

(2) INFORMATION FOR SEQ ID NO:1398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1398:

Met Glu Leu Tyr Ala Asn Glu Val Pro Lys Thr Ala Glu Asn Phe Arg
1 5 10 15
Ala Leu Cys Thr Gly Glu Lys Gly Val Gly Lys Ser Gly Lys Pro Leu
20 25 30
His Tyr Lys Gly Ser Thr Phe His Arg Val Ile Pro Xaa Phe Met Cys
35 40 45
Gln Gly Gly Asp Phe
50

(2) INFORMATION FOR SEQ ID NO:1399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..507
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1399:

acgatattaa ccgacccaaa taagctagt gtagcagttg gaggggtaac agcacttgct 60
gcagggatat acacaacaag ggagggtgca agagtagtct ggggctatgt tgatcgatt 120
ctgggtcagc catcactgat aaggagagca tcacgtggga aatatccctg gtctgggttc 180
ctctcacgtg ctacaagtac cctgactagc aaactgaaga atggaagcaa cctaggggaag 240
gacagaaatg ggtttggtga tggtattcta aatccttctc tccagaagag agtgaagcag 300
cttgctaattg ccacagccaa tacaaaactt catcaagctc ctttcaggaa catgcttttc 360
tatgggcctc ctggcacagg gaaaaccatg gcagcacgag aacttgctcg caattctgga 420
ttagattatg cactaatgac tgggtggagat gttgcacatc tgggatcaca agcagtcacc 480
aagattcatc agttgtttga ctgggag

(2) INFORMATION FOR SEQ ID NO:1400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1400:

Thr Ile Leu Thr Asp Gln Asn Lys Leu Val Val Ala Val Gly Gly Val
1 5 10 15
Thr Ala Leu Ala Ala Gly Ile Tyr Thr Thr Arg Glu Gly Ala Arg Val
20 25 30
Val Trp Gly Tyr Val Asp Arg Ile Leu Gly Gln Pro Ser Leu Ile Arg
35 40 45
Glu Ser Ser Arg Gly Lys Tyr Pro Trp Ser Gly Phe Leu Ser Arg Ala
50 55 60

Thr Ser Thr Leu Thr Ser Lys Leu Lys Asn Gly Ser Asn Leu Gly Lys
65 70 75 80
Asp Arg Asn Gly Phe Gly Asp Val Ile Leu Asn Pro Ser Leu Gln Lys
85 90 95
Arg Val Lys Gln Leu Ala Asn Ala Thr Ala Asn Thr Lys Leu His Gln
100 105 110
Ala Pro Phe Arg Asn Met Leu Phe Tyr Gly Pro Pro Gly Thr Gly Lys
115 120 125
Thr Met Ala Ala Arg Glu Leu Ala Arg Asn Ser Gly Leu Asp Tyr Ala
130 135 140
Leu Met Thr Gly Gly Asp Val Ala Pro Leu Gly Ser Gln Ala Val Thr
145 150 155 160
Lys Ile His Gln Leu Phe Asp Trp Ala
165

(2) INFORMATION FOR SEQ ID NO:1401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..536
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1401:

aaaagccagg attcctctgc tcttctctgt tagggtttcc ccctctctct gctcctgccg	60
gatgcgatgg cgattccgcc gcggactcct tccccgccgc catcgtggtc gcgctctgta	120
accgagaccg ttcggggggtc ccaccagttc accgtacggg gctactccct cgccaagggc	180
atggggccccg gccgctacct cgccagcgac gtcttcgccg tcggaggata ccactgggac	240
gtctacctct accccgacgg caagaacgcc gaggacaact ccaactacgt ctccgttttc	300
gtcgcctctg cttccgacgg catcgacgtc cgagccctct tcgagctcac cctcctcgac	360
cagtycggcm gcggctgcma caaggttcac tcgcactttg accgctcgct caagttcggc	420
ccatacaccc tcaagtacag gggatccatg tggggttaca agcgcttcta caaaagaaca	480
ctcttggaag aatctgattt cttaaagaat gattgcctag tgatgaactg cacagt	

(2) INFORMATION FOR SEQ ID NO:1402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1402:

Lys Pro Gly Phe Leu Cys Ser Ser Cys Leu Gly Phe Pro Pro Leu Ser
1 5 10 15
Ala Pro Ala Gly Cys Asp Gly Asp Ser Ala Ala Asp Ser Phe Pro Ala
20 25 30
Ala Ile Val Val Ala Leu Cys Asn Arg Asp Arg Ser Gly Val Pro Pro
35 40 45
Val His Arg Thr Gly Leu Leu Pro Arg Gln Gly His Gly Pro Arg Pro
50 55 60
Leu Pro Arg Gln Arg Arg Leu Arg Arg Arg Arg Ile Pro Leu Gly Arg
65 70 75 80
Leu Pro Leu Pro Arg Arg Gln Glu Arg Arg Gly Gln Leu Gln Leu Arg
85 90 95
Leu Arg Phe Arg Arg Pro Arg Phe Arg Arg His Arg Arg Pro Ser Pro
100 105 110

Leu Arg Ala His Pro Pro Arg Pro Xaa Arg Xaa Arg Leu Xaa Gln Gly
115 120 125
Ser Leu Ala Leu
130

(2) INFORMATION FOR SEQ ID NO:1403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1500181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1403:

Met Ala Ile Pro Pro Arg Thr Pro Ser Pro Pro Pro Ser Trp Ser Arg
1 5 10 15
Ser Val Thr Glu Thr Val Arg Gly Ser His Gln Phe Thr Val Arg Gly
20 25 30
Tyr Ser Leu Ala Lys Gly Met Gly Pro Gly Arg Tyr Leu Ala Ser Asp
35 40 45
Val Phe Ala Val Gly Gly Tyr His Trp Ala Val Tyr Leu Tyr Pro Asp
50 55 60
Gly Lys Asn Ala Glu Asp Asn Ser Asn Tyr Val Ser Val Phe Val Ala
65 70 75 80
Leu Ala Ser Asp Gly Ile Asp Val Arg Ala Leu Phe Glu Leu Thr Leu
85 90 95
Leu Asp Gln Xaa Gly Xaa Gly Cys Xaa Lys Val His Ser His Phe Asp
100 105 110
Arg Ser Leu Lys Phe Gly Pro Tyr Thr Leu Lys Tyr Arg Gly Ser Met
115 120 125
Trp Gly Tyr Lys Arg Phe Tyr Lys Arg Thr Leu Leu Glu Glu Ser Asp
130 135 140
Phe Leu Lys Asn Asp Cys Leu Val Met Asn Cys Thr
145 150 155

(2) INFORMATION FOR SEQ ID NO:1404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1500182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1404:

Met Gly Pro Gly Arg Tyr Leu Ala Ser Asp Val Phe Ala Val Gly Gly
1 5 10 15
Tyr His Trp Ala Val Tyr Leu Tyr Pro Asp Gly Lys Asn Ala Glu Asp
20 25 30
Asn Ser Asn Tyr Val Ser Val Phe Val Ala Leu Ala Ser Asp Gly Ile
35 40 45
Asp Val Arg Ala Leu Phe Glu Leu Thr Leu Leu Asp Gln Xaa Gly Xaa
50 55 60
Gly Cys Xaa Lys Val His Ser His Phe Asp Arg Ser Leu Lys Phe Gly
65 70 75 80
Pro Tyr Thr Leu Lys Tyr Arg Gly Ser Met Trp Gly Tyr Lys Arg Phe
85 90 95
Tyr Lys Arg Thr Leu Leu Glu Glu Ser Asp Phe Leu Lys Asn Asp Cys

100 105 110
Leu Val Met Asn Cys Thr
115

(2) INFORMATION FOR SEQ ID NO:1405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..540
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1405:

ggccacacct	tccgtccccc	ggcctccgct	cgccctgcgcg	ccgcctgtgc	cctgtctgtc	60
tctctctctc	ctcgctgagt	cgccgccagc	catgaacaac	ctcctcacgg	attcctttga	120
gctcccccgg	cgggactcct	caagagatgc	agacattgaa	atgggaatgc	atcaagctga	180
tgcttcagac	aacttaaaag	atttcttgaa	gaaggtcgat	acaattgaga	gtttaattgc	240
aaagctgaca	aatctattga	ataagctaca	gactgcaaat	gaggaatcca	aagcagttac	300
aaaagcaagt	tccatgaaag	caattaagca	gcggatggag	aaagatattg	atgaagtggg	360
gaaaattgct	cgtcaggcga	agacaaaagt	tgatgaattg	gaaaaagaca	acttatcaaa	420
taggcaaaaa	cctggatgtg	gaaaagggtc	tgccgtggac	cgatcaagag	agcaaamtac	480
tggagcagtg	aaaaagaaat	tgaaggagcg	gatggatgac	tttcagacct	tgagagaagc	540

(2) INFORMATION FOR SEQ ID NO:1406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1406:

Ala Thr Pro Ser Val Pro Arg Pro Pro Leu Ala Ser Pro Pro Ala Cys	
1 5 10 15	
Pro Cys Leu Ser Leu Ser Leu Leu Ala Glu Ser Pro Pro Ala Met Asn	
20 25 30	
Asn Leu Leu Thr Asp Ser Phe Glu Leu Pro Arg Arg Asp Ser Ser Arg	
35 40 45	
Asp Ala Asp Ile Glu Met Gly Met His Gln Ala Asp Ala Ser Asp Asn	
50 55 60	
Leu Lys Asp Phe Leu Lys Lys Val Asp Thr Ile Glu Ser Leu Ile Ala	
65 70 75 80	
Lys Leu Thr Asn Leu Asn Lys Leu Gln Thr Ala Asn Glu Glu Ser	
85 90 95	
Lys Ala Val Thr Lys Ala Ser Ser Met Lys Ala Ile Lys Gln Arg Met	
100 105 110	
Glu Lys Asp Ile Asp Glu Val Gly Lys Ile Ala Arg Gln Ala Lys Thr	
115 120 125	
Lys Val Asp Glu Leu Glu Lys Asp Asn Leu Ser Asn Arg Gln Lys Pro	
130 135 140	
Gly Cys Gly Lys Gly Ser Ala Val Asp Arg Ser Arg Glu Gln Xaa Thr	
145 150 155 160	
Gly Ala Val Lys Lys Lys Leu Lys Glu Arg Met Asp Asp Phe Gln Thr	
165 170 175	
Leu Arg Glu	

(2) INFORMATION FOR SEQ ID NO:1407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1407:

Met Asn Asn Leu Leu Thr Asp Ser Phe Glu Leu Pro Arg Arg Asp Ser
1 5 10 15
Ser Arg Asp Ala Asp Ile Glu Met Gly Met His Gln Ala Asp Ala Ser
20 25 30
Asp Asn Leu Lys Asp Phe Leu Lys Lys Val Asp Thr Ile Glu Ser Leu
35 40 45
Ile Ala Lys Leu Thr Asn Leu Leu Asn Lys Leu Gln Thr Ala Asn Glu
50 55 60
Glu Ser Lys Ala Val Thr Lys Ala Ser Ser Met Lys Ala Ile Lys Gln
65 70 75 80
Arg Met Glu Lys Asp Ile Asp Glu Val Gly Lys Ile Ala Arg Gln Ala
85 90 95
Lys Thr Lys Val Asp Glu Leu Glu Lys Asp Asn Leu Ser Asn Arg Gln
100 105 110
Lys Pro Gly Cys Gly Lys Gly Ser Ala Val Asp Arg Ser Arg Glu Gln
115 120 125
Xaa Thr Gly Ala Val Lys Lys Lys Leu Lys Glu Arg Met Asp Asp Phe
130 135 140
Gln Thr Leu Arg Glu
145

(2) INFORMATION FOR SEQ ID NO:1408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1408:

Met Gly Met His Gln Ala Asp Ala Ser Asp Asn Leu Lys Asp Phe Leu
1 5 10 15
Lys Lys Val Asp Thr Ile Glu Ser Leu Ile Ala Lys Leu Thr Asn Leu
20 25 30
Leu Asn Lys Leu Gln Thr Ala Asn Glu Glu Ser Lys Ala Val Thr Lys
35 40 45
Ala Ser Ser Met Lys Ala Ile Lys Gln Arg Met Glu Lys Asp Ile Asp
50 55 60
Glu Val Gly Lys Ile Ala Arg Gln Ala Lys Thr Lys Val Asp Glu Leu
65 70 75 80
Glu Lys Asp Asn Leu Ser Asn Arg Gln Lys Pro Gly Cys Gly Lys Gly
85 90 95
Ser Ala Val Asp Arg Ser Arg Glu Gln Xaa Thr Gly Ala Val Lys Lys
100 105 110
Lys Leu Lys Glu Arg Met Asp Asp Phe Gln Thr Leu Arg Glu
115 120 125

(2) INFORMATION FOR SEQ ID NO:1409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1473
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1409:

```
agaaagaaga agataacaca atgctcttct tcttattctt cttctactta ctcttatctt      60
catcctccga tctagtcttc gccgaccgtc gtgtactcca cgaaccattc ttccctatag      120
attcgccacc accgtcacca ccataccacc caccacttcc taaactacca ttctcttcaa      180
ccactcctcc atcttcatca gacccaaatg cttctccttt cttcccttta tacccttcat      240
ctccaccacc accttctcca gcctccttcg cttcttttcc ggcgaaatgc tcactctctaa      300
tcgtccctca cgccactaaa tccccaccta actccaaaaa actccttato gtcgctatct      360
ccgcccgttc ctcgctgtgt ttagtcgtct tacttatcgc tttactctat tggcgaagaa      420
gcaaacgtaa ccaagatctt aacttctccg atgatagcaa aacatacacc accgacagta      480
gccgccgtgt ctaccctcct cctccggcaa cggcgccctc aacacgacgc aatgcggagg      540
ctagaagtaa acagaggacc accacgagct ccaccaataa caacagctct gagtttcttt      600
acttaggaac aatgggtgaat caaagaggaa tcgatgaaca atctcttagt aataatggat      660
caagctcaag aaaacttgaa tctccagatc ttcaaccact tcctccattg atgaaacgaa      720
gtttccggtt aaatccagat gttggttcaa tcggagaaga agatgaagaa gatgagtttt      780
actctccacg tggctcacia agcgggcgag aaccgttaaa ccgggtcgga cttccgggtc      840
aaaatcctag atctgttaac aatgacacta tctcttgctc atcttcaagc tctggttcac      900
caggaagatc aacattttatc agtatctctc cttcaatgag tcctaagaga tctgaaccaa      960
aaccgccggt tatctccaca ccagaaccgg cggagttaac cgattataga tttgttcggt      1020
ctccgtcact gtcgttagct tctttatcgt cgggattgaa aaactccgat gaagtaggat      1080
tgaatcaaat ctttagatct ccgacgggta catctctaac aacttcaccg gagaataaca      1140
aaaaagagaa ctctccatta tcacttactt caacttcacc ggaacgacga ccaaatagata      1200
caccagaagc ttacttgaga tctccgtcgc attcttctgc ttctacatca ccgtatagat      1260
gttttcagaa atctccggag gtcttaccgg cgtttatgag taatctccgg caagggttgc      1320
aatctcagtt actatcttct ctttctaact ctcatggagg acaagggttc cttaagcagt      1380
tagatgcatt acgttctcgt tcaccgtcgt cgtcttcttc ttctgtttgt tcttcaccgg      1440
agaaagcttc tcataagtea ccagttacat ctc
```

(2) INFORMATION FOR SEQ ID NO:1410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..490
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1410:

```
Lys Glu Glu Asp Asn Thr Met Leu Phe Phe Leu Phe Phe Tyr Leu
1          5          10          15
Leu Leu Ser Ser Ser Ser Asp Leu Val Phe Ala Asp Arg Arg Val Leu
          20          25          30
His Glu Pro Phe Phe Pro Ile Asp Ser Pro Pro Pro Ser Pro Pro Ser
          35          40          45
Pro Pro Pro Leu Pro Lys Leu Pro Phe Ser Ser Thr Thr Pro Pro Ser
          50          55          60
Ser Ser Asp Pro Asn Ala Ser Pro Phe Phe Pro Leu Tyr Pro Ser Ser
65          70          75          80
Pro Pro Pro Pro Ser Pro Ala Ser Phe Ala Ser Phe Pro Ala Asn Ile
          85          90          95
Ser Ser Leu Ile Val Pro His Ala Thr Lys Ser Pro Pro Asn Ser Lys
```

(2) INFORMATION FOR SEQ ID NO:1411:

(A) LENGTH: 484 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..484

(D) OTHER INFORMATION: / Ceres Seq. ID 1500192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1411:

	Met	Leu	Phe	Phe	Leu	Phe	Phe	Phe	Tyr	Leu	Leu	Leu	Ser	Ser	Ser	Ser
1				5						10					15	
Asp	Leu	Val	Phe 20	Ala	Asp	Arg	Arg	Val 25	Leu	His	Glu	Pro	Phe 30	Phe	Pro	
Ile	Asp	Ser 35	Pro	Pro	Pro	Ser	Pro	Pro	Ser	Pro	Pro	Pro	Leu 45	Pro	Lys	
Leu	Pro	Phe	Ser	Ser	Thr	Thr	Pro	Pro	Ser	Ser	Ser	Asp	Pro	Asn	Ala	
	50				55					60						
Ser	Pro	Phe	Phe	Pro	Leu	Tyr	Pro	Ser	Ser	Pro	Pro	Pro	Pro	Ser	Pro	
65				70						75					80	
Ala	Ser	Phe	Ala	Ser 85	Phe	Pro	Ala	Asn	Ile	Ser	Ser	Leu	Ile	Val 95	Pro	
His	Ala	Thr	Lys 100	Ser	Pro	Pro	Asn	Ser 105	Lys	Lys	Leu	Leu	Ile 110	Val	Ala	
Ile	Ser	Ala	Val	Ser	Ser	Ala	Ala	Leu 120	Val	Ala	Leu	Leu	Ile 125	Ala	Leu	
Leu	Tyr	Trp	Arg	Arg	Ser	Lys	Arg	Asn	Gln	Asp	Leu	Asn	Phe	Ser	Asp	
	130				135					140						
Asp	Ser	Lys	Thr	Tyr	Thr	Thr	Asp	Ser	Ser	Arg	Arg	Val	Tyr	Pro	Pro	
145				150						155					160	
Pro	Pro	Ala	Thr	Ala	Pro	Pro	Thr	Arg	Arg	Asn	Ala	Glu	Ala	Arg	Ser	
				165					170					175		
Lys	Gln	Arg	Thr 180	Thr	Thr	Ser	Ser	Thr 185	Asn	Asn	Asn	Ser	Ser 190	Glu	Phe	
Leu	Tyr	Leu	Gly	Thr	Met	Val	Asn	Gln	Arg	Gly	Ile	Asp	Glu 205	Gln	Ser	
	195						200					205				
Leu	Ser	Asn	Asn	Gly	Ser	Ser	Ser	Arg	Lys	Leu	Glu	Ser	Pro	Asp	Leu	
	210				215					220						
Gln	Pro	Leu	Pro	Pro	Leu	Met	Lys	Arg	Ser	Phe	Arg	Leu	Asn	Pro	Asp	
225				230						235					240	
Val	Gly	Ser	Ile	Gly 245	Glu	Glu	Asp	Glu	Glu	Asp	Glu	Phe	Tyr	Ser 255	Pro	
Arg	Gly	Ser	Gln 260	Ser	Gly	Arg	Glu	Pro 265	Leu	Asn	Arg	Val	Gly 270	Leu	Pro	
Gly	Gln	Asn	Pro	Arg	Ser	Val	Asn	Asn	Asp	Thr	Ile	Ser	Cys 285	Ser	Ser	
	275						280					285				
Ser	Ser	Ser	Gly	Ser	Pro	Gly	Arg	Ser	Thr	Phe	Ile	Ser	Ile	Ser	Pro	
	290				295					300						
Ser	Met	Ser	Pro	Lys	Arg	Ser	Glu	Pro	Lys	Pro	Val	Ile	Ser	Thr		
305				310						315					320	
Pro	Glu	Pro	Ala	Glu	Leu	Thr	Asp	Tyr	Arg	Phe	Val	Arg	Ser	Pro	Ser	
				325					330					335		
Leu	Ser	Leu	Ala 340	Ser	Leu	Ser	Ser	Gly 345	Leu	Lys	Asn	Ser	Asp 350	Glu	Val	
Gly	Leu	Asn	Gln	Ile	Phe	Arg	Ser	Pro	Thr	Val	Thr	Ser	Leu 365	Thr	Thr	
	355						360					365				
Ser	Pro	Glu	Asn	Asn	Lys	Lys	Glu	Asn	Ser	Pro	Leu	Ser	Ser	Thr	Ser	
	370				375					380						
Thr	Ser	Pro	Glu	Arg	Arg	Pro	Asn	Asp	Thr	Pro	Glu	Ala	Tyr	Leu	Arg	
385</																

(2) INFORMATION FOR SEQ ID NO:1412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..287
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1412:

Met	Val	Asn	Gln	Arg	Gly	Ile	Asp	Glu	Gln	Ser	Leu	Ser	Asn	Asn	Gly
1				5				10						15	
Ser	Ser	Ser	Arg	Lys	Leu	Glu	Ser	Pro	Asp	Leu	Gln	Pro	Leu	Pro	Pro
			20					25					30		
Leu	Met	Lys	Arg	Ser	Phe	Arg	Leu	Asn	Pro	Asp	Val	Gly	Ser	Ile	Gly
		35					40					45			
Glu	Glu	Asp	Glu	Glu	Asp	Glu	Phe	Tyr	Ser	Pro	Arg	Gly	Ser	Gln	Ser
	50					55					60				
Gly	Arg	Glu	Pro	Leu	Asn	Arg	Val	Gly	Leu	Pro	Gly	Gln	Asn	Pro	Arg
65					70					75				80	
Ser	Val	Asn	Asn	Asp	Thr	Ile	Ser	Cys	Ser	Ser	Ser	Ser	Ser	Gly	Ser
			85					90						95	
Pro	Gly	Arg	Ser	Thr	Phe	Ile	Ser	Ile	Ser	Pro	Ser	Met	Ser	Pro	Lys
			100					105					110		
Arg	Ser	Glu	Pro	Lys	Pro	Pro	Val	Ile	Ser	Thr	Pro	Glu	Pro	Ala	Glu
			115					120				125			
Leu	Thr	Asp	Tyr	Arg	Phe	Val	Arg	Ser	Pro	Ser	Leu	Ser	Leu	Ala	Ser
	130					135					140				
Leu	Ser	Ser	Gly	Leu	Lys	Asn	Ser	Asp	Glu	Val	Gly	Leu	Asn	Gln	Ile
				150						155					160
Phe	Arg	Ser	Pro	Thr	Val	Thr	Ser	Leu	Thr	Thr	Ser	Pro	Glu	Asn	Asn
				165					170					175	
Lys	Lys	Glu	Asn	Ser	Pro	Leu	Ser	Ser	Thr	Ser	Thr	Ser	Pro	Glu	Arg
			180					185					190		
Arg	Pro	Asn	Asp	Thr	Pro	Glu	Ala	Tyr	Leu	Arg	Ser	Pro	Ser	His	Ser
		195					200					205			
Ser	Ala	Ser	Thr	Ser	Pro	Tyr	Arg	Cys	Phe	Gln	Lys	Ser	Pro	Glu	Val
	210					215					220				
Leu	Pro	Ala	Phe	Met	Ser	Asn	Leu	Arg	Gln	Gly	Leu	Gln	Ser	Gln	Leu
225				230						235					240
Leu	Ser	Ser	Pro	Ser	Asn	Ser	His	Gly	Gly	Gln	Gly	Phe	Leu	Lys	Gln
			245						250					255	
Leu	Asp	Ala	Leu	Arg	Ser	Arg	Ser	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Val
		260					265					270			
Cys	Ser	Ser	Pro	Glu	Lys	Ala	Ser	His	Lys	Ser	Pro	Val	Thr	Ser	
		275					280					285			

(2) INFORMATION FOR SEQ ID NO:1413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 503 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..503
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1413:

```
gccatttttr gtgartgcgc cttttccctt cctccccaga tccccgtccc cgttttccac      60
ttttgcctcc gcccacaattc ggataacaaa cccctccgcc tcgtcgcgtc tcctcccagc      120
cgagccgata cggtagagag agggagargg agggactgar ggaggaggag ctggggttccg      180
gtcccggccg cccggccgnc ntgcgcgatt cgattgcagc tctcgtcccc gggcgggcgtc      240
caggatgggtg cggggcaaga cgcagatgaa gcggatagag aaccgcacca gccgccaggt      300
caccttctcc aagcgccgca acggcctgct caagaaggcg ttcgarctct ccgtcctctg      360
cramgccgag gtgcgccctcg tmgctctctc cmcgcgcggc aagctctacg aattcgccag      420
cggaagtrcg cagaaaacga ttgaacgtta tagaacatac acaaaggata atgtcagcaa      480
caagacagtg cagcaggata ttg
```

(2) INFORMATION FOR SEQ ID NO:1414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1414:

```
Ala Ile Phe Xaa Cys Ala Leu Ser Leu Pro Pro Gln Ile Pro Val
1           5           10           15
Pro Val Phe His Phe Cys Leu Arg Pro Asn Ser Asp Asn Lys Pro Leu
          20           25           30
Arg Leu Val Ala Ser Pro Pro Ser Arg Ala Asp Pro Val Glu Arg Gly
          35           40           45
Arg Xaa Arg Asp
          50
```

(2) INFORMATION FOR SEQ ID NO:1415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1415:

```
Met Val Arg Gly Lys Thr Gln Met Lys Arg Ile Glu Asn Pro Thr Ser
1           5           10           15
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Leu Leu Lys Lys Ala
          20           25           30
Phe Xaa Leu Ser Val Leu Cys Xaa Ala Glu Val Ala Leu Xaa Val Phe
          35           40           45
Ser Xaa Arg Gly Lys Leu Tyr Glu Phe Ala Ser Gly Ser Xaa Gln Lys
          50           55           60
Thr Ile Glu Arg Tyr Arg Thr Tyr Thr Lys Asp Asn Val Ser Asn Lys
          65           70           75           80
Thr Val Gln Gln Asp Ile
          85
```

(2) INFORMATION FOR SEQ ID NO:1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1500201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1416:

Met	Lys	Arg	Ile	Glu	Asn	Pro	Thr	Ser	Arg	Gln	Val	Thr	Phe	Ser	Lys
1				5				10						15	
Arg	Arg	Asn	Gly	Leu	Leu	Lys	Lys	Ala	Phe	Xaa	Leu	Ser	Val	Leu	Cys
			20					25					30		
Xaa	Ala	Glu	Val	Ala	Leu	Xaa	Val	Phe	Ser	Xaa	Arg	Gly	Lys	Leu	Tyr
		35					40					45			
Glu	Phe	Ala	Ser	Gly	Ser	Xaa	Gln	Lys	Thr	Ile	Glu	Arg	Tyr	Arg	Thr
	50					55					60				
Tyr	Thr	Lys	Asp	Asn	Val	Ser	Asn	Lys	Thr	Val	Gln	Gln	Asp	Ile	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:1417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 892 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..892
(D) OTHER INFORMATION: / Ceres Seq. ID 1500202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1417:

atcctcggca	tccgtcccgc	tttgcccttg	tttaattcca	aaggtttcat	tttctgcagg	60
gataacattt	gtvgggggtg	gtgagccggc	cggccctata	gaatcctgct	cctgctcctg	120
cgcccgcccc	cttttcatgt	tgttttccct	ttcctcctct	tcttcctcct	cacctcaccg	180
gctcacctcc	tatttagccg	tccgaattgc	ttgtcagcat	cttcccagct	tcttcttctt	240
cttccaaccg	cgctacgctc	tcttgtcccc	ggtgctcgct	tggattcttc	tctcttcata	300
ggaaggaagg	attggctacc	gagatattcc	tactagtcca	gggctgtagt	gcatacctgcg	360
cgcttggttt	attctgcagc	cataaccagt	accagtaccc	ccagcctgav	ccggtgagga	420
gaggagatag	agagagcgag	cgggagcggn	gagcagagga	ggagggccat	ggaaggcgac	480
agcttytccg	gcggcgccat	ggccaacggc	ggcggcgggc	gcggcagcgg	cggcgggcag	540
gtgggtggac	ggaagctgat	ccacacgttc	cacaggagct	tcgtgcaggt	gcagagcctg	600
ctggaccaga	accggatgct	catcagcgag	atcaaccaga	accacgagtc	ccgcgcgcgt	660
gntmstccgc	tgtctgttgc	gcgggataga	tatagcgctt	ccacttaatt	tcttctgtct	720
ttttcggttt	cttcttcttc	tctggttccc	gctgcttgta	ttgtattgta	tctagtatgt	780
atcgctgtcc	atccctccgg	cgggctctga	gatgtacctc	cattcctcct	cgtgtaccgg	840
tctcgatgca	gatgataccg	gggcatgtga	atgaacagag	ctggttccga	cc	

(2) INFORMATION FOR SEQ ID NO:1418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..99
(D) OTHER INFORMATION: / Ceres Seq. ID 1500203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1418:

Ser	Ser	Ala	Ser	Val	Pro	Leu	Cys	Pro	Cys	Leu	Ile	Pro	Lys	Val	Ser
1				5				10					15		
Phe	Ser	Ala	Gly	Ile	Thr	Phe	Xaa	Gly	Gly	Gly	Glu	Pro	Ala	Gly	Pro
			20					25					30		
Ile	Glu	Ser	Cys	Ser	Cys	Ser	Cys	Ala	Arg	Pro	Leu	Phe	Met	Leu	Leu
	35					40					45				
Ser	Leu	Ser	Ser	Ser	Ser	Ser	Ser	Pro	His	Arg	Leu	Thr	Ser	Tyr	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:1419:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(A) NAME/KEY: peptide

(B) LOCATION: 1-79

(D) OTHER INFORMATION

(D) OTHER INFORMATION: / Ceres Seq. ID 1500204
SEQUENCE DESCRIPTION: SEQ ID NO:1419.

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1419:
Gly Gly Asp Ser Yaa Ser Gly Gly Ala Met Al

(2) INFORMATION FOR SEQ ID NO:1420:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:1420:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1420:
Ala Asn Gly Gly Gly Gly Gly Gly Ser Gly Gly

(2) INFORMATION FOR SEQ ID NO:1421:

(A) LENGTH: 756 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

```
(ix) FEATURE:
```

(A) NAM

(B) LOCATION: 1

(D) OTHER INFORMATION

(D) OTHER: _____

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1421:

ataggggtct	aagcctcggc	cgtttcttcg	tctccacagc	tcccgccgcc	gaggaccagc	60
gcgtcactct	accgggttcc	ggcgtctccc	cgtaccgcga	gcgcggcatc	catggcggas	120
agacggaaag	ggctttcttg	aagcagccca	aggtgtttct	ctgttccaag	aaggccacca	180
aggtaaacia	acctggcaag	ggaggaaaca	gattctggaa	gaacattggc	cttggtttca	240
agacaccag	ggaagccatt	gaaggaacct	acattgataa	gaagtgtcca	ttcaccggca	300
ctgtgtctat	caggggtcgc	atcatcgccg	gaacatgcca	cagtgtctaa	atgaatagga	360
ccatcattgt	tcgtaggaat	tatcttctac	tcgtcaagaa	gtaccagagg	tatgagaaga	420
gacactccaa	catccctgcg	cacatttcac	catgcttccg	tgtcaaggaa	ggagatcatg	480
tgatcattgg	ccagtgcagg	ccagtgtcga	agactgntaa	ggttcaatgt	ggtcaaagtt	540
attcctgcag	gttcgaagag	tggagcagtg	aagaaagctt	tactgcccgc	ttaagatcat	600
gacgagttca	tcattccatg	cccggaaaag	ctctgtgtta	taacgttttg	atgctgccta	660
ttagcctttt	tccccgtaac	tactatatgt	gtacttggaa	ttggacttga	attacatcca	720
gaacttgaaa	tcctgaaaaa	aatcataaac	cctttg			

(2) INFORMATION FOR SEQ ID NO:1422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1422:

Met	Asn	Arg	Thr	Ile	Ile	Val	Arg	Arg	Asn	Tyr	Leu	His	Phe	Val	Lys
1				5					10					15	
Lys	Tyr	Gln	Arg	Tyr	Glu	Lys	Arg	His	Ser	Asn	Ile	Pro	Ala	His	Ile
			20					25					30		
Ser	Pro	Cys	Phe	Arg	Val	Lys	Glu	Gly	Asp	His	Val	Ile	Ile	Gly	Gln
		35				40					45				
Cys	Arg	Pro	Val	Ser	Lys	Thr	Xaa	Lys	Val	Gln	Cys	Gly	Gln	Ser	Tyr
	50				55					60					
Ser	Cys	Arg	Phe	Glu	Glu	Trp	Ser	Ser	Glu	Glu	Ser	Phe	His	Cys	Arg
65					70				75					80	
Leu	Arg	Ser													

(2) INFORMATION FOR SEQ ID NO:1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1034
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500234

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1423:

gtgtctcttta	tttctttgtg	tgtttggttg	ctggaaagg	agtggacttt	tacaacttct	60
catgtcccta	ttgttgggag	ggttcggagt	ccggatcggg	atttgccaca	accagattgt	120
tcaacactcg	gaaggetcac	caaatcgctc	tacgtctctg	cttcctcctc	cacgaggtga	180
ggaaacccta	gcgactgacc	atggcgttgc	tcccgcgcac	cgcacgggtg	gccttctct	240
ctaccccgcg	gtcgtactcc	gccgcggccg	ctgcgggcgc	ctccccgacc	tccccagcgc	300
catacggggg	cgcgccccca	ccggcgatgt	cgaagaggnc	cgagttcgtg	gtctccaagg	360
ttgatgacct	gatgaactgg	gcgcgtaagg	gctcgatttg	gcccattgacc	tttgggctcg	420
cctgctgcrc	ggtcgagatg	atgcacgccg	gcgcgtcccc	ctacgacttc	gaccgggttc	480
ggcgtcatct	tccgtccctc	gccgcgcma	tccgattgca	tgatcgtcgc	cggcacgytc	540
accaacaaaa	tggctccagc	cctccgcaag	gtttatgacc	aaatgcctga	gcctagatgg	600
gttattttcaa	tgggcagctg	tgccaacggt	ggtggatact	accattactc	ctactctgtt	660

gtacgtggat gtgaccgtat agtccccgtg gacatctacg tccctgggtg cccaccaact 720
gctgaggcac tgctgtacgg tgttcttcag ctccaaaaga agatcaacag gcgtaaggat 780
ttccttcact ggtggaccaa gtgaagcatg cttctgctgt tgctcgcttg ctacgtttct 840
ttgcactcga cctacctgtc ttatctgaaa taaggacgga ctttgctcgg attcacaaat 900
ttgttgtgcc tggaaggatg tatgccagcagg ttgtgacgaa catataactt gtgtacttgg 960
agtcagttcg cctgtaatgg acaccagacc tgctgtgaat ctgtttttta gcttccattg 1020
taatacagca atac

(2) INFORMATION FOR SEQ ID NO:1424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1424:

Cys Leu Leu Phe Leu Cys Val Phe Gly Cys Trp Lys Gly Ser Gly Leu
1 5 10 15
Leu Gln Leu Leu Met Ser Leu Leu Leu Gly Gly Phe Gly Val Arg Ile
20 25 30
Gly Ile Cys His Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn
35 40 45
Arg Pro Thr Leu Leu Leu Pro Pro Arg Gly Glu Glu Thr Leu Ala
50 55 60
Thr Asp His Gly Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu
65 70 75 80
Tyr Pro Ala Val Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp
85 90 95
Leu Pro Ser Ala Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu
100 105 110
Xaa Arg Val Arg Gly Leu Gln Gly
115 120

(2) INFORMATION FOR SEQ ID NO:1425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1425:

Met Ser Leu Leu Leu Gly Gly Phe Gly Val Arg Ile Gly Ile Cys His
1 5 10 15
Asn Gln Ile Val Gln His Ser Glu Gly Ser Pro Asn Arg Pro Thr Leu
20 25 30
Leu Leu Pro Pro Pro Arg Gly Glu Glu Thr Leu Ala Thr Asp His Gly
35 40 45
Val Ala Pro Ala His Arg Thr Val Gly Leu Pro Leu Tyr Pro Ala Val
50 55 60
Val Leu Arg Arg Arg Arg Cys Gly Arg Leu Pro Asp Leu Pro Ser Ala
65 70 75 80
Ile Arg Gly Arg Ala Pro Thr Gly Asp Val Glu Glu Xaa Arg Val Arg
85 90 95
Gly Leu Gln Gly
100

(2) INFORMATION FOR SEQ ID NO:1426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1426:

Met	Ala	Leu	Leu	Pro	Arg	Thr	Ala	Arg	Leu	Ala	Phe	Leu	Ser	Thr	Pro	
1				5					10					15		
Arg	Ser	Tyr	Ser	Ala	Ala	Ala	Ala	Ala	Gly	Ala	Ser	Pro	Thr	Ser	Pro	
			20					25					30			
Ala	Pro	Tyr	Gly	Gly	Ala	Pro	Pro	Pro	Ala	Met	Ser	Lys	Arg	Xaa	Glu	
		35					40					45				
Phe	Val	Val	Ser	Lys	Val	Asp	Asp	Leu	Met	Asn	Trp	Ala	Arg	Lys	Gly	
	50				55					60						
Ser	Ile	Trp	Pro	Met	Thr	Phe	Gly	Leu	Ala	Cys	Cys	Xaa	Val	Glu	Met	
65				70						75				80		
Met	His	Ala	Gly	Ala	Ser	Arg	Tyr	Asp	Phe	Asp	Arg	Val	Arg	Arg	His	
			85						90				95			
Leu	Pro	Ser	Leu	Ala	Ala	Xaa	Val	Arg	Leu	His	Asp	Arg	Arg	Arg	His	
			100					105					110			
Xaa	His	Gln	Asn	Gly	Ser	Ser	Pro	Pro	Gln	Gly	Leu					
		115				120					125					

(2) INFORMATION FOR SEQ ID NO:1427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..539
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1427:

aaccacacca	ctcgavcgcg	cgcgacggcc	caccgctccg	ccgctgcccg	cccgcgcgca	60
tgcgagggat	cctctcctct	tcctccgctc	tcctccggcg	agccggcgcc	cagctctcgc	120
gcacggactg	cagtagcccc	tcagcgctccg	cgacctctcc	tctccgcccg	tccccctctc	180
agaatgggaa	aagagacaca	ttttgttcgc	tttggttcaa	aggtcgttcg	gtatcaacca	240
cagttgatat	gcagttagac	tatgagagtg	atccccctct	tgacgataca	aaagctattg	300
agaaggagtc	atcacttaat	gttgctgttt	ctcaactcgc	aattgacttc	gatagagact	360
ctaatttatg	twtgagcgga	ttttcccgtg	caaggaaagc	atctgtagtc	tctactgggt	420
ctcttaagct	tgamctcgct	ctcggcggtg	gaggattacc	gaaggtagaa	tggtggagat	480
atatgggaaa	gaagcatctg	ggaagacaac	actcgcgctt	catgttatta	aggaagctc	

(2) INFORMATION FOR SEQ ID NO:1428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1428:

Pro His His Ser Xaa Ala Arg Asp Gly Pro Pro Leu Arg Arg Cys Pro
1 5 10 15
Pro Ala Ala Met Arg Gly Ile Leu Ser Ser Ser Ala Leu Leu Arg
20 25 30
Arg Ala Gly Ala Gln Leu Ser Arg Thr Asp Cys Ser Ser Pro Ser Ala
35 40 45
Ser Ala Thr Ser Pro Leu Arg Arg Ser Pro Leu Gln Asn Gly Lys Arg
50 55 60
Asp Thr Phe Cys Ser Leu Trp Phe Lys Gly Arg Ser Val Ser Thr Thr
65 70 75 80
Val Asp Met Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr
85 90 95
Lys Ala Ile Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu
100 105 110
Ala Ile Asp Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser
115 120 125
Arg Ala Arg Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa
130 135 140
Leu Ala Leu Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr
145 150 155 160
Met Gly Lys Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu
165 170 175
Arg Lys Leu

(2) INFORMATION FOR SEQ ID NO:1429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1500248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1429:

Met Arg Gly Ile Leu Ser Ser Ser Ser Ala Leu Leu Arg Arg Ala Gly
1 5 10 15
Ala Gln Leu Ser Arg Thr Asp Cys Ser Ser Pro Ser Ala Ser Ala Thr
20 25 30
Ser Pro Leu Arg Arg Ser Pro Leu Gln Asn Gly Lys Arg Asp Thr Phe
35 40 45
Cys Ser Leu Trp Phe Lys Gly Arg Ser Val Ser Thr Thr Val Asp Met
50 55 60
Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr Lys Ala Ile
65 70 75 80
Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu Ala Ile Asp
85 90 95
Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser Arg Ala Arg
100 105 110
Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa Leu Ala Leu
115 120 125
Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr Met Gly Lys
130 135 140
Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu Arg Lys Leu
145 150 155 160

(2) INFORMATION FOR SEQ ID NO:1430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..97
(D) OTHER INFORMATION: / Ceres Seq. ID 1500249
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1430:
Met Gln Leu Asp Tyr Glu Ser Asp Pro Pro Leu Asp Asp Thr Lys Ala
1 5 10 15
Ile Glu Lys Glu Ser Ser Leu Asn Val Ala Val Ser Gln Leu Ala Ile
20 25 30
Asp Phe Asp Arg Asp Ser Asn Leu Cys Xaa Glu Arg Phe Ser Arg Ala
35 40 45
Arg Lys Ala Ser Val Val Ser Thr Gly Ser Leu Lys Leu Xaa Leu Ala
50 55 60
Leu Gly Val Gly Gly Leu Pro Lys Val Glu Trp Trp Arg Tyr Met Gly
65 70 75 80
Lys Lys His Leu Gly Arg Gln His Ser Arg Phe Met Leu Leu Arg Lys
85 90 95
Leu

(2) INFORMATION FOR SEQ ID NO:1431:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 749 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..749
(D) OTHER INFORMATION: / Ceres Seq. ID 1500250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1431:

agccgactgg	gactgagaag	aaacctccaa	acacctacct	ctctacgaac	tacctgccgc	60
cggaaaaccc	tagagcgctc	gaccatggat	ccgcagcagc	cggagcctgt	cagttacctc	120
tgcggagatt	gcggactgag	aacaccttga	agcccggaga	tgcatccag	tgccgtgaat	180
gtggctaccg	catcctctac	aagaagcgg	agccacattc	acggcactgg	aagacctctg	240
agggtgaact	gcggggccacc	gccacctaga	gatggatccg	caccaagagc	accaaggggt	300
ggtggtggtg	gcggcggcgg	cagcagcttt	gtcgattcag	ggaacaaggt	atacgtgggg	360
aaccttgcat	ggggcggtga	caactcgact	ctggagaacc	tattcagtga	gcaaggacag	420
gtgctggatg	ctaaggtcat	ctacgacagg	gatagcggca	ggtcaagggg	gtttggtttc	480
gtcacctatg	gctctgccga	ggaggtcaac	aatgccatat	caaaccttga	tggcatagac	540
ttggatggta	gacagatccg	agtcacgggt	gcagaatcaa	agcccaggcg	tgaattttga	600
gattttgtta	aggtggttta	gaggtcaata	gcgtgtgttc	acaagttcta	gtttgtagcg	660
tctattcttt	cttccgtatg	agtaacaaga	agatgctgat	aatgagagac	tggaagtga	720
actgctgtcc	acaggaagat	atTTTTccc				

(2) INFORMATION FOR SEQ ID NO:1432:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..146
(D) OTHER INFORMATION: / Ceres Seq. ID 1500251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1432:

Met Ser Ser Ser Ala Val Asn Val Ala Thr Ala Ser Ser Thr Arg Ser

1 5 10 15
Gly Ser His Ile His Gly Thr Gly Arg Pro Leu Arg Val Asn Cys Gly
20 25 30
Pro Pro Pro Pro Arg Asp Gly Ser Ala Pro Arg Ala Pro Arg Gly Gly
35 40 45
Gly Gly Gly Gly Gly Ser Ser Phe Val Asp Ser Gly Asn Lys Val
50 55 60
Tyr Val Gly Asn Leu Ala Trp Gly Val Asp Asn Ser Thr Leu Glu Asn
65 70 75 80
Leu Phe Ser Glu Gln Gly Gln Val Leu Asp Ala Lys Val Ile Tyr Asp
85 90 95
Arg Asp Ser Gly Arg Ser Arg Gly Phe Val Thr Tyr Gly Ser
100 105 110
Ala Glu Glu Val Asn Asn Ala Ile Ser Asn Leu Asp Gly Ile Asp Leu
115 120 125
Asp Gly Arg Gln Ile Arg Val Thr Val Ala Glu Ser Lys Pro Arg Arg
130 135 140
Glu Phe
145

(2) INFORMATION FOR SEQ ID NO:1433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500252

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1433:

Met Asp Pro His Gln Glu His Gln Gly Val Val Val Val Ala Ala Ala
1 5 10 15
Ala Ala Ala Leu Ser Ile Gln Gly Thr Arg Tyr Thr Trp Gly Thr Leu
20 25 30
His Gly Ala Leu Thr Thr Arg Leu Trp Arg Thr Tyr Ser Val Ser Lys
35 40 45
Asp Arg Cys Trp Met Leu Arg Ser Ser Thr Thr Gly Ile Ala Ala Gly
50 55 60
Gln Gly Gly Leu Val Ser Ser Pro Met Ala Leu Pro Arg Arg Ser Thr
65 70 75 80
Met Pro Tyr Gln Thr Leu Met Ala
85

(2) INFORMATION FOR SEQ ID NO:1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1250
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1434:

ctctctctct ctctctcttc tcgcttctct tctcctctcc gatcttctct gtgacctctt 60
tcttcttcga tttccttttg gtttcttctc cgaatcgccg gagaaaaaaa cccttctttg 120
aatctaaaga gactgttttt ttgaagctat tgactgattg attgataagg aagaataagc 180
attgatcgat ctgaattttg ggtacaagat gtcgagattc agagacagga cggaggattt 240
caaggattct gttcgggaagt ccgctgtttc gataggttat aatgagtcta aagtggcatc 300
aacaatggcg tctttttatta tacataagcc aaaggagaga tcgcctttca cgaaagctgc 360

tttcaaaacg	cttcatagca	tcaaggagtt	ggaactgttt	atgttgaagc	atcgaaagga	420
ttatgttgat	ctgcaccgga	ctacagaaca	ggaaaaggat	agtattgaac	aagaagttgc	480
tgctttttatt	aaagcttgca	aagaacagat	cgatattctc	ataaacagta	ttagaaatga	540
agaagcaaac	tccaaaggat	ggcttggcct	ccccgcagat	aacttcaatg	ctgattctat	600
agcacacaaa	catggagtgg	ttttgattct	gagtgaagaa	cttcattcag	tcactgccc	660
gtttgatcag	cttagagcta	ctcgtttcca	agatattata	aacagagcta	tgccgagaag	720
aaaacctaag	agggtcataa	aggaagctac	cccaattaat	acaactctgg	gaaattcgga	780
gtccatagaa	ccggatgaaa	tccaggccca	acctcgtaga	ttacaacaac	aacaacttct	840
agacgatgaa	acacaagccc	ttcaggtaga	gctaagtaat	cttttagatg	gtgctaggca	900
gacagaaact	aagatgggtg	agatgtctgc	attaaaccac	ttgatggcaa	ctcatgttct	960
gcagcaagcc	caacagatag	agttttctta	tgaccaggca	gttgaggcaa	caaagaacgt	1020
ggagcttgga	aacaaagagc	tttctcaagc	aatccaacga	aacagcagca	gcagaacctt	1080
tctcttactg	tttttcttcg	tccttacttt	ctccgtcttg	ttcttggtg	ggtacagtta	1140
aaaaaccatt	ctccaacaac	aacttcacac	agtttttgta	gatttttgatt	gttaactata	1200
aattatgaaa	aattggaaat	gggtttaaat	gttaaaacaa	aaataatgag		

(2) INFORMATION FOR SEQ ID NO:1435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..310

(D) OTHER INFORMATION: / Ceres Seq. ID 1500264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1435:

Met	Ser	Arg	Phe	Arg	Asp	Arg	Thr	Glu	Asp	Phe	Lys	Asp	Ser	Val	Arg
1			5					10						15	
Lys	Ser	Ala	Val	Ser	Ile	Gly	Tyr	Asn	Glu	Ser	Lys	Val	Ala	Ser	Thr
			20					25					30		
Met	Ala	Ser	Phe	Ile	Ile	His	Lys	Pro	Lys	Glu	Arg	Ser	Pro	Phe	Thr
			35				40					45			
Lys	Ala	Ala	Phe	Lys	Thr	Leu	Asp	Ser	Ile	Lys	Glu	Leu	Glu	Leu	Phe
			50			55					60				
Met	Leu	Lys	His	Arg	Lys	Asp	Tyr	Val	Asp	Leu	His	Arg	Thr	Thr	Glu
65					70				75					80	
Gln	Glu	Lys	Asp	Ser	Ile	Glu	Gln	Glu	Val	Ala	Ala	Phe	Ile	Lys	Ala
			85					90					95		
Cys	Lys	Glu	Gln	Ile	Asp	Ile	Leu	Ile	Asn	Ser	Ile	Arg	Asn	Glu	Glu
			100				105					110			
Ala	Asn	Ser	Lys	Gly	Trp	Leu	Gly	Leu	Pro	Ala	Asp	Asn	Phe	Asn	Ala
			115				120					125			
Asp	Ser	Ile	Ala	His	Lys	His	Gly	Val	Val	Leu	Ile	Leu	Ser	Glu	Lys
			130			135					140				
Leu	His	Ser	Val	Thr	Ala	Gln	Phe	Asp	Gln	Leu	Arg	Ala	Thr	Arg	Phe
145					150				155					160	
Gln	Asp	Ile	Ile	Asn	Arg	Ala	Met	Pro	Arg	Arg	Lys	Pro	Lys	Arg	Val
			165					170					175		
Ile	Lys	Glu	Ala	Thr	Pro	Ile	Asn	Thr	Leu	Gly	Asn	Ser	Glu	Ser	
			180				185					190			
Ile	Glu	Pro	Asp	Glu	Ile	Gln	Ala	Gln	Pro	Arg	Arg	Leu	Gln	Gln	Gln
			195				200					205			
Gln	Leu	Leu	Asp	Asp	Glu	Thr	Gln	Ala	Leu	Gln	Val	Glu	Leu	Ser	Asn
			210			215					220				
Leu	Leu	Asp	Gly	Ala	Arg	Gln	Thr	Glu	Thr	Lys	Met	Val	Glu	Met	Ser
225					230					235				240	
Ala	Leu	Asn	His	Leu	Met	Ala	Thr	His	Val	Leu	Gln	Gln	Ala	Gln	Gln
			245					250					255		
Ile	Glu	Phe	Leu	Tyr	Asp	Gln	Ala	Val	Glu	Ala	Thr	Lys	Asn	Val	Glu
			260				265						270		

Leu Gly Asn Lys Glu Leu Ser Gln Ala Ile Gln Arg Asn Ser Ser Ser
275 280 285
Arg Thr Phe Leu Leu Leu Phe Phe Val Leu Thr Phe Ser Val Leu
290 295 300
Phe Leu Asp Trp Tyr Ser
305 310

(2) INFORMATION FOR SEQ ID NO:1436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..278

(D) OTHER INFORMATION: / Ceres Seq. ID 1500265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1436:

Met Ala Ser Phe Ile Ile His Lys Pro Lys Glu Arg Ser Pro Phe Thr
1 5 10 15
Lys Ala Ala Phe Lys Thr Leu Asp Ser Ile Lys Glu Leu Glu Leu Phe
20 25 30
Met Leu Lys His Arg Lys Asp Tyr Val Asp Leu His Arg Thr Thr Glu
35 40 45
Gln Glu Lys Asp Ser Ile Glu Gln Glu Val Ala Ala Phe Ile Lys Ala
50 55 60
Cys Lys Glu Gln Ile Asp Ile Leu Ile Asn Ser Ile Arg Asn Glu Glu
65 70 75 80
Ala Asn Ser Lys Gly Trp Leu Gly Leu Pro Ala Asp Asn Phe Asn Ala
85 90 95
Asp Ser Ile Ala His Lys His Gly Val Val Leu Ile Leu Ser Glu Lys
100 105 110
Leu His Ser Val Thr Ala Gln Phe Asp Gln Leu Arg Ala Thr Arg Phe
115 120 125
Gln Asp Ile Ile Asn Arg Ala Met Pro Arg Arg Lys Pro Lys Arg Val
130 135 140
Ile Lys Glu Ala Thr Pro Ile Asn Thr Thr Leu Gly Asn Ser Glu Ser
145 150 155 160
Ile Glu Pro Asp Glu Ile Gln Ala Gln Pro Arg Arg Leu Gln Gln Gln
165 170 175
Gln Leu Leu Asp Asp Glu Thr Gln Ala Leu Gln Val Glu Leu Ser Asn
180 185 190
Leu Leu Asp Gly Ala Arg Gln Thr Glu Thr Lys Met Val Glu Met Ser
195 200 205
Ala Leu Asn His Leu Met Ala Thr His Val Leu Gln Gln Ala Gln Gln
210 215 220
Ile Glu Phe Leu Tyr Asp Gln Ala Val Glu Ala Thr Lys Asn Val Glu
225 230 235 240
Leu Gly Asn Lys Glu Leu Ser Gln Ala Ile Gln Arg Asn Ser Ser Ser
245 250 255
Arg Thr Phe Leu Leu Phe Phe Phe Val Leu Thr Phe Ser Val Leu
260 265 270
Phe Leu Asp Trp Tyr Ser
275

(2) INFORMATION FOR SEQ ID NO:1437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..246

(D) OTHER INFORMATION: / Ceres Seq. ID 1500266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1437:

```
Met Leu Lys His Arg Lys Asp Tyr Val Asp Leu His Arg Thr Thr Glu
1      5      10      15
Gln Glu Lys Asp Ser Ile Glu Gln Glu Val Ala Ala Phe Ile Lys Ala
20      25      30
Cys Lys Glu Gln Ile Asp Ile Leu Ile Asn Ser Ile Arg Asn Glu Glu
35      40      45
Ala Asn Ser Lys Gly Trp Leu Gly Leu Pro Ala Asp Asn Phe Asn Ala
50      55      60
Asp Ser Ile Ala His Lys His Gly Val Val Leu Ile Leu Ser Glu Lys
65      70      75      80
Leu His Ser Val Thr Ala Gln Phe Asp Gln Leu Arg Ala Thr Arg Phe
85      90      95
Gln Asp Ile Ile Asn Arg Ala Met Pro Arg Arg Lys Pro Lys Arg Val
100     105     110
Ile Lys Glu Ala Thr Pro Ile Asn Thr Thr Leu Gly Asn Ser Glu Ser
115     120     125
Ile Glu Pro Asp Glu Ile Gln Ala Gln Pro Arg Arg Leu Gln Gln Gln
130     135     140
Gln Leu Leu Asp Asp Glu Thr Gln Ala Leu Gln Val Glu Leu Ser Asn
145     150     155     160
Leu Leu Asp Gly Ala Arg Gln Thr Glu Thr Lys Met Val Glu Met Ser
165     170     175
Ala Leu Asn His Leu Met Ala Thr His Val Leu Gln Gln Ala Gln Gln
180     185     190
Ile Glu Phe Leu Tyr Asp Gln Ala Val Glu Ala Thr Lys Asn Val Glu
195     200     205
Leu Gly Asn Lys Glu Leu Ser Gln Ala Ile Gln Arg Asn Ser Ser Ser
210     215     220
Arg Thr Phe Leu Leu Leu Phe Phe Phe Val Leu Thr Phe Ser Val Leu
225     230     235     240
Phe Leu Asp Trp Tyr Ser
245
```

(2) INFORMATION FOR SEQ ID NO:1438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 529 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..529

(D) OTHER INFORMATION: / Ceres Seq. ID 1500283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1438:

```
agagtcccag cgacctgtag cctcctctct cegtgcacct cgctctcgcc tcgccgcctc 60
cgaccgcgag cagcgctcc attgctctct ctcacgagtc ccggcggttc agtggggggc 120
attcatggcg gggcagtcg acccgacct ctccatcttc tcgccctccg aggtggagtt 180
cgtggctgag gatgagatt tcgaaatcgt cccaacatc cgcatggacg ccctcaacat 240
gatctgcggg gatttcgggc ccttcttccc ccagattccc accaaggtgc ctctctggct 300
cgctgtcgcg ctcaagaagc gtasaagtgc accatccgca ccccgactg gatgactgtt 360
gaccgcttga cacaggtatt ggaagcgga agagagtcgc cagcagaatt ccagccatta 420
ccattccact atattgaaat ttctaagctt ctgtttgatc atgctcgtga tgacatctca 480
gatgcatacc tggttaagatc tctaattgag gacatcagag atgtcagat
```

(2) INFORMATION FOR SEQ ID NO:1439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1500284
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1439:
Arg Val Pro Ala Thr Cys Ser Leu Leu Ser Pro Ser Thr Ser Leu Ser
1 5 10 15
Pro Arg Arg Leu Arg Pro Ala Ala Ala Pro Pro Leu Leu Ser Leu Thr
20 25 30
Ser Pro Gly Val Pro Val Gly Gly Ile His Gly Gly Ala Val Arg Pro
35 40 45
Ala Pro Leu His Leu Leu Ala Leu Arg Gly Gly Val Arg Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO:1440:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..117
(D) OTHER INFORMATION: / Ceres Seq. ID 1500285
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1440:
Glu Ser Gln Arg Pro Val Ala Ser Ser Leu Arg Arg Pro Arg Ser Arg
1 5 10 15
Leu Ala Ala Ser Asp Pro Gln Gln Arg Leu His Cys Ser Leu Ser Arg
20 25 30
Val Pro Ala Phe Gln Trp Gly Ala Phe Met Ala Gly Gln Ser Asp Pro
35 40 45
His Leu Ser Ile Phe Ser Pro Ser Glu Val Glu Phe Val Ala Glu Asp
50 55 60
Glu Ile Val Glu Ile Val Pro Asn Ile Arg Met Asp Ala Leu Asn Met
65 70 75 80
Ile Cys Gly Asp Phe Gly Pro Phe Phe Pro Gln Ile Pro Thr Lys Val
85 90 95
Pro Leu Trp Leu Ala Val Ala Leu Lys Lys Arg Xaa Ser Ala Pro Ser
100 105 110
Ala Pro Arg Thr Gly
115

(2) INFORMATION FOR SEQ ID NO:1441:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..76
(D) OTHER INFORMATION: / Ceres Seq. ID 1500286
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1441:
Met Ala Gly Gln Ser Asp Pro His Leu Ser Ile Phe Ser Pro Ser Glu
1 5 10 15
Val Glu Phe Val Ala Glu Asp Glu Ile Val Glu Ile Val Pro Asn Ile
20 25 30

Arg Met Asp Ala Leu Asn Met Ile Cys Gly Asp Phe Gly Pro Phe Phe
35 40 45
Pro Gln Ile Pro Thr Lys Val Pro Leu Trp Leu Ala Val Ala Leu Lys
50 55 60
Lys Arg Xaa Ser Ala Pro Ser Ala Pro Arg Thr Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:1442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..442
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1442:

tactacatgc aatttgggaa atgtaaattt caatcagctt gtatattcaa tcattcaaaa	60
gacatacttt caagtvgrtg gcatccagca gaatgcccat tctacatgaa aactaggaca	120
tgccaatttg gatcagcttg tgagttttat caccctaaaag atcggvgctc cttcaagang	180
rctgggaaca ggcaggcgcc ctaccagccg ccgaabgccc tgacgctgcg tggcasacga	240
catgtaccct gcrntcgccg cagargcggc ggcggcgagg gggctctcggc gctcgaracg	300
ggcaccaagc tctacatctc caacctggac tttrgggttt cgaacgacga tatcaaggag	360
ctgttctctg agctaggtga tctgaagcgt ttttcgataa tatatgadcg aagtrggagg	420
tctaagggaa cagctgaagt tg	

(2) INFORMATION FOR SEQ ID NO:1443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1443:

Tyr Tyr Met Gln Phe Gly Lys Cys Lys Phe Gln Ser Ala Cys Ile Phe	
1 5 10 15	
Asn His Ser Lys Asp Ile Leu Ser Ser Xaa Trp His Pro Ala Glu Cys	
20 25 30	
Pro Phe Tyr Met Lys Thr Arg Thr Cys Gln Phe Gly Ser Ala Cys Glu	
35 40 45	
Phe Tyr His Pro Lys Asp Arg Xaa Ser Phe Lys Xaa Xaa Gly Asn Arg	
50 55 60	
Gln Ala Pro Tyr Gln Pro Pro Xaa Ala Leu Thr Leu Arg Gly Xaa Arg	
65 70 75 80	
His Val Pro Cys Xaa Arg Arg Arg Xaa Gly Gly Gly Arg Val Ser	
85 90 95	
Ala Leu Xaa Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Phe Xaa	
100 105 110	
Val Ser Asn Asp Asp Ile Lys Glu Leu Phe Ser Glu Leu Gly Asp Leu	
115 120 125	
Lys Arg Phe Ser Ile Ile Tyr Xaa Arg Ser Xaa Arg Ser Lys Gly Thr	
130 135 140	
Ala Glu Val	
145	

(2) INFORMATION FOR SEQ ID NO:1444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..145
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500300
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1444:

```
Met Gln Phe Gly Lys Cys Lys Phe Gln Ser Ala Cys Ile Phe Asn His
1          5          10          15
Ser Lys Asp Ile Leu Ser Ser Xaa Trp His Pro Ala Glu Cys Pro Phe
          20          25          30
Tyr Met Lys Thr Arg Thr Cys Gln Phe Gly Ser Ala Cys Glu Phe Tyr
          35          40          45
His Pro Lys Asp Arg Xaa Ser Phe Lys Xaa Xaa Gly Asn Arg Gln Ala
          50          55          60
Pro Tyr Gln Pro Pro Xaa Ala Leu Thr Leu Arg Gly Xaa Arg His Val
65          70          75          80
Pro Cys Xaa Arg Arg Arg Xaa Gly Gly Gly Gly Arg Val Ser Ala Leu
          85          90          95
Xaa Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Phe Xaa Val Ser
          100          105          110
Asn Asp Asp Ile Lys Glu Leu Phe Ser Glu Leu Gly Asp Leu Lys Arg
          115          120          125
Phe Ser Ile Ile Tyr Xaa Arg Ser Xaa Arg Ser Lys Gly Thr Ala Glu
130          135          140
Val
145
```

- (2) INFORMATION FOR SEQ ID NO:1445:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500301
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1445:

```
Met Lys Thr Arg Thr Cys Gln Phe Gly Ser Ala Cys Glu Phe Tyr His
1          5          10          15
Pro Lys Asp Arg Xaa Ser Phe Lys Xaa Xaa Gly Asn Arg Gln Ala Pro
          20          25          30
Tyr Gln Pro Pro Xaa Ala Leu Thr Leu Arg Gly Xaa Arg His Val Pro
          35          40          45
Cys Xaa Arg Arg Arg Xaa Gly Gly Gly Gly Arg Val Ser Ala Leu Xaa
          50          55          60
Thr Gly Thr Lys Leu Tyr Ile Ser Asn Leu Asp Phe Xaa Val Ser Asn
65          70          75          80
Asp Asp Ile Lys Glu Leu Phe Ser Glu Leu Gly Asp Leu Lys Arg Phe
          85          90          95
Ser Ile Ile Tyr Xaa Arg Ser Xaa Arg Ser Lys Gly Thr Ala Glu Val
100          105          110
```

- (2) INFORMATION FOR SEQ ID NO:1446:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..501
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1446:

aacttggccc	caaatcgtgg	agtggaaacc	ctactcgtcc	ccttcgcgat	cgccgccc	60
ttccccacc	caattccac	tctccgctcg	acagatccat	acatgatggg	agaggccaag	120
gagaacgacg	tttatgagga	ggagctcctg	gactacgagg	aggacgacga	caagacggtc	180
gatggctccg	ctgctaagcc	caccggagag	gtcgcaaaga	agggctacgt	cgggatccac	240
agttccgggt	tcagagactt	cctgctcaag	ccagagctgc	tccgtgctat	ccaggattgt	300
ggttttragc	atccttccga	agtgcaacac	gagtgtatcc	ctcaagccat	tcttggaatg	360
gatgtcatct	gtcaagctaa	atctgggatg	gggaaaactg	ctgtttttgt	cctttcatcc	420
ctccaacaaa	ttgaccctgt	tcggggtcag	gtagcagcac	ttgtactgtg	ccacacaarg	480
gaactggctt	atcagatatg	c				

(2) INFORMATION FOR SEQ ID NO:1447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..167
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1447:

Asn	Leu	Ala	Pro	Asn	Arg	Gly	Val	Glu	Thr	Leu	Leu	Val	Pro	Phe	Arg	
1				5					10					15		
Ile	Ala	Ala	Gln	Phe	Pro	His	Pro	Ile	Pro	Thr	Leu	Arg	Ser	Thr	Asp	
			20					25					30			
Pro	Tyr	Met	Met	Gly	Glu	Ala	Lys	Glu	Asn	Asp	Val	Tyr	Glu	Glu	Glu	
		35					40					45				
Leu	Leu	Asp	Tyr	Glu	Glu	Asp	Asp	Asp	Lys	Thr	Val	Asp	Gly	Ser	Ala	
	50					55					60					
Ala	Lys	Pro	Thr	Gly	Glu	Val	Ala	Lys	Lys	Gly	Tyr	Val	Gly	Ile	His	
65				70					75					80		
Ser	Ser	Gly	Phe	Arg	Asp	Phe	Leu	Leu	Lys	Pro	Glu	Leu	Leu	Arg	Ala	
			85						90					95		
Ile	Gln	Asp	Cys	Gly	Phe	Xaa	His	Pro	Ser	Glu	Val	Gln	His	Glu	Cys	
		100						105					110			
Ile	Pro	Gln	Ala	Ile	Leu	Gly	Met	Asp	Val	Ile	Cys	Gln	Ala	Lys	Ser	
		115					120					125				
Gly	Met	Gly	Lys	Thr	Ala	Val	Phe	Val	Leu	Ser	Ser	Leu	Gln	Gln	Ile	
	130					135					140					
Asp	Pro	Val	Ala	Gly	Gln	Val	Ala	Ala	Leu	Val	Leu	Cys	His	Thr	Xaa	
145				150					155						160	
Glu	Leu	Ala	Tyr	Gln	Ile	Cys										
				165												

(2) INFORMATION FOR SEQ ID NO:1448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1500307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1448:

Met Met Gly Glu Ala Lys Glu Asn Asp Val Tyr Glu Glu Glu Leu Leu
1 5 10 15
Asp Tyr Glu Glu Asp Asp Asp Lys Thr Val Asp Gly Ser Ala Ala Lys
20 25 30
Pro Thr Gly Glu Val Ala Lys Lys Gly Tyr Val Gly Ile His Ser Ser
35 40 45
Gly Phe Arg Asp Phe Leu Leu Lys Pro Glu Leu Leu Arg Ala Ile Gln
50 55 60
Asp Cys Gly Phe Xaa His Pro Ser Glu Val Gln His Glu Cys Ile Pro
65 70 75 80
Gln Ala Ile Leu Gly Met Asp Val Ile Cys Gln Ala Lys Ser Gly Met
85 90 95
Gly Lys Thr Ala Val Phe Val Leu Ser Ser Leu Gln Gln Ile Asp Pro
100 105 110
Val Ala Gly Gln Val Ala Ala Leu Val Leu Cys His Thr Xaa Glu Leu
115 120 125
Ala Tyr Gln Ile Cys
130

(2) INFORMATION FOR SEQ ID NO:1449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1500308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1449:

Met Gly Glu Ala Lys Glu Asn Asp Val Tyr Glu Glu Glu Leu Leu Asp
1 5 10 15
Tyr Glu Glu Asp Asp Asp Lys Thr Val Asp Gly Ser Ala Ala Lys Pro
20 25 30
Thr Gly Glu Val Ala Lys Lys Gly Tyr Val Gly Ile His Ser Ser Gly
35 40 45
Phe Arg Asp Phe Leu Leu Lys Pro Glu Leu Leu Arg Ala Ile Gln Asp
50 55 60
Cys Gly Phe Xaa His Pro Ser Glu Val Gln His Glu Cys Ile Pro Gln
65 70 75 80
Ala Ile Leu Gly Met Asp Val Ile Cys Gln Ala Lys Ser Gly Met Gly
85 90 95
Lys Thr Ala Val Phe Val Leu Ser Ser Leu Gln Gln Ile Asp Pro Val
100 105 110
Ala Gly Gln Val Ala Ala Leu Val Leu Cys His Thr Xaa Glu Leu Ala
115 120 125
Tyr Gln Ile Cys
130

(2) INFORMATION FOR SEQ ID NO:1450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1540
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1450:

atcatcatcg	tattcaccgt	tgtcctttct	ttcattgaca	cttgccagtt	tacatcgaca	60
aacaaaagaa	atcagaatgg	atttctcagg	gagattcttt	gtcatcttcg	ttaccttctt	120
ctttctccct	cctctgtctt	cagctgggag	ctacgattct	ggttcggggtc	tcgagtcact	180
cgctcgcggg	atgcttcatt	cagccaagga	tcctgagttc	ttcgagtggga	tgagaggaat	240
taggagaaaag	attcatgaga	acccagagac	agggtttcag	gagttcaaaa	cgagtcaact	300
cgttcgagac	gagcttgact	cgcttgagg	gaagtataag	tatcctgtgg	cgaagactgg	360
cgctgctcrt	tggatcggat	cctgttcgaa	acctgttttc	ggacttagag	ccgacatgga	420
cgcaattccg	gttacaggga	attagtggaa	tgggaatcsa	aaagtaaagt	agatggaaaag	480
atgcatgctt	gtggtcatga	tactcatgtt	gctatgcttc	ttgggtgctgc	taagcttctt	540
caaaccacaa	aacacctcat	caaggggaca	gtaaaacttg	tgtttcaacc	aggcgaggaa	600
ggttatgcag	gtgcttatga	aatgctaaaa	gacgagattc	tagacgactt	msatgggata	660
ctcagtggtc	atgtctttcc	atcgatccca	tcagggtgga	ttggttctag	gcctgggacc	720
gttcttgtag	gtgcaggatt	gtttacagtc	acggttcacg	gtcaaggtag	ccacgcagct	780
acaccgcact	tctctaaara	cccggttctt	gcagcttctt	ccgctgttgt	tgctttgcaa	840
cagattgttt	cgcggggaact	ggatccactc	gaagctgggtg	tggttacagt	tggatatatt	900
gaaggagggtc	atgctcaaaa	cgtaataaccg	cagagtgcga	aatttggagg	tactttcaga	960
magcttaagc	aacgatgggc	ttctattttat	ccaaagacgg	atcaaagaga	tttcagaggc	1020
acaagcatcg	gtataccgat	gcaaagcaga	agtaaacttc	gaagagaaaa	agccgtcgct	1080
tcacmccggt	aatgaataac	gacgagggtc	tatacbgagc	acggtaaaaa	agtagcggaa	1140
gcgatgattg	gaaagaataa	cttccatgat	ttcccggtga	caatgggagg	agaggatttc	1200
agcnttcttc	actcaaaaaga	cntaaggctg	cgattttcgt	gctggggata	aagaatgaga	1260
cgctaggcgc	tggttaagccg	cttcaactcgc	cttacttctt	tggtgatgaa	gaagctcttc	1320
ctggttggggc	tgctcttcac	gcagctatgg	ccgtttctta	tttgacgaa	catgscata	1380
gccatgaaga	agagggttaag	agtgaattat	agaaggtgtt	gggagaaaaat	cagcttatat	1440
tagtcatcat	ctatttgat	ttgaacttga	aagttagggtg	aggttagggtt	tcgggttggg	1500
aagaatgttt	gttaatatgtc	acgagaaaacc	aaccactttc			

(2) INFORMATION FOR SEQ ID NO:1451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..203
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1451:

Met	His	Ala	Cys	Gly	His	Asp	Thr	His	Val	Ala	Met	Leu	Leu	Gly	Ala
1				5					10					15	
Ala	Lys	Leu	Leu	Gln	Thr	Thr	Lys	His	Leu	Ile	Lys	Gly	Thr	Val	Lys
			20					25					30		
Leu	Val	Phe	Gln	Pro	Gly	Glu	Glu	Gly	Tyr	Ala	Gly	Ala	Tyr	Glu	Met
			35				40					45			
Leu	Lys	Asp	Glu	Ile	Leu	Asp	Asp	Xaa	Xaa	Gly	Ile	Leu	Ser	Val	His
			50				55				60				
Val	Phe	Pro	Ser	Ile	Pro	Ser	Gly	Gly	Ile	Gly	Ser	Arg	Pro	Gly	Thr
65					70				75					80	
Val	Leu	Ala	Gly	Ala	Gly	Leu	Phe	Thr	Val	Thr	Val	His	Gly	Gln	Gly
				85				90						95	
Ser	His	Ala	Ala	Thr	Pro	His	Phe	Ser	Lys	Xaa	Pro	Val	Leu	Ala	Ala
				100				105					110		
Ser	Ser	Ala	Val	Val	Ala	Leu	Gln	Ile	Val	Ser	Arg	Glu	Leu	Asp	
			115				120				125				
Pro	Leu	Glu	Ala	Gly	Val	Val	Thr	Val	Gly	Tyr	Ile	Glu	Gly	Gly	His
			130				135				140				
Ala	Gln	Asn	Val	Ile	Pro	Gln	Ser	Ala	Lys	Phe	Gly	Gly	Thr	Phe	Arg
145					150				155					160	
Xaa	Leu	Lys	Gln	Arg	Trp	Ala	Ser	Ile	Tyr	Pro	Lys	Thr	Asp	Gln	Arg
			165						170					175	

Asp Phe Arg Gly Thr Ser Ile Gly Ile Pro Met Gln Ser Arg Ser Lys
180 185 190
Leu Arg Arg Glu Lys Ala Val Ala Ser Xaa Arg
195 200

(2) INFORMATION FOR SEQ ID NO:1452:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1500315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1452:

Met Leu Leu Gly Ala Lys Leu Leu Gln Thr Thr Lys His Leu Ile
1 5 10 15
Lys Gly Thr Val Lys Leu Val Phe Gln Pro Gly Glu Glu Gly Tyr Ala
20 25 30
Gly Ala Tyr Glu Met Leu Lys Asp Glu Ile Leu Asp Asp Xaa Xaa Gly
35 40 45
Ile Leu Ser Val His Val Phe Pro Ser Ile Pro Ser Gly Ile Gly
50 55 60
Ser Arg Pro Gly Thr Val Leu Ala Gly Ala Gly Leu Phe Thr Val Thr
65 70 75 80
Val His Gly Gln Gly Ser His Ala Ala Thr Pro His Phe Ser Lys Xaa
85 90 95
Pro Val Leu Ala Ala Ser Ser Ala Val Val Ala Leu Gln Gln Ile Val
100 105 110
Ser Arg Glu Leu Asp Pro Leu Glu Ala Gly Val Val Thr Val Gly Tyr
115 120 125
Ile Glu Gly Gly His Ala Gln Asn Val Ile Pro Gln Ser Ala Lys Phe
130 135 140
Gly Gly Thr Phe Arg Xaa Leu Lys Gln Arg Trp Ala Ser Ile Tyr Pro
145 150 155 160
Lys Thr Asp Gln Arg Asp Phe Arg Gly Thr Ser Ile Gly Ile Pro Met
165 170 175
Gln Ser Arg Ser Lys Leu Arg Arg Glu Lys Ala Val Ala Ser Xaa Arg
180 185 190

(2) INFORMATION FOR SEQ ID NO:1453:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1500316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1453:

Met Leu Lys Asp Glu Ile Leu Asp Asp Xaa Xaa Gly Ile Leu Ser Val
1 5 10 15
His Val Phe Pro Ser Ile Pro Ser Gly Gly Ile Gly Ser Arg Pro Gly
20 25 30
Thr Val Leu Ala Gly Ala Gly Leu Phe Thr Val Thr Val His Gly Gln
35 40 45
Gly Ser His Ala Ala Thr Pro His Phe Ser Lys Xaa Pro Val Leu Ala

50		55		60
Ala Ser Ser Ala Val Val	Ala Leu Gln Gln Ile	Val Ser Arg Glu Leu		
65		70		75
Asp Pro Leu Glu Ala Gly	Val Val Thr Val Gly Tyr	Ile Glu Gly Gly		80
	85	90		95
His Ala Gln Asn Val Ile	Pro Gln Ser Ala Lys Phe	Gly Gly Thr Phe		
	100	105		110
Arg Xaa Leu Lys Gln Arg	Trp Ala Ser Ile Tyr Pro	Lys Thr Asp Gln		
	115	120		125
Arg Asp Phe Arg Gly Thr	Ser Ile Gly Ile Pro Met	Gln Ser Arg Ser		
	130	135		140
Lys Leu Arg Arg Glu Lys	Ala Val Ala Ser Xaa Arg			
145	150	155		

(2) INFORMATION FOR SEQ ID NO:1454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..498
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1454:

gcttgctcgc taacaatcag tgaactgaac accttccgcc tcccgggtctc ctccctgccc	60
ggtgctgaag aaccctgcca tccccggaac tggatcgatc tgccgccaac tctgaaaatc	120
catccgatcc atctctgtcg tccaagtcta ctccccgatg gacattattt accaggacag	180
cagttgtctt gccctagagc aggcgtaca tgatgaaggc gtgggaccaa tcgacctacc	240
tttcatgctt ctcagggcca tcacaaaaga tttctctgat actcaactaa ttggcagggg	300
tgggttcgga gaggtttaca aggtatgcat ggggtatttg gcacctgaat ttctgagcag	360
caatgcaatc acattcaagg cggacatata cagtctargt gttataatca ctgagattct	420
gacgggggca taargratgc accartgttg acaaaggkgc ttgaaarctg gacggacatg	480
tttcagacat taggaagc	

(2) INFORMATION FOR SEQ ID NO:1455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1455:

Ala Cys Ser Leu Thr Ile Ser Glu Leu Asn Thr Phe Arg Leu Pro Val	
1	5
Ser Ser Leu Pro Gly Ala Glu Glu Pro Cys His Pro Arg Asn Trp Ile	10
	15
	20
Asp Leu Pro Pro Thr Leu Lys Ile His Pro Ile His Leu Cys Arg Pro	25
	30
	35
Ser Leu Leu Pro Asp Gly His Tyr Leu Pro Gly Gln Gln Leu Ser Cys	40
	45
	50
Pro Arg Ala Gly Ala Thr	55
	60
65	70

(2) INFORMATION FOR SEQ ID NO:1456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..91
(D) OTHER INFORMATION: / Ceres Seq. ID 1500323
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1456:
Met Asp Ile Ile Tyr Gln Asp Ser Ser Cys Leu Ala Leu Glu Gln Ala
1 5 10 15
Leu His Asp Glu Gly Val Gly Pro Ile Asp Leu Pro Phe Met Leu Leu
20 25 30
Arg Ala Ile Thr Lys Asp Phe Ser Asp Thr Gln Leu Ile Gly Arg Gly
35 40 45
Gly Phe Gly Glu Val Tyr Lys Val Cys Met Gly Tyr Leu Ala Pro Glu
50 55 60
Phe Leu Ser Ser Asn Ala Ile Thr Phe Lys Ala Asp Ile Tyr Ser Leu
65 70 75 80
Xaa Val Ile Ile Thr Glu Ile Leu Thr Gly Ala
85 90

(2) INFORMATION FOR SEQ ID NO:1457:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1500324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1457:

Met Leu Leu Arg Ala Ile Thr Lys Asp Phe Ser Asp Thr Gln Leu Ile
1 5 10 15
Gly Arg Gly Gly Phe Gly Glu Val Tyr Lys Val Cys Met Gly Tyr Leu
20 25 30
Ala Pro Glu Phe Leu Ser Ser Asn Ala Ile Thr Phe Lys Ala Asp Ile
35 40 45
Tyr Ser Leu Xaa Val Ile Ile Thr Glu Ile Leu Thr Gly Ala
50 55 60

(2) INFORMATION FOR SEQ ID NO:1458:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 368 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..368

(D) OTHER INFORMATION: / Ceres Seq. ID 1500367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1458:

tcacactctg	cccagctaag	ctaagctccc	tccgtccatc	ggcatggcga	ctaccactac	60
taccatcctc	ctcctcctcc	tcgtcgcagc	cacagccgtc	tcggcggccg	acctctccgt	120
gtaccacaac	gtgcaccgcg	cgctcccgcg	cccgcctcgag	tccatcatcg	cgctcgcgccg	180
cgccgacgac	gcgcggctcc	tcttcccttc	atccaaggcg	gcctcgtccg	gcggcggtcac	240
ctccgctccc	gtcgccctcg	gccagactcc	gcmctcgtag	gtmgtccgcg	cggggctcgg	300
caccccggtc	cagcagctgc	tcctcgcgct	cgacaccagc	gccgacgcca	cctggctcgca	360
ctgcgcgc						

(2) INFORMATION FOR SEQ ID NO:1459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500368
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1459:

Thr	Leu	Cys	Pro	Ala	Lys	Leu	Ser	Ser	Leu	Arg	Pro	Ser	Ala	Trp	Arg
1			5						10					15	
Leu	Pro	Leu	Leu	Pro	Ser	Ser	Ser	Ser	Ser	Ser	Gln	Pro	Gln	Pro	
			20						25				30		
Ser	Arg	Arg	Pro	Thr	Ser	Pro	Cys	Thr	Thr	Thr	Cys	Thr	Arg	Arg	Pro
			35				40					45			
Arg	Pro	Arg	Ser	Ser	Pro	Ser	Ser	Arg	Ser	Pro	Ala	Pro	Thr	Thr	Arg
			50				55				60				
Gly	Ser	Ser	Ser	Ser	His	Pro	Arg	Arg	Pro	Arg	Pro	Ala	Ala	Ser	Pro
65					70					75				80	
Pro	Leu	Pro	Ser	Pro	Pro	Ala	Arg	Leu	Arg	Xaa	Arg	Thr	Xaa	Ser	Ala
					85				90					95	
Arg	Gly	Ser	Ala	Pro	Arg	Ser	Ser	Ser	Cys	Ser	Ser	Arg	Ser	Thr	Pro
			100						105				110		
Ala	Pro	Thr	Pro	Pro	Gly	Arg	Thr	Ala	Arg						
			115				120								

(2) INFORMATION FOR SEQ ID NO:1460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..108
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500369
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1460:

Met	Ala	Thr	Thr	Thr	Thr	Ile	Leu	Leu	Leu	Leu	Val	Ala	Ala		
1														15	
Thr	Ala	Val	Ser	Ala	Ala	Asp	Leu	Ser	Val	Tyr	His	Asn	Val	His	Pro
			20						25				30		
Pro	Ser	Pro	Ser	Pro	Leu	Glu	Ser	Ile	Ile	Ala	Leu	Ala	Arg	Ala	Asp
			35				40					45			
Asp	Ala	Arg	Leu	Leu	Phe	Leu	Ser	Ser	Lys	Ala	Ala	Ser	Ser	Gly	Gly
			50				55				60				
Val	Thr	Ser	Ala	Pro	Val	Ala	Ser	Gly	Gln	Thr	Pro	Xaa	Ser	Tyr	Xaa
65					70					75				80	
Val	Arg	Ala	Gly	Leu	Gly	Thr	Pro	Val	Gln	Gln	Leu	Leu	Leu	Ala	Leu
					85				90					95	
Asp	Thr	Ser	Ala	Asp	Ala	Thr	Trp	Ser	His	Cys	Ala				
			100					105							

(2) INFORMATION FOR SEQ ID NO:1461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 921 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..921

(D) OTHER INFORMATION: / Ceres Seq. ID 1500370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1461:

atcctctagc	tctctctctc	tctcttctct	cacacacaca	cacagtcaca	gacaccccta	60
tcacttagac	tgtgctagta	ggtagcggcc	gcgtaatgga	gcaggagctc	agccttgagc	120
tcacccctct	ccacccctcg	gcctcgccgc	cggagccacc	gggctacttc	gtctgcatgt	180
actgcgaccg	caagttcttc	agctcgagc	ctctcggtgg	ccaccagaac	gcgcacaagt	240
acgagcgcas	ctggccaagc	gccgcaggga	gatagccgcc	gccctgcgcg	cgcacggggc	300
ggccgccacc	gmacggggcg	cycggaggga	cgacgmcgyc	gccgcgatgg	gctctgcgca	360
tgtccccgcc	aggccacaag	gcacgggtac	cggagtcgtc	gtcgttgaag	atgagagtgc	420
aaccaggatg	atgggacaag	cagaaggctc	ctgctgctga	tgacgasstc	ccgcgaccgc	480
gtcgtcgagc	aacatgaaga	ggtcgtcgga	gtacgggtac	ggcgtcgagg	agctggatct	540
ctccctcagg	ctttgattgg	ttcctcttcc	tcctccacyn	nnanatataa	ttcgccccgt	600
tngtcnagat	aattcgatct	ttgtggtcag	tgcaatcatc	tgtttcgcgt	gcgtgggtatc	660
tcagtgtctg	atccgtcact	ttcttcctca	tgtagttggt	gtgcagttat	attcttccat	720
ccgatgatgg	aacctatcgg	caagaactat	tgtcggccca	tcctgctatc	caaagggcgt	780
ggtatttggt	gtgctctttt	cgtttttctg	ccttgagtct	tccttgtgcg	atctaaattc	840
gcagcttggt	ttttccaaaa	ggcggaagc	agttttgccg	caatttcggt	tggacctttt	900
tcaagtgact	ctaaattggg	c				

(2) INFORMATION FOR SEQ ID NO:1462:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1500371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1462:

Met	Glu	Gln	Glu	Leu	Ser	Leu	Glu	Leu	Thr	Leu	Leu	His	Pro	Ser	Ala
1				5					10					15	
Ser	Pro	Pro	Glu	Pro	Pro	Gly	Tyr	Phe	Val	Cys	Met	Tyr	Cys	Asp	Arg
			20					25					30		
Lys	Phe	Phe	Ser	Ser	Gln	Ala	Leu	Gly	Gly	His	Gln	Asn	Ala	His	Lys
			35				40					45			
Tyr	Glu	Arg	Xaa	Trp	Pro	Ser	Ala	Ala	Gly	Arg					
	50					55									

(2) INFORMATION FOR SEQ ID NO:1463:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1500372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1463:

Met	Gly	Ser	Arg	Asp	Val	Pro	Ala	Arg	Pro	Gln	Gly	Thr	Gly	Thr	Gly
1					5				10					15	
Val	Val	Val	Val	Glu	Asp	Glu	Ser	Ala	Thr	Arg	Met	Met	Gly	Gln	Ala
				20				25					30		
Glu	Gly	Ser	Ser	Cys	Cys										
				35											

(2) INFORMATION FOR SEQ ID NO:1464:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..50
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1464:

Met	Thr	Xaa	Ser	Arg	Asp	Arg	Val	Val	Glu	Gln	His	Glu	Glu	Val	Val
1			5						10					15	
Gly	Val	Arg	Leu	Arg	Arg	Arg	Gly	Ala	Gly	Ser	Leu	Pro	Gln	Ala	Leu
			20					25					30		
Ile	Gly	Ser	Ser	Ser	Ser	Ser	Xaa	Xaa	Xaa	Tyr	Asn	Ser	Pro	Arg	Xaa
		35					40						45		
Xaa	Arg														
	50														

(2) INFORMATION FOR SEQ ID NO:1465:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..380
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1465:

aaaatagagt	tcacacgcac	aaccgcgcgc	cgcacgcgcg	gatctcgata	gactctggct	60
gccgcggaaa	gcggaaagaa	ggcagggatc	gtggccaaga	tgcagatctt	cgtgaagacg	120
ctgtcgtcga	caaggacgat	cacgctggag	gttgagcctt	cggacacggt	ggcggacgtr	180
aaggccaagg	tgtacgagtc	ggagggcgtc	ccgtacacct	tggccttcca	gaactagagc	240
gcggcagata	gctaggtcgc	ttcgtactcc	ccccatttgc	aatgacaaa	cgtttttacc	300
tttctagata	tgcacttatg	tctagataca	tagattatct	tatacttttd	wcgttctktt	360
ttatttatcg	tgttttagtt					

(2) INFORMATION FOR SEQ ID NO:1466:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1466:

Asn	Arg	Val	His	Thr	His	Asn	Pro	Pro	Pro	His	Ala	Gly	Ile	Ser	Ile
1			5						10					15	
Asp	Ser	Gly	Cys	Arg	Gly	Lys	Arg	Lys	Glu	Gly	Arg	Asp	Arg	Gly	Gln
			20					25				30			
Asp	Ala	Asp	Leu	Arg	Glu	Asp	Ala	Val	Val	Asp	Lys	Asp	Asp	His	Ala
			35				40				45				
Gly	Gly														
	50														

(2) INFORMATION FOR SEQ ID NO:1467:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1500376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1467:

```
Met Gln Ile Phe Val Lys Thr Leu Ser Ser Thr Arg Thr Ile Thr Leu
1           5           10           15
Glu Val Glu Pro Ser Asp Thr Val Ala Asp Xaa Lys Ala Lys Val Tyr
20           25           30
Glu Ser Glu Gly Val Pro Tyr Thr Leu Ala Phe Gln Asn
35           40           45
```

(2) INFORMATION FOR SEQ ID NO:1468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..33

(D) OTHER INFORMATION: / Ceres Seq. ID 1500377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1468:

```
Met Thr Lys Arg Phe Tyr Leu Ser Arg Tyr Ala Leu Met Ser Arg Tyr
1           5           10           15
Ile Asp Tyr Leu Ile Leu Xaa Xaa Phe Xaa Phe Ile Tyr Arg Val Leu
20           25           30
Val
```

(2) INFORMATION FOR SEQ ID NO:1469:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1326 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1326

(D) OTHER INFORMATION: / Ceres Seq. ID 1500387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1469:

```
aaaaaaccaa atcgaagatc tttgaaagtt tccttttttc cgaaatctga gcttgggtat 60
tggttgataa gcttctcgga gattgagatt gaggattttg ataggtgagg agattgaaag 120
atttgatttt ttgggcggca aaaatggtga tgcagacgga agctagggtt ggtgtgagct 180
caggacatgg cgtagcttcg tcttctcatc gtttaacgca ggaccagaga tcacatatcg 240
aatcggcgtc gcagctctta gccggaggac tcgctggtgc ttttagcaag acttgtactg 300
ctcctctatc tcgtctcacc attctcttcc aggtgcaagg tatgcacaca aatgctgcag 360
ctttaagaaa gccaaagcata ttacacgagg cttcacggat attgaatgaa gaaggattga 420
aagctttttg gaaagggaaat ctagtacta ttgctcaccg gcttccatat tcttctgtta 480
atttctacgc atatgaacac tacaagaagt tcatgtatat ggttactggg atggaaaatc 540
acaaggagag tataagttca aacctttttg tacattttgt agccggtggt ttggctggaa 600
tcacagctgc ttctgccact tatccacttg atcttgtag aactcgtctt gctgctcaga 660
caaaagtaat ctactactcg ggtatctggc atactctgcg ctctattaca accgatgaag 720
gtatcttggg cctctacaag ggactaggaa caacgcttgt ggtgtttggg cctagtattg 780
ccattagctt ttctgtgtat gaatcattga gatcttattg gaggtcaact aggcccatg 840
attcccctat catggtcagt ctagcttggt gaagtctttc aggaatagca tcttcaacag 900
ctacgtttcc attggatctg gtgagaagaa cgaagcagct ggaaggaata ggcgggag 960
cggtagtgtg caagacaggt ttgttaggca cattaaagcg tattgttcaa acggaaggag 1020
cgagaggcct gtacagagga attcttccag agtactacaa agtggtacct ggtgtaggga 1080
tttgcttcat gacctacgag acactcaagc tttacttcaa ggatctttct tcgaatctat 1140
aacggtttta aaggttggtg gatttggtta ggtctatttt tgggtgagagg aaaaaaactg 1200
```

taaaaaccaa acagcggaaa atgataatgt atacgaaatg tagaattata tatgtagttg 1260
ttggatgtag cttatacgag attaacattt gtattggtac aatccttttc cattgttaca 1320
tggctt

(2) INFORMATION FOR SEQ ID NO:1470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..332
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1470:

Met	Val	Met	Gln	Thr	Glu	Ala	Arg	Val	Gly	Val	Ser	Ser	Gly	His	Gly
1			5						10					15	
Val	Ala	Ser	Ser	Ser	His	Arg	Leu	Thr	Gln	Asp	Gln	Arg	Ser	His	Ile
			20					25					30		
Glu	Ser	Ala	Ser	Gln	Leu	Leu	Ala	Gly	Gly	Leu	Ala	Gly	Ala	Phe	Ser
		35					40					45			
Lys	Thr	Cys	Thr	Ala	Pro	Leu	Ser	Arg	Leu	Thr	Ile	Leu	Phe	Gln	Val
	50					55					60				
Gln	Gly	Met	His	Thr	Asn	Ala	Ala	Ala	Leu	Arg	Lys	Pro	Ser	Ile	Leu
65					70					75				80	
His	Glu	Ala	Ser	Arg	Ile	Leu	Asn	Glu	Glu	Gly	Leu	Lys	Ala	Phe	Trp
			85						90					95	
Lys	Gly	Asn	Leu	Val	Thr	Ile	Ala	His	Arg	Leu	Pro	Tyr	Ser	Ser	Val
		100						105					110		
Asn	Phe	Tyr	Ala	Tyr	Glu	His	Tyr	Lys	Lys	Phe	Met	Tyr	Met	Val	Thr
		115					120					125			
Gly	Met	Glu	Asn	His	Lys	Glu	Ser	Ile	Ser	Ser	Asn	Leu	Phe	Val	His
	130					135					140				
Phe	Val	Ala	Gly	Gly	Leu	Ala	Gly	Ile	Thr	Ala	Ala	Ser	Ala	Thr	Tyr
145					150					155				160	
Pro	Leu	Asp	Leu	Val	Arg	Thr	Arg	Leu	Ala	Ala	Gln	Thr	Lys	Val	Ile
			165						170					175	
Tyr	Tyr	Ser	Gly	Ile	Trp	His	Thr	Leu	Arg	Ser	Ile	Thr	Thr	Asp	Glu
		180						185					190		
Gly	Ile	Leu	Gly	Leu	Tyr	Lys	Gly	Leu	Gly	Thr	Thr	Leu	Val	Gly	Val
	195					200						205			
Gly	Pro	Ser	Ile	Ala	Ile	Ser	Phe	Ser	Val	Tyr	Glu	Ser	Leu	Arg	Ser
	210					215					220				
Tyr	Trp	Arg	Ser	Thr	Arg	Pro	His	Asp	Ser	Pro	Ile	Met	Val	Ser	Leu
225				230						235				240	
Ala	Cys	Gly	Ser	Leu	Ser	Gly	Ile	Ala	Ser	Ser	Thr	Ala	Thr	Phe	Pro
			245						250					255	
Leu	Asp	Leu	Val	Arg	Arg	Thr	Lys	Gln	Leu	Glu	Gly	Ile	Gly	Gly	Arg
		260						265					270		
Ala	Val	Val	Tyr	Lys	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Lys	Arg	Ile	Val
		275					280					285			
Gln	Thr	Glu	Gly	Ala	Arg	Gly	Leu	Tyr	Arg	Gly	Ile	Leu	Pro	Glu	Tyr
	290					295					300				
Tyr	Lys	Val	Val	Pro	Gly	Val	Gly	Ile	Cys	Phe	Met	Thr	Tyr	Glu	Thr
305				310						315				320	
Leu	Lys	Leu	Tyr	Phe	Lys	Asp	Leu	Ser	Ser	Asn	Leu				
			325						330						

(2) INFORMATION FOR SEQ ID NO:1471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..330
(D) OTHER INFORMATION: / Ceres Seq. ID 1500389
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1471:

Met	Gln	Thr	Glu	Ala	Arg	Val	Gly	Val	Ser	Ser	Gly	His	Gly	Val	Ala
1				5				10						15	
Ser	Ser	Ser	His	Arg	Leu	Thr	Gln	Asp	Gln	Arg	Ser	His	Ile	Glu	Ser
			20					25					30		
Ala	Ser	Gln	Leu	Leu	Ala	Gly	Gly	Leu	Ala	Gly	Ala	Phe	Ser	Lys	Thr
		35					40					45			
Cys	Thr	Ala	Pro	Leu	Ser	Arg	Leu	Thr	Ile	Leu	Phe	Gln	Val	Gln	Gly
	50					55					60				
Met	His	Thr	Asn	Ala	Ala	Leu	Arg	Lys	Pro	Ser	Ile	Leu	His	Glu	
65				70				75						80	
Ala	Ser	Arg	Ile	Leu	Asn	Glu	Glu	Gly	Leu	Lys	Ala	Phe	Trp	Lys	Gly
			85					90						95	
Asn	Leu	Val	Thr	Ile	Ala	His	Arg	Leu	Pro	Tyr	Ser	Ser	Val	Asn	Phe
		100						105					110		
Tyr	Ala	Tyr	Glu	His	Tyr	Lys	Lys	Phe	Met	Tyr	Met	Val	Thr	Gly	Met
		115					120					125			
Glu	Asn	His	Lys	Glu	Ser	Ile	Ser	Ser	Asn	Leu	Phe	Val	His	Phe	Val
	130					135					140				
Ala	Gly	Gly	Leu	Ala	Gly	Ile	Thr	Ala	Ala	Ser	Ala	Thr	Tyr	Pro	Leu
145				150						155					160
Asp	Leu	Val	Arg	Thr	Arg	Leu	Ala	Ala	Gln	Thr	Lys	Val	Ile	Tyr	Tyr
			165					170						175	
Ser	Gly	Ile	Trp	His	Thr	Leu	Arg	Ser	Ile	Thr	Thr	Asp	Glu	Gly	Ile
		180						185					190		
Leu	Gly	Leu	Tyr	Lys	Gly	Leu	Gly	Thr	Thr	Leu	Val	Gly	Val	Gly	Pro
		195					200					205			
Ser	Ile	Ala	Ile	Ser	Phe	Ser	Val	Tyr	Glu	Ser	Leu	Arg	Ser	Tyr	Trp
	210					215					220				
Arg	Ser	Thr	Arg	Pro	His	Asp	Ser	Pro	Ile	Met	Val	Ser	Leu	Ala	Cys
225				230						235					240
Gly	Ser	Leu	Ser	Gly	Ile	Ala	Ser	Ser	Thr	Ala	Thr	Phe	Pro	Leu	Asp
			245						250					255	
Leu	Val	Arg	Arg	Thr	Lys	Gln	Leu	Glu	Gly	Ile	Gly	Gly	Arg	Ala	Val
		260						265					270		
Val	Tyr	Lys	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Lys	Arg	Ile	Val	Gln	Thr
		275					280					285			
Glu	Gly	Ala	Arg	Gly	Leu	Tyr	Arg	Gly	Ile	Leu	Pro	Glu	Tyr	Tyr	Lys
	290					295					300				
Val	Val	Pro	Gly	Val	Gly	Ile	Cys	Phe	Met	Thr	Tyr	Glu	Thr	Leu	Lys
305				310						315					320
Leu	Tyr	Phe	Lys	Asp	Leu	Ser	Ser	Asn	Leu						
			325					330							

(2) INFORMATION FOR SEQ ID NO:1472:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 266 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..266
(D) OTHER INFORMATION: / Ceres Seq. ID 1500390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1472:

Met	His	Thr	Asn	Ala	Ala	Ala	Leu	Arg	Lys	Pro	Ser	Ile	Leu	His	Glu
1			5						10				15		
Ala	Ser	Arg	Ile	Leu	Asn	Glu	Glu	Gly	Leu	Lys	Ala	Phe	Trp	Lys	Gly
		20					25						30		
Asn	Leu	Val	Thr	Ile	Ala	His	Arg	Leu	Pro	Tyr	Ser	Ser	Val	Asn	Phe
		35					40					45			
Tyr	Ala	Tyr	Glu	His	Tyr	Lys	Lys	Phe	Met	Tyr	Met	Val	Thr	Gly	Met
	50					55					60				
Glu	Asn	His	Lys	Glu	Ser	Ile	Ser	Ser	Asn	Leu	Phe	Val	His	Phe	Val
65					70					75					80
Ala	Gly	Gly	Leu	Ala	Gly	Ile	Thr	Ala	Ala	Ser	Ala	Thr	Tyr	Pro	Leu
			85					90						95	
Asp	Leu	Val	Arg	Thr	Arg	Leu	Ala	Ala	Gln	Thr	Lys	Val	Ile	Tyr	Tyr
			100				105						110		
Ser	Gly	Ile	Trp	His	Thr	Leu	Arg	Ser	Ile	Thr	Thr	Asp	Glu	Gly	Ile
		115					120					125			
Leu	Gly	Leu	Tyr	Lys	Gly	Leu	Gly	Thr	Thr	Leu	Val	Gly	Val	Gly	Pro
	130					135					140				
Ser	Ile	Ala	Ile	Ser	Phe	Ser	Val	Tyr	Glu	Ser	Leu	Arg	Ser	Tyr	Trp
145					150					155					160
Arg	Ser	Thr	Arg	Pro	His	Asp	Ser	Pro	Ile	Met	Val	Ser	Leu	Ala	Cys
				165					170					175	
Gly	Ser	Leu	Ser	Gly	Ile	Ala	Ser	Ser	Thr	Ala	Thr	Phe	Pro	Leu	Asp
			180					185					190		
Leu	Val	Arg	Arg	Thr	Lys	Gln	Leu	Glu	Gly	Ile	Gly	Gly	Arg	Ala	Val
	195						200					205			
Val	Tyr	Lys	Thr	Gly	Leu	Leu	Gly	Thr	Leu	Lys	Arg	Ile	Val	Gln	Thr
	210					215					220				
Glu	Gly	Ala	Arg	Gly	Leu	Tyr	Arg	Gly	Ile	Leu	Pro	Glu	Tyr	Tyr	Lys
225					230					235					240
Val	Val	Pro	Gly	Val	Gly	Ile	Cys	Phe	Met	Thr	Tyr	Glu	Thr	Leu	Lys
				245					250					255	
Leu	Tyr	Phe	Lys	Asp	Leu	Ser	Ser	Asn	Leu						
			260					265							

(2) INFORMATION FOR SEQ ID NO:1473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 686 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..686
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1473:

tcccaagtga	taatgcaagt	aatgaaatgg	aaaggcgtcc	accccggaag	cgaaagtttc	60
aggaacttcc	agctgattgt	aaggttccag	aaaaagacaa	acagcaatcg	gagttagcaa	120
tgacaggtga	tgttactcca	tcagcaaata	gagtgcggtc	gccgccttca	ccaagatctg	180
taatgcctcc	tcctccacca	aagaccatcg	caccaccgcc	ttctaagacc	atgtctctctc	240
catcatcaaa	aagcatgctt	cctccaccac	cacgttctaa	gaccatgtct	cctctaacat	300
caaaaagcat	gcttcctcca	ccaccgcgat	ttacactgac	aactcaacct	tcaagattac	360
aggacaacca	catcagtgtg	aagaaaccaa	atccagttcc	agatacggtg	ataaagctga	420
tggaatatgg	agacgatgaa	gacgatgatg	acgatcctga	tgagccattg	acaactagat	480
cgtgacagtg	tattagatta	cagaaccttc	ttatctggca	acaaaatgtc	aatttgtgtt	540
tgtaacaata	gaaagaaatg	ttggtctctt	actgatttgg	aacttcattg	cctaaggcta	600
ttagttaaat	atttaagaca	ttagctactt	gttttgcaag	gcactgctcg	ttttgttgta	660
tttcttatca	ttaatacata	atggtt				

(2) INFORMATION FOR SEQ ID NO:1474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..160
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500392
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1474:

```
Pro Ser Asp Asn Ala Ser Asn Glu Met Glu Arg Arg Pro Pro Arg Lys
1          5          10          15
Arg Lys Phe Gln Glu Leu Pro Ala Asp Cys Lys Val Pro Glu Lys Asp
          20          25          30
Lys Gln Gln Ser Glu Leu Ala Met Thr Gly Asp Val Thr Pro Ser Ala
          35          40          45
Asn Arg Val Arg Ser Pro Pro Ser Pro Arg Ser Val Met Pro Pro Pro
          50          55          60
Pro Pro Lys Thr Ile Ala Pro Pro Pro Ser Lys Thr Met Ser Pro Pro
65          70          75          80
Ser Ser Lys Ser Met Leu Pro Pro Pro Pro Arg Ser Lys Thr Met Ser
          85          90          95
Pro Leu Thr Ser Lys Ser Met Leu Pro Pro Pro Pro Arg Phe Thr Leu
          100          105          110
Thr Thr Gln Pro Ser Arg Leu Gln Asp Asn His Ile Ser Val Lys Lys
          115          120          125
Pro Asn Pro Val Pro Asp Thr Leu Ile Lys Leu Met Glu Tyr Gly Asp
          130          135          140
Asp Glu Asp Asp Asp Asp Asp Pro Asp Glu Pro Leu Thr Thr Arg Ser
145          150          155          160
```

(2) INFORMATION FOR SEQ ID NO:1475:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..152
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500393
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1475:

```
Met Glu Arg Arg Pro Pro Arg Lys Arg Lys Phe Gln Glu Leu Pro Ala
1          5          10          15
Asp Cys Lys Val Pro Glu Lys Asp Lys Gln Gln Ser Glu Leu Ala Met
          20          25          30
Thr Gly Asp Val Thr Pro Ser Ala Asn Arg Val Arg Ser Pro Pro Ser
          35          40          45
Pro Arg Ser Val Met Pro Pro Pro Pro Pro Lys Thr Ile Ala Pro Pro
          50          55          60
Pro Ser Lys Thr Met Ser Pro Pro Ser Ser Lys Ser Met Leu Pro Pro
65          70          75          80
Pro Pro Arg Ser Lys Thr Met Ser Pro Leu Thr Ser Lys Ser Met Leu
          85          90          95
Pro Pro Pro Pro Arg Phe Thr Leu Thr Thr Gln Pro Ser Arg Leu Gln
          100          105          110
Asp Asn His Ile Ser Val Lys Lys Pro Asn Pro Val Pro Asp Thr Leu
          115          120          125
Ile Lys Leu Met Glu Tyr Gly Asp Asp Glu Asp Asp Asp Asp Pro
```

130 135 140
Asp Glu Pro Leu Thr Thr Arg Ser
145 150
(2) INFORMATION FOR SEQ ID NO:1476:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..121
(D) OTHER INFORMATION: / Ceres Seq. ID 1500394
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1476:
Met Thr Gly Asp Val Thr Pro Ser Ala Asn Arg Val Arg Ser Pro Pro
1 5 10 15
Ser Pro Arg Ser Val Met Pro Pro Pro Pro Pro Lys Thr Ile Ala Pro
20 25 30
Pro Pro Ser Lys Thr Met Ser Pro Pro Ser Ser Lys Ser Met Leu Pro
35 40 45
Pro Pro Pro Arg Ser Lys Thr Met Ser Pro Leu Thr Ser Lys Ser Met
50 55 60
Leu Pro Pro Pro Pro Arg Phe Thr Leu Thr Thr Gln Pro Ser Arg Leu
65 70 75 80
Gln Asp Asn His Ile Ser Val Lys Lys Pro Asn Pro Val Pro Asp Thr
85 90 95
Leu Ile Lys Leu Met Glu Tyr Gly Asp Asp Glu Asp Asp Asp Asp Asp
100 105 110
Pro Asp Glu Pro Leu Thr Thr Arg Ser
115 120

(2) INFORMATION FOR SEQ ID NO:1477:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..441
(D) OTHER INFORMATION: / Ceres Seq. ID 1500395
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1477:
ccagacttta ttccccaaaa accaaaataa tcgccaccgc tctccgcacg gaaccgaagc 60
ggcggcgatg gcggcggaga agccgggctcc cgtgcgcgtg ctctactgcg gcgtctgcgg 120
cctcccggcc gagtactgcg agttcggccc cgacttcgag cgctgcaagc cctggctgcg 180
cgcgcatgns ccggcgtcta ccccgcacgaa cttgtcgccg cmtcctcctc ctcateccgcm 240
ggcggcgaca aggacgtcga cagggtcggg gatcgccctcc agggcgctcg gatctccgac 300
ggctccacca gcgcgcagc gatgcttccg cgtctaagcc ccaagaggcg aaacgcctgc 360
mtggtggtaa gctcaagaaa aaggagaagc aagaagtggc cattgagaag attgtccgta 420
acaagcgcaa atgtgttact g

(2) INFORMATION FOR SEQ ID NO:1478:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1500396

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1478:

Gln	Thr	Leu	Phe	Pro	Lys	Asn	Gln	Asn	Asn	Arg	His	Arg	Ser	Pro	His
1				5					10					15	
Gly	Thr	Glu	Ala	Ala	Ala	Met	Ala	Ala	Glu	Lys	Pro	Ala	Pro	Val	Arg
			20					25					30		
Val	Leu	Tyr	Cys	Gly	Val	Cys	Gly	Leu	Pro	Ala	Glu	Tyr	Cys	Glu	Phe
		35				40					45				
Gly	Pro	Asp	Phe	Glu	Arg	Cys	Lys	Pro	Trp	Leu	Arg	Ala	His	Xaa	Pro
	50					55					60				
Ala	Ser	Thr	Pro	Thr	Asn	Leu	Ser	Pro	Xaa	Pro	Pro	Pro	His	Pro	Xaa
65					70					75				80	
Ala	Ala	Thr	Arg	Thr	Ser	Thr	Gly	Ser	Gly	Ile	Ala	Ser	Arg	Ala	Ser
			85					90						95	
Gly	Ser	Pro	Thr	Ala	Pro	Pro	Ala	Pro	Gln	Gly	Cys	Phe	Arg	Val	
		100						105						110	

(2) INFORMATION FOR SEQ ID NO:1479:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1500397

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1479:

Arg	Leu	Tyr	Ser	Pro	Lys	Thr	Lys	Ile	Ile	Ala	Thr	Ala	Leu	Arg	Thr
1				5					10					15	
Glu	Pro	Lys	Arg	Arg	Arg	Trp	Arg	Arg	Arg	Ser	Arg	Leu	Pro	Cys	Ala
			20					25					30		
Cys	Ser	Thr	Ala	Ala	Ser	Ala	Ala	Ser	Arg	Pro	Ser	Thr	Ala	Ser	Ser
		35				40						45			
Ala	Pro	Thr	Ser	Ser	Ala	Ala	Ser	Pro	Gly	Cys	Ala	Arg	Met	Xaa	Arg
	50					55					60				
Arg	Leu	Pro	Arg	Arg	Thr	Cys	Arg	Arg	Xaa	Leu	Leu	Ile	Arg	Xaa	
65					70					75				80	
Arg	Arg	Gln	Gly	Arg	Arg	Gln	Gly	Arg	Gly	Ser	Pro	Pro	Gly	Arg	Arg
			85					90						95	
Asp	Leu	Arg	Arg	Leu	His	Gln	Arg	Arg	Arg	Asp	Ala	Ser	Ala	Ser	Lys
		100						105					110		
Pro	Gln	Glu	Ala	Lys	Arg	Leu	Xaa	Gly	Gly	Lys	Leu	Lys	Lys	Lys	Glu
		115					120						125		
Lys	Gln	Glu	Val	Val	Ile	Glu	Lys	Ile	Val	Arg	Asn	Lys	Arg	Lys	Cys
	130					135					140				
Val	Thr														
145															

(2) INFORMATION FOR SEQ ID NO:1480:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1500398

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1480:

Met Ala Ala Glu Lys Pro Ala Pro Val Arg Val Leu Tyr Cys Gly Val

1 5 10 15
Cys Gly Leu Pro Ala Glu Tyr Cys Glu Phe Gly Pro Asp Phe Glu Arg
20 25 30
Cys Lys Pro Trp Leu Arg Ala His Xaa Pro Ala Ser Thr Pro Thr Asn
35 40 45
Leu Ser Pro Xaa Pro Pro Pro His Pro Xaa Ala Ala Thr Arg Thr Ser
50 55 60
Thr Gly Ser Gly Ile Ala Ser Arg Ala Ser Gly Ser Pro Thr Ala Pro
65 70 75 80
Pro Ala Pro Gln Gly Cys Phe Arg Val
85

(2) INFORMATION FOR SEQ ID NO:1481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..431
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1481:

atccctccct	ccctcatcgc	gttttattat	tcccgtcctt	cttcattcgg	cccttcgcgc	60
ctgctatatt	tcgcggccgc	cttgccctcct	aataatagcm	gccgcggcag	tggataccgc	120
caccgccatg	ggagcgctcg	aggaggccca	cctcgcggcc	gccgcgtgcg	cgtgcgagga	180
ggaggaggaa	agcgactaca	tcggcctcct	cgcaggggaa	gcggcggcgg	gcgacgccgt	240
ggagccggcc	gtgcgcgccc	tgctgctggg	gctcggtag	gacgaccgcc	gcgarggcct	300
gctccggacg	cccaagcgcg	tcgccaaggc	cttccgcgac	ggcaccgag	gctacaggca	360
aaaagtaaaa	gacatagtgc	aagggtgctct	gtttccarag	gttggtgtgg	ataaaaggac	420
tggatctgct	g					

(2) INFORMATION FOR SEQ ID NO:1482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1482:

Ile Pro Pro Ser Leu Ile Ala Phe Tyr Tyr Ser Arg Pro Ser Ser Phe
1 5 10 15
Gly Pro Ser Pro Leu Leu Tyr Phe Ala Ala Ala Leu Pro Pro Asn Asn
20 25 30
Ser Xaa Arg Gly Ser Gly Tyr Arg His Arg His Gly Ser Ala Arg Gly
35 40 45
Gly Pro Pro Arg Gly Arg Arg Val Arg Val Arg Gly Gly Gly Gly Lys
50 55 60
Arg Leu His Arg Pro Pro Arg Arg Gly Ser Gly Gly Gly Arg Arg Arg
65 70 75 80
Gly Ala Gly Arg Ala Arg Pro Ala Ala Gly Ala Arg
85 90

(2) INFORMATION FOR SEQ ID NO:1483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1500409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1483:

```
Ser Leu Pro Pro Ser Ser Arg Phe Ile Ile Pro Val Leu Leu His Ser
1          5          10          15
Ala Leu Arg Arg Cys Tyr Ile Ser Arg Pro Pro Cys Leu Leu Ile Ile
20          25          30
Xaa Ala Ala Val Asp Thr Ala Thr Ala Met Gly Ala Leu Glu Glu
35          40          45
Ala His Leu Ala Ala Ala Ala Cys Ala Cys Glu Glu Glu Glu Ser
50          55          60
Asp Tyr Ile Gly Leu Leu Ala Gly Glu Ala Ala Ala Gly Asp Ala Val
65          70          75          80
Glu Pro Ala Val Arg Ala Leu Leu Leu Gly Leu Gly Glu Asp Asp Arg
85          90          95
Arg Xaa Gly Leu Leu Arg Thr Pro Lys Arg Val Ala Lys Ala Phe Arg
100          105          110
Asp Gly Thr Arg Gly Tyr Arg Gln Lys Val Lys Asp Ile Val Gln Gly
115          120          125
Ala Leu Phe Pro Xaa Val Gly Val Asp Lys Arg Thr Gly Ser Ala
130          135          140
```

(2) INFORMATION FOR SEQ ID NO:1484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1500410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1484:

```
Met Gly Ala Leu Glu Glu Ala His Leu Ala Ala Ala Cys Ala Cys
1          5          10          15
Glu Glu Glu Glu Glu Ser Asp Tyr Ile Gly Leu Leu Ala Gly Glu Ala
20          25          30
Ala Ala Gly Asp Ala Val Glu Pro Ala Val Arg Ala Leu Leu Leu Gly
35          40          45
Leu Gly Glu Asp Asp Arg Arg Xaa Gly Leu Leu Arg Thr Pro Lys Arg
50          55          60
Val Ala Lys Ala Phe Arg Asp Gly Thr Arg Gly Tyr Arg Gln Lys Val
65          70          75          80
Lys Asp Ile Val Gln Gly Ala Leu Phe Pro Xaa Val Gly Val Asp Lys
85          90          95
Arg Thr Gly Ser Ala
100
```

(2) INFORMATION FOR SEQ ID NO:1485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 470 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..470

(D) OTHER INFORMATION: / Ceres Seq. ID 1500422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1485:

agcaaacccct	agcgcannc	anccacccac	ccactcgctt	cagcgcctc	cgcgcgcggt	60
acaagcaggt	ggagacagga	tgccggctgg	ccacggcctg	cgctcgcgga	cgcgcgacct	120
cttcgcgcgc	cccttcgcga	agaagggtta	catccgcgtc	accacctacc	tccgcacctta	180
caagatcggc	gattacgtcg	atgtcaaggt	gaacggcgcc	gtccacaagg	ggatgccgca	240
caagttctac	cacggccgca	ccggtcgcgt	ctggaacgtc	accaagcgcg	ccatcggcgt	300
cgaggtcaac	aagcaggtag	acaacgcgga	tccttttttc	gcagaggcaa	ttacgattag	360
tcgcgtggcg	catcttttga	tcgtttcatt	ctaggaaatg	taacgsttta	atatagaatg	420
gsggctatatt	gctgacggtg	ttgtttgatt	tqattttata	qaattttgac		

(2) INFORMATION FOR SEQ ID NO:1486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..130
(D) OTHER INFORMATION: / Ceres Seq. ID 1500423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1486:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..69
(D) OTHER INFORMATION: / Ceres Seq. ID 1500424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1487:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1500425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1488:

Met	Pro	Ala	Gly	His	Gly	Leu	Arg	Ser	Arg	Thr	Arg	Asp	Leu	Phe	Ala
1				5					10					15	
Arg	Pro	Phe	Arg	Lys	Lys	Gly	Tyr	Ile	Pro	Leu	Thr	Thr	Tyr	Leu	Arg
			20				25						30		
Thr	Tyr	Lys	Ile	Gly	Asp	Tyr	Val	Asp	Val	Lys	Val	Asn	Gly	Ala	Val
		35				40						45			
His	Lys	Gly	Met	Pro	His	Lys	Phe	Tyr	His	Gly	Arg	Thr	Gly	Arg	Val
	50					55				60					
Trp	Asn	Val	Thr	Lys	Arg	Ala	Ile	Gly	Val	Glu	Val	Asn	Lys	Gln	Val
65				70						75				80	
Asp	Asn	Ala	Asp	Pro	Phe	Phe	Ala	Glu	Ala	Ile	Thr	Ile	Ser	Ala	Leu
			85					90						95	
Ala	His	Leu	Leu	Ile	Val	Ser	Phe								
			100												

(2) INFORMATION FOR SEQ ID NO:1489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1500464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1489:

aatcggaaaca	attccgcgtt	gccatccat	cccggaata	tccccaagga	aaccctcgcc	60
cccctccttc	cccgccgccc	gtcgccagat	ctccggtcat	ggacgacgac	ggcggggcct	120
cccggtcgcc	ctcgccgtcc	ccgtcgcgt	ctccgtcccc	gctccccgtg	gccgaccccg	180
tcacggtcgc	ngcggcgccc	cccggccacg	tcgcccgtgc	tatccccctc	cgcaagcact	240
cgcccttcctc	cggcggcgcc	ggcggcgggc	gcggccggna	gggacgattg	ggagcgacgg	300
cgccacctcc	acgtcatcg	acgcctgggg	ggagcgcttc	gtggcgctgg	gccggggcag	360
cctccgccac	ccgcagtggc	aggaggctgc	cgaggctgct	tcctctcgcg	acagytactc	420
caaggcgccc	caaatccgac	gtcccagtgc	aag			

(2) INFORMATION FOR SEQ ID NO:1490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1500465

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1490:

Asn	Arg	Asn	Asn	Ser	Ala	Leu	Pro	Ile	His	Pro	Gly	Asn	Ile	Pro	Lys
1				5				10				15			
Glu	Thr	Leu	Ala	Pro	Leu	Leu	Pro	Arg	Arg	Arg	Ser	Pro	Asp	Leu	Arg

[illegible]

(2) INFORMATION FOR SEQ ID NO:1491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..150
(D) OTHER INFORMATION: / Ceres Seq. ID 1500466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1491:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..150
(D) OTHER INFORMATION: / Ceres Seq. ID 1500467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1492:

Ser Glu Gln Phe Arg Val Ala His Pro Ser Arg Lys Tyr Pro Gln Gly
1 5 10 15
Asn Pro Arg Pro Pro Pro Ser Pro Pro Pro Val Ala Arg Ser Pro Val
20 25 30
Met Asp Asp Asp Gly Gly Ala Ser Arg Ser Pro Ser Ser Pro Ser
35 40 45
Arg Ser Pro Ser Pro Leu Pro Val Ala Asp Pro Val Thr Val Xaa Ala
50 55 60
Ala Pro Pro Gly His Val Ala Val Ala Ile Pro Leu Arg Lys His Ser
65 70 75 80
Pro Ser Ser Gly Gly Gly Gly Gly Gly Arg Xaa Gly Arg Leu
85 90 95
Gly Ala Thr Ala Pro Pro Pro Arg Ser Ser Thr Pro Gly Gly Ser Ala
100 105 110
Ser Trp Arg Trp Ala Gly Ala Ala Ser Ala Thr Arg Ser Gly Arg Arg
115 120 125
Ser Pro Arg Ser Ser Pro Leu Ala Thr Xaa Thr Pro Arg Arg Pro Lys
130 135 140
Ser Asp Val Pro Val Gln
145 150

(2) INFORMATION FOR SEQ ID NO:1493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..654
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1493:

ggacctttct atcgcgcgca ttttctttcc gaccagccga vcgccgccgc cctccggcag	60
gtcttctttcc cggccacgac caccacgccc aggtctttccc ggccccgaac gcgagcaccc	120
agccctctctc caggtctttcc ccggcgacga gcgcgtagaa gaggggatcc ttagcacaat	180
ggaagaagga gcaccagggc cgtcgcaagc catcccggat tctggagaca cgtaccgcaa	240
cagctccacc gcgcccgtgg gcagcagctc accgtctgtc gcgaagctcc ggaagctgct	300
gttcggcgcg atgtctcatcg gcgtcaacga cggccgctac ttccacggcc tgttccactg	360
catcgacaag cagggcaaca tcatcctcca ggacgcgta gactaccgca gcgcccgcga	420
ctgctcgccct ccgacggagc agcgggtgcct ggggctcatc ctgatcccgg ccgcctgccg	480
gtcgtcgtgc caggtcgatt gctccgttga agagaagatg tcgctcctgt gttttgagtg	540
aatcgtgctt caaaggaat acactacgca tgtactaagt tactggggct catctctgct	600
atctgaaact gagaggcatg attggtgttt cctatttttg aaggattgtt tatt	

(2) INFORMATION FOR SEQ ID NO:1494:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1494:

Asp Leu Ser Ile Ala Arg Ile Phe Phe Pro Thr Ser Arg Xaa Pro Pro
1 5 10 15
Pro Ser Gly Arg Ser Ser Ser Arg Pro Arg Pro Pro Thr Pro Gly Leu
20 25 30
Pro Gly Pro Glu Arg Glu His Pro Ala Leu Leu Gln Val Phe Pro Gly
35 40 45

Asp Glu Arg Val Glu Glu Gly Ile Leu Ser Thr Met Glu Glu Gly Ala
50 55 60
Pro Gly Pro Ser Gln Ala Ile Pro Asp Ser Gly Asp Thr Tyr Arg Asn
65 70 75 80
Ser Ser Thr Ala Pro Val Gly Ser Ser Ser Pro Ser Val Ala Lys Leu
85 90 95
Arg Lys Leu Leu Phe Arg Arg Met Leu Ile Gly Val Asn Asp Gly Arg
100 105 110
Tyr Phe His Gly Leu Phe His Cys Ile Asp Lys Gln Gly Asn Ile Ile
115 120 125
Leu Gln Asp Ala Val Glu Tyr Arg Ser Ala Arg His Cys Ser Pro Pro
130 135 140
Thr Glu Gln Arg Cys Leu Gly Leu Ile Leu Ile Pro Ala Ala Cys Arg
145 150 155 160
Ser Ser Cys Gln Val Asp Cys Ser Val Glu Glu Lys Met Ser Leu Leu
165 170 175
Cys Phe Glu

(2) INFORMATION FOR SEQ ID NO:1495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1500470

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1495:

Met Glu Glu Gly Ala Pro Gly Pro Ser Gln Ala Ile Pro Asp Ser Gly
1 5 10 15
Asp Thr Tyr Arg Asn Ser Ser Thr Ala Pro Val Gly Ser Ser Ser Pro
20 25 30
Ser Val Ala Lys Leu Arg Lys Leu Leu Phe Arg Arg Met Leu Ile Gly
35 40 45
Val Asn Asp Gly Arg Tyr Phe His Gly Leu Phe His Cys Ile Asp Lys
50 55 60
Gln Gly Asn Ile Ile Leu Gln Asp Ala Val Glu Tyr Arg Ser Ala Arg
65 70 75 80
His Cys Ser Pro Pro Thr Glu Gln Arg Cys Leu Gly Leu Ile Leu Ile
85 90 95
Pro Ala Ala Cys Arg Ser Ser Cys Gln Val Asp Cys Ser Val Glu Glu
100 105 110
Lys Met Ser Leu Leu Cys Phe Glu
115 120

(2) INFORMATION FOR SEQ ID NO:1496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 410 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..410

(D) OTHER INFORMATION: / Ceres Seq. ID 1500474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1496:

gtgcttcaag aattgatccg ttgcggtgc gacctccagc tccaggagca gcaccaatcc 60
ccaagccgc catggccgc gacccacgc tgctgcttct cgtaccttcc ctcgccatcc 120
ccctctactt cttcttgcc accagacgta ggacgccacg cgggggcgcg cggctccgcg 180

cggggccggtg ggcgctgccc gtggtcgggc acctgcatca cctagcccgg ggccctcccg 240
accgcgtcat gcgcgamctg gcgargcgcc acggcccgt catgatgctc cggttcggcg 300
agggtcccggt ggtggtggcc tctcgccgg cmgcrgcgcg cgaggtgatg cggacccacg 360
acgcggcggtt crcgtcgcg cccatcggtc ccgtgtmccg gctctggttc

(2) INFORMATION FOR SEQ ID NO:1497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..74
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1497:

Val Leu Gln Glu Leu Ile Arg Ser Arg Cys Asp Leu Gln Leu Glu
1 5 10 15
Gln His Gln Ser Pro Lys Pro Pro Trp Pro Pro Thr Pro Arg Cys Cys
20 25 30
Phe Ser Tyr Leu Ser Ser Pro Ser Pro Ser Thr Ser Ser Trp Pro Pro
35 40 45
Asp Val Gly Arg His Ala Gly Ala Arg Gly Ser Arg Arg Gly Arg Gly
50 55 60
Arg Cys Pro Trp Ser Gly Thr Cys Ile Thr
65 70

(2) INFORMATION FOR SEQ ID NO:1498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1498:

Ala Ser Arg Ile Asp Pro Phe Ala Val Arg Pro Pro Ala Pro Gly Ala
1 5 10 15
Ala Pro Ile Pro Gln Ala Ala Met Ala Ala Asp Pro Thr Leu Leu Leu
20 25 30
Leu Val Pro Phe Leu Ala Ile Pro Leu Tyr Phe Phe Leu Ala Thr Arg
35 40 45
Arg Arg Thr Pro Arg Gly Gly Ala Arg Leu Pro Pro Gly Pro Trp Ala
50 55 60
Leu Pro Val Val Gly His Leu His His Leu Ala Arg Gly Leu Pro His
65 70 75 80
Arg Val Met Arg Xaa Leu Ala Xaa Arg His Gly Pro Leu Met Met Leu
85 90 95
Arg Phe Gly Glu Val Pro Val Val Val Ala Ser Ser Pro Xaa Xaa Ala
100 105 110
Arg Glu Val Met Arg Thr His Asp Ala Ala Phe Xaa Ser Arg Pro Ile
115 120 125
Gly Pro Val Xaa Arg Leu Trp Phe
130 135

(2) INFORMATION FOR SEQ ID NO:1499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1500477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1499:

```
Met Ala Ala Asp Pro Thr Leu Leu Leu Leu Val Pro Phe Leu Ala Ile
1      5      10      15
Pro Leu Tyr Phe Phe Leu Ala Thr Arg Arg Arg Thr Pro Arg Gly Gly
20      25      30
Ala Arg Leu Pro Pro Gly Pro Trp Ala Leu Pro Val Val Gly His Leu
35      40      45
His His Leu Ala Arg Gly Leu Pro His Arg Val Met Arg Xaa Leu Ala
50      55      60
Xaa Arg His Gly Pro Leu Met Met Leu Arg Phe Gly Glu Val Pro Val
65      70      75      80
Val Val Ala Ser Ser Pro Xaa Xaa Ala Arg Glu Val Met Arg Thr His
85      90      95
Asp Ala Ala Phe Xaa Ser Arg Pro Ile Gly Pro Val Xaa Arg Leu Trp
100      105      110
Phe
```

(2) INFORMATION FOR SEQ ID NO:1500:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..328
(D) OTHER INFORMATION: / Ceres Seq. ID 1500478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1500:

```
cagatcttat cccttcaggt tccaggcagc atccccagcc tgacgaagga attgaggacg      60
ctcgagctcg agctacgtca ggrtccaaca ccascagtgt tacgggaaca agaggacggt      120
cgtgctctac ccgtcgtctg gcgtgggcca cctgatcccg atgggtggagc tggccaagca      180
cctcttgccg cacggccacg gcgcgtctcat cgccgtggtc aaccgcgccg acascgagcg      240
cgtgtcggcc gcmgcggtkg agcgccctkc ggcggycaac ccggccatcg cgttccgcct      300
cctgccggtc ccggccagcc cggacgcc
```

(2) INFORMATION FOR SEQ ID NO:1501:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 1500479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1501:

```
Gln Ile Leu Ser Leu Pro Val Pro Gly Ser Ile Pro Ser Leu Thr Lys
1      5      10      15
Glu Leu Arg Thr Leu Glu Leu Glu Leu Arg Gln Xaa Pro Thr Pro Xaa
20      25      30
Trp Leu Arg Glu Gln Glu Asp Val Arg Ala Leu Pro Val Ala Gly Arg
35      40      45
Gly Pro Pro Asp Pro Asp Gly Gly Ala Gly Gln Ala Pro Leu Ala Pro
50      55      60
```

Arg Pro Arg Arg Ala His Arg Arg Gly Gln Pro Ala Arg Xaa Arg Arg
65 70 75 80
Arg Val Gly Arg Xaa Gly Xaa Ala Pro Xaa Gly Xaa Gln Pro Gly His
85 90 95
Arg Val Pro Pro Pro Ala Gly Pro Gly Gln Pro Gly Arg
100 105

(2) INFORMATION FOR SEQ ID NO:1502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1502:

Met Val Glu Leu Ala Lys His Leu Leu Arg His Gly His Gly Ala Leu
1 5 10 15
Ile Ala Val Val Asn Pro Pro Asp Xaa Asp Ala Val Ser Ala Xaa Ala
20 25 30
Xaa Glu Arg Leu Xaa Ala Xaa Asn Pro Ala Ile Ala Phe Arg Leu Leu
35 40 45
Pro Val Pro Ala Ser Pro Asp Ala
50 55

(2) INFORMATION FOR SEQ ID NO:1503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..531
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1503:

atcaaaactgc acagcttctc ctgcattgcc cttccaggaa tatccacctg gaataaacact 60
tgtacctatg aagagtagga cactagcgcc attccgtaca actaatcttg tggtagtacg 120
atcaaccaat ggtgctggtg gatctacatg ttctgatttt ttgcttcgg gggaagctct 180
gcttatagat cctggatgca gctctcaggt tcatgcagag cttgcagatc tcattgattc 240
ccttccaaaa aggttattag ttcttggttac acatcatcat caggatcaca ttgagggtct 300
ttcagtcgtt cagagatgca atcctgatgc tggtcttctg acacacccaaa gtacaatgga 360
tcgcattggg aaaggaactt ggcagattga ctacacttca gtaactgggt gtgaaaagat 420
atgcataggt gaccaagaac tacaagttgt ttttgcacct ggtcatacag atggtcatat 480
ggggcttctc catgtaaata ccaatacatt ggttggtgga gatcattgtg t

(2) INFORMATION FOR SEQ ID NO:1504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..176
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1504:

Ser Asn Cys Thr Ala Ser Pro Ala Leu Pro Phe Gln Glu Tyr Pro Pro
1 5 10 15

Gly	Ile	Thr	Leu	Val	Pro	Met	Lys	Ser	Arg	Thr	Leu	Ala	Pro	Phe	Arg	
			20					25					30			
Thr	Thr	Asn	Leu	Val	Val	Val	Arg	Ser	Thr	Asn	Gly	Ala	Gly	Gly	Ser	
		35					40					45				
Thr	Cys	Ser	Asp	Phe	Phe	Ala	Ser	Gly	Glu	Ala	Leu	Leu	Ile	Asp	Pro	
	50					55					60					
Gly	Cys	Ser	Ser	Gln	Val	His	Ala	Glu	Leu	Ala	Asp	Leu	Ile	Asp	Ser	
65					70					75					80	
Leu	Pro	Lys	Arg	Leu	Leu	Val	Leu	Val	Thr	His	His	His	Gln	Asp	His	
				85					90					95		
Ile	Glu	Gly	Leu	Ser	Val	Val	Gln	Arg	Cys	Asn	Pro	Asp	Ala	Val	Leu	
			100					105					110			
Leu	Thr	His	Gln	Ser	Thr	Met	Asp	Arg	Ile	Gly	Lys	Gly	Thr	Trp	Gln	
		115					120					125				
Ile	Asp	Tyr	Thr	Ser	Val	Thr	Gly	Gly	Glu	Lys	Ile	Cys	Ile	Gly	Asp	
	130					135					140					
Gln	Glu	Leu	Gln	Val	Val	Phe	Ala	Pro	Gly	His	Thr	Asp	Gly	His	Met	
145					150					155					160	
Gly	Leu	Leu	His	Val	Asn	Thr	Asn	Thr	Leu	Val	Val	Gly	Asp	His	Cys	
			165						170					175		

(2) INFORMATION FOR SEQ ID NO:1505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1500483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1505:

Met	Lys	Ser	Arg	Thr	Leu	Ala	Pro	Phe	Arg	Thr	Thr	Asn	Leu	Val	Val	
1				5					10					15		
Val	Arg	Ser	Thr	Asn	Gly	Ala	Gly	Gly	Ser	Thr	Cys	Ser	Asp	Phe	Phe	
		20						25					30			
Ala	Ser	Gly	Glu	Ala	Leu	Leu	Ile	Asp	Pro	Gly	Cys	Ser	Ser	Gln	Val	
	35						40					45				
His	Ala	Glu	Leu	Ala	Asp	Leu	Ile	Asp	Ser	Leu	Pro	Lys	Arg	Leu	Leu	
	50					55					60					
Val	Leu	Val	Thr	His	His	Gln	Asp	His	Ile	Glu	Gly	Leu	Ser	Val		
65				70					75					80		
Val	Gln	Arg	Cys	Asn	Pro	Asp	Ala	Val	Leu	Leu	Thr	His	Gln	Ser	Thr	
			85						90					95		
Met	Asp	Arg	Ile	Gly	Lys	Gly	Thr	Trp	Gln	Ile	Asp	Tyr	Thr	Ser	Val	
		100					105						110			
Thr	Gly	Gly	Glu	Lys	Ile	Cys	Ile	Gly	Asp	Gln	Glu	Leu	Gln	Val	Val	
		115					120					125				
Phe	Ala	Pro	Gly	His	Thr	Asp	Gly	His	Met	Gly	Leu	Leu	His	Val	Asn	
	130					135					140					
Thr	Asn	Thr	Leu	Val	Val	Gly	Asp	His	Cys							
145					150											

(2) INFORMATION FOR SEQ ID NO:1506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..555

(D) OTHER INFORMATION: / Ceres Seq. ID 1500487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1506:

gactccacgc	cgccagtcac	gaccacgccg	cgcctccgcc	tggaaccctt	tagccgagcg	60
gasaagggaa	gaaatgggga	aggggtacgg	cagcttcggc	aagcgccgga	acaagacgca	120
cacgctctgc	atccgctgcg	gcggccggcg	tggagcgggc	gcgtcaagaa	cccggatcta	180
aatcggggcg	ccagccccga	gagctccgac	gccgagtgac	atgagaagcg	agcgagcagc	240
agcagcagca	gccaccgcaa	aggctcaacg	acgacgacgt	ccgttggtgc	gacggcgccc	300
agcgcagcat	gccgctgtcg	tcttcgttcg	tatccacgta	cgtacgacgg	cccagctgac	360
ccgcttgcc	accggtccgt	tctgtgcgac	tggatggtcg	gtcggcgggc	gtcgcggcga	420
gggctttcgg	tacgtcgtgg	ataagcacga	ggggagggcg	ggcaggcggg	aacggaggcg	480
gaggcgggcg	ccccaaagtgg	cggctctttcc	aaatgtcaaa	aaggacagct	gtaacagtga	540
taagaaaaac	aagtc					

(2) INFORMATION FOR SEQ ID NO:1507:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1500488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1507:

Asp	Ser	Thr	Pro	Pro	Val	Thr	Thr	Thr	Thr	Arg	Leu	Arg	Leu	Glu	Pro
1			5						10					15	
Phe	Ser	Arg	Ala	Xaa	Lys	Gly	Arg	Asn	Gly	Glu	Gly	Tyr	Gly	Gln	Leu
			20					25					30		
Arg	Gln	Ala	Pro	Glu	Gln	Asp	Ala	His	Ala	Leu	His	Pro	Leu	Arg	Arg
			35				40					45			
Pro	Ala	Trp	Ser	Gly	Arg	Val	Lys	Asn	Pro	Asp	Leu	Asn	Arg	Ala	Pro
			50				55				60				
Ser	Pro	Glu	Ser	Ser	Asp	Ala	Glu								
65						70									

(2) INFORMATION FOR SEQ ID NO:1508:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1500489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1508:

Thr	Pro	Arg	Arg	Gln	Ser	Arg	Pro	Arg	Arg	Ala	Ser	Ala	Trp	Asn	Pro
1				5						10				15	
Leu	Ala	Glu	Arg	Xaa	Arg	Glu	Glu	Met	Gly	Lys	Gly	Thr	Gly	Ser	Phe
				20				25					30		
Gly	Lys	Arg	Arg	Asn	Lys	Thr	His	Thr	Leu	Cys	Ile	Arg	Cys	Gly	Gly
				35			40					45			
Arg	Arg	Gly	Ala	Gly	Ala	Ser	Arg	Thr	Arg	Ile					
				50			55								

(2) INFORMATION FOR SEQ ID NO:1509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..111
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1509:

```
Met Arg Ser Glu Arg Ala Ala Ala Ala Thr Ala Lys Ala Gln
1          5          10          15
Arg Arg Arg Arg Pro Leu Leu Arg Arg Pro Ala Gln His Ala Ala
20          25          30
Val Val Phe Val Arg Ile His Val Arg Thr Thr Ala Gln Leu Thr Arg
35          40          45
Leu Pro Thr Arg Pro Phe Cys Ala Thr Gly Trp Ser Val Gly Gly Arg
50          55          60
Arg Gly Glu Gly Phe Arg Tyr Val Val Asp Lys His Glu Gly Arg Ala
65          70          75          80
Gly Arg Arg Glu Arg Arg Arg Arg Arg Arg Pro Gln Val Ala Val Phe
85          90          95
Pro Asn Val Lys Lys Asp Ser Cys Asn Ser Asp Lys Lys Asn Lys
100         105         110
```

(2) INFORMATION FOR SEQ ID NO:1510:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 825 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..825
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1510:

```
attaaaaagc taatatggct actagggaag agagagataa gtatagatca gtccttgaag      60
atgcatgaca gggttcaatgg aggtatgata accctccaga cttcaatagt gtgaaccagc      120
tctttgaaga aggccagact aagggtgtggc cagaagggtc gttagaagag acagtgcaaa      180
acgcgatcaa gtcatgggag atggagttct cacataagat ccgtttacag gacttcaaga      240
ctataaacc tgaagaagttt aagctctttg tcaatggttt atcagctgaa gagacgctta      300
ggcttgggag ttacaatgct ttgctcaaga actctttgcc tgaagagttt cagtactata      360
agcccgagga agagagcttt gagtcacac atgacgcctt tagatctgct ttaccacgcg      420
ggtttgctg ggaaatactc tctgtgtact cggggccgcc tgttatagcc ttcaaattta      480
gacactgggg atactttgaa ggaactttca aaggtcatgc tcctactggg gaaatgggtc      540
aattcctggg tctaggagtt ctaaagggtg acgaatcact tagagcagag gagattgaga      600
tttactatga tccaggagag ctgttcgggg gactactcaa gggacctcct atatcagaga      660
ccaaaaccac agacagtggg gacaacactg cagagaaaca aagctgccc ttcacacact      720
aagataataa gaaaagcaga agtgattttg accctttaa gaatatattg taacagtctc      780
ttggttattg atgcatggaa taaattataa gttatgttag gcgcc
```

(2) INFORMATION FOR SEQ ID NO:1511:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 173 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..173
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1511:

```
Met Glu Phe Ser His Lys Ile Arg Leu Gln Asp Phe Lys Thr Ile Asn
```

1	5	10	15												
Pro	Glu	Lys	Phe	Lys	Leu	Phe	Val	Asn	Gly	Leu	Ser	Ala	Glu	Thr	
	20							25					30		
Leu	Arg	Leu	Gly	Ser	Tyr	Asn	Ala	Leu	Leu	Lys	Asn	Ser	Leu	Pro	Glu
	35						40					45			
Glu	Phe	Gln	Tyr	Tyr	Lys	Pro	Glu	Glu	Glu	Ser	Phe	Glu	Ser	Ser	His
	50					55					60				
Asp	Ala	Phe	Arg	Ser	Ala	Leu	Pro	Arg	Gly	Phe	Ala	Trp	Glu	Ile	Leu
65					70					75					80
Ser	Val	Tyr	Ser	Gly	Pro	Pro	Val	Ile	Ala	Phe	Lys	Phe	Arg	His	Trp
			85						90					95	
Gly	Tyr	Phe	Glu	Gly	Thr	Phe	Lys	Gly	His	Ala	Pro	Thr	Gly	Glu	Met
		100						105					110		
Val	Gln	Phe	Leu	Gly	Leu	Gly	Val	Leu	Lys	Val	Asp	Glu	Ser	Leu	Arg
	115						120					125			
Ala	Glu	Glu	Ile	Glu	Ile	Tyr	Tyr	Asp	Pro	Gly	Glu	Leu	Phe	Gly	Gly
	130					135					140				
Leu	Leu	Lys	Gly	Pro	Pro	Ile	Ser	Glu	Thr	Lys	Thr	Thr	Asp	Ser	Gly
145					150					155					160
Asp	Asn	Thr	Ala	Glu	Lys	Gln	Ser	Cys	Pro	Phe	Thr	His			
			165						170						

(2) INFORMATION FOR SEQ ID NO:1512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..668
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1512:

agtacttact	cactctcccc	ccaccgcgc	caggccagac	agactaactg	agcaccgcgt	60
gcaaggagtc	cgcgcccatg	gcgagcacca	acatggcgtc	ggccacctcg	cggttcatgc	120
tggccgcggg	cgtgcccacc	ggcagcagcg	gcggccgcgt	caacttcgcc	tcggcgccca	180
accggcttgg	caggaggctc	gtggcccggg	ccgacaacga	ggccgcgcga	gctgaggcgg	240
cggaagggga	gggtgccgtg	gccaccaagc	ccaaggccga	gaagccgccg	ccgatcgggc	300
ccaatagggg	cgccaagggtg	aagatcctta	ggaggagtc	ctactggtag	aacgggatcg	360
gcaacgtcgt	caccgtcgat	caggatccca	acaccgccta	cccgggtggt	gtgcggttca	420
acaagggtgaa	ctacgccggc	gtgtccacca	acaactacgc	cttggacgag	gtcttagagg	480
tgaatagagt	ggggccggcc	ggctcaaggg	tccgcgctag	ctaccgtgtg	attgatttgt	540
agtagttgtg	aaatgaggct	gtgaagctgc	atgctgtgct	ggctagcgtc	acaacatcga	600
tcctatgtgt	aatagcataa	tccacataat	catatcatgt	aattgcttgc	tttattcacc	660
gtgtactc						

(2) INFORMATION FOR SEQ ID NO:1513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1513:

Met	Ala	Ser	Thr	Asn	Met	Ala	Ser	Ala	Thr	Ser	Arg	Phe	Met	Leu	Ala
1					5				10				15		
Ala	Gly	Val	Pro	Thr	Gly	Ser	Ser	Gly	Gly	Arg	Val	Asn	Phe	Ala	Ser
			20					25					30		

Ala Pro Asn Arg Leu Gly Arg Arg Leu Val Ala Arg Ala Asp Asn Glu
35 40 45
Ala Ala Ala Ala Glu Ala Ala Glu Gly Glu Gly Ala Val Ala Thr Lys
50 55 60
Pro Lys Ala Glu Lys Pro Pro Ile Gly Pro Asn Arg Gly Ala Lys
65 70 75 80
Val Lys Ile Leu Arg Arg Glu Ser Tyr Trp Tyr Asn Gly Ile Gly Asn
85 90 95
Val Val Thr Val Asp Gln Asp Pro Asn Thr Arg Tyr Pro Val Val Val
100 105 110
Arg Phe Asn Lys Val Asn Tyr Ala Gly Val Ser Thr Asn Asn Tyr Ala
115 120 125
Leu Asp Glu Val Leu Glu Val Lys
130 135

(2) INFORMATION FOR SEQ ID NO:1514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1514:

Met Ala Ser Ala Thr Ser Arg Phe Met Leu Ala Ala Gly Val Pro Thr
1 5 10 15
Gly Ser Ser Gly Gly Arg Val Asn Phe Ala Ser Ala Pro Asn Arg Leu
20 25 30
Gly Arg Arg Leu Val Ala Arg Ala Asp Asn Glu Ala Ala Ala Glu
35 40 45
Ala Ala Glu Gly Glu Gly Ala Val Ala Thr Lys Pro Lys Ala Glu Lys
50 55 60
Pro Pro Pro Ile Gly Pro Asn Arg Gly Ala Lys Val Lys Ile Leu Arg
65 70 75 80
Arg Glu Ser Tyr Trp Tyr Asn Gly Ile Gly Asn Val Val Thr Val Asp
85 90 95
Gln Asp Pro Asn Thr Arg Tyr Pro Val Val Arg Phe Asn Lys Val
100 105 110
Asn Tyr Ala Gly Val Ser Thr Asn Asn Tyr Ala Leu Asp Glu Val Leu
115 120 125
Glu Val Lys
130

(2) INFORMATION FOR SEQ ID NO:1515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500498

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1515:

Met Leu Ala Ala Gly Val Pro Thr Gly Ser Ser Gly Gly Arg Val Asn
1 5 10 15
Phe Ala Ser Ala Pro Asn Arg Leu Gly Arg Arg Leu Val Ala Arg Ala
20 25 30
Asp Asn Glu Ala Ala Ala Ala Glu Ala Ala Glu Gly Glu Gly Ala Val

35 40 45
Ala Thr Lys Pro Lys Ala Glu Lys Pro Pro Pro Ile Gly Pro Asn Arg
50 55 60
Gly Ala Lys Val Lys Ile Leu Arg Arg Glu Ser Tyr Trp Tyr Asn Gly
65 70 75 80
Ile Gly Asn Val Val Thr Val Asp Gln Asp Pro Asn Thr Arg Tyr Pro
85 90 95
Val Val Val Arg Phe Asn Lys Val Asn Tyr Ala Gly Val Ser Thr Asn
100 105 110
Asn Tyr Ala Leu Asp Glu Val Leu Glu Val Lys
115 120

(2) INFORMATION FOR SEQ ID NO:1516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..425
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1516:

gacaacaccg	cgcgcgcaat	acacgggaca	cacacgcaga	tccgagctaa	ccaccatcga	60
cgagcgccas	cgccagcagc	cgagccggac	cgaccttttc	ttttttcttt	tacacagcgg	120
gacggagaaa	ggagtcaatc	agccaaagcc	acccaccgct	tttaccacc	gatcggcggt	180
gccgccgcta	gcattgtcgg	cttcagctcc	atccaaatcc	accgccagca	agcaagcaag	240
caagccggcg	ccatgggtct	gccgatgagg	agggagaggg	acgcggaggc	ggagctgaac	300
ctgccgcggg	ggttcgggtt	ccacccacc	gacgacgagc	tggtggagca	ctacctgtrc	360
cgcaaggggc	ggggcagcgc	ctccccgtgc	ccatcatcgc	cgaggtggac	ctgtacaggt	420
tcgac						

(2) INFORMATION FOR SEQ ID NO:1517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1517:

Asp	Asn	Thr	Ala	Arg	Ala	Ile	His	Gly	Thr	His	Thr	Gln	Ile	Arg	Ala	
1			5					10					15			
Asn	His	His	Arg	Arg	Ala	Pro	Xaa	Pro	Ala	Ala	Glu	Pro	Asp	Arg	Pro	
			20					25					30			
Phe	Leu	Phe	Ser	Phe	Thr	Gln	Arg	Asp	Gly	Glu	Arg	Ser	Gln	Ser	Ala	
			35					40					45			
Lys	Ala	Thr	His	Arg	Phe	Tyr	Pro	Pro	Ile	Gly	Val	Ala	Ala	Ala	Ser	
			50					55					60			
Ile	Val	Gly	Phe	Ser	Ser	Ile	Gln	Ile	His	Arg	Gln	Gln	Ala	Ser	Lys	
Gln	Ala	Gly	Ala	Met	Gly	Leu	Pro	Met	Arg	Arg	Glu	Arg	Asp	Ala	Glu	
Ala	Glu	Leu	Asn	Leu	Pro	Pro	Gly	Phe	Arg	Phe	His	Pro	Thr	Asp	Asp	
Glu	Leu	Val	Glu	His	Tyr	Leu	Xaa	Arg	Lys	Gly	Arg	Gly	Ser	Ala	Ser	
Pro	Cys	Pro	Ser	Ser	Pro	Arg	Trp	Thr	Cys	Thr	Gly	Ser				
130								135					140			

(2) INFORMATION FOR SEQ ID NO:1518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1500503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1518:

Thr	Thr	Pro	Arg	Ala	Gln	Tyr	Thr	Gly	His	Thr	Arg	Arg	Ser	Glu	Leu
1				5					10					15	
Thr	Thr	Ile	Asp	Glu	Arg	Xaa	Arg	Gln	Gln	Pro	Ser	Arg	Thr	Asp	Leu
			20					25					30		
Phe	Phe	Phe	Leu	Leu	His	Ser	Gly	Thr	Glu	Lys	Gly	Val	Asn	Gln	Pro
		35					40					45			
Lys	Pro	Pro	Thr	Ala	Phe	Thr	His	Arg	Ser	Ala	Leu	Pro	Pro	Leu	Ala
	50					55					60				
Leu	Ser	Ala	Ser	Ala	Pro	Ser	Lys	Ser	Thr	Ala	Ser	Lys	Gln	Ala	Ser
65					70				75					80	
Lys	Pro	Ala	Pro	Trp	Val	Cys	Arg								
				85											

(2) INFORMATION FOR SEQ ID NO:1519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1500504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1519:

attcttcttg	cctcctccct	ccaccagcat	ccctgagtct	gccatgggca	actgctgggg	60
aaccaagatt	agctctgaca	ccgccgcctc	cccttccaca	tcaccgttcc	ctcgcagcga	120
gggtgagatt	ctccggtgtg	ccaatgtcag	gagcttcacc	ttgacggagc	tgatgacctc	180
cacccggaac	ttccggcccg	acagcgctct	cggcgaggga	ggcttcggct	ccgtcttcaa	240
ggggtggatc	gacgagacca	ccttcgcccc	ggccaggccc	ggcacaggga	tggtcatcgc	300
tgtcaagaag	ctcaaccagc	agggattgca	ggggcacagg	gagtggcttg	ctgaagtcaa	360
ctacctgggc	cagttgtctc	amcccagttc	cgtaargctc	gtagggtact	gcctccaaga	420
cgagcagcgc	cttctcgtct	acgagttcat	gccgcgarga	agcttkgaga	accatctttt	480
caggacctca	cgt					

(2) INFORMATION FOR SEQ ID NO:1520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1500505

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1520:

Phe	Phe	Leu	Pro	Pro	Pro	Ser	Thr	Ser	Ile	Pro	Glu	Ser	Ala	Met	Gly
1				5					10					15	
Asn	Cys	Trp	Gly	Thr	Lys	Ile	Ser	Ser	Asp	Thr	Ala	Ala	Ser	Pro	Ser
			20					25					30		

Thr Ser Pro Phe Pro Arg Ser Glu Gly Glu Ile Leu Arg Cys Ala Asn
35 40 45
Val Arg Ser Phe Thr Leu Thr Glu Leu Met Thr Ser Thr Arg Asn Phe
50 55 60
Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly Ser Val Phe Lys
65 70 75 80
Gly Trp Ile Asp Glu Thr Thr Phe Ala Pro Ala Arg Pro Gly Thr Gly
85 90 95
Met Val Ile Ala Val Lys Lys Leu Asn Gln Gln Gly Leu Gln Gly His
100 105 110
Arg Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln Leu Ser Xaa Pro
115 120 125
Ser Leu Val Xaa Leu Val Gly Tyr Cys Leu Gln Asp Glu Gln Arg Leu
130 135 140
Leu Val Tyr Glu Phe Met Pro Arg Xaa Ser Xaa Glu Asn His Leu Phe
145 150 155 160
Arg Thr Ser Arg

(2) INFORMATION FOR SEQ ID NO:1521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500506

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1521:

Met Gly Asn Cys Trp Gly Thr Lys Ile Ser Ser Asp Thr Ala Ala Ser
1 5 10 15
Pro Ser Thr Ser Pro Phe Pro Arg Ser Glu Gly Glu Ile Leu Arg Cys
20 25 30
Ala Asn Val Arg Ser Phe Thr Leu Thr Glu Leu Met Thr Ser Thr Arg
35 40 45
Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly Ser Val
50 55 60
Phe Lys Gly Trp Ile Asp Glu Thr Thr Phe Ala Pro Ala Arg Pro Gly
65 70 75 80
Thr Gly Met Val Ile Ala Val Lys Lys Leu Asn Gln Gln Gly Leu Gln
85 90 95
Gly His Arg Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln Leu Ser
100 105 110
Xaa Pro Ser Leu Val Xaa Leu Val Gly Tyr Cys Leu Gln Asp Glu Gln
115 120 125
Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Xaa Ser Xaa Glu Asn His
130 135 140
Leu Phe Arg Thr Ser Arg
145 150

(2) INFORMATION FOR SEQ ID NO:1522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1500507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1522:

Met Thr Ser Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly
1 5 10 15
Gly Phe Gly Ser Val Phe Lys Gly Trp Ile Asp Glu Thr Thr Phe Ala
20 25 30
Pro Ala Arg Pro Gly Thr Gly Met Val Ile Ala Val Lys Lys Leu Asn
35 40 45
Gln Gln Gly Leu Gln Gly His Arg Glu Trp Leu Ala Glu Val Asn Tyr
50 55 60
Leu Gly Gln Leu Ser Xaa Pro Ser Leu Val Xaa Leu Val Gly Tyr Cys
65 70 75 80
Leu Gln Asp Glu Gln Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Xaa
85 90 95
Ser Xaa Glu Asn His Leu Phe Arg Thr Ser Arg
100 105

(2) INFORMATION FOR SEQ ID NO:1523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1523:

acgaacccaa cccagtcgaa ccacctcgcc agtgagcgcc cccctcccggt cctctttccc	60
tgctggccag aactccgaat gaaatcgctg ctccaccagc tttctttacc ttcagcaagc	120
gagccggtag catcaagcta gatcgcgggg aagctcctcg tttcccccat cggcgtgct	180
ctggcgggga gaagcgtcct ctcacggcgg cggggaagac caatccgcgc cgccagtccc	240
tgcggcggtt tccgtgaggt ggtcttggt cctggggcgg cgtgttcgtg gcggccggcg	300
agatgagcag ccacgcggtt ggaacaagca acggcggatc cggatgatgc gccgccgggg	360
gcgcggccag gaggaacacc aggatgcccc aatattccaa gttcacacag caggagctgc	420
ccgcttkcaa gccgattctt actccaaaat gggttgtctc tgt	

(2) INFORMATION FOR SEQ ID NO:1524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1524:

Thr Asn Pro Thr Gln Ser Asn His Leu Ala Ser Glu Arg Pro Pro Pro
1 5 10 15
Val Leu Phe Pro Cys Trp Pro Glu Leu Arg Met Lys Ser Leu Leu His
20 25 30
Gln Leu Ser Leu Pro Ser Ala Ser Glu Pro Val Ala Ser Ser
35 40 45

(2) INFORMATION FOR SEQ ID NO:1525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1500518
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1525:
Met Ser Ser His Ala Val Gly Thr Ser Asn Gly Gly Ser Gly Asp Ala
1 5 10 15
Ala Ala Gly Gly Ala Ala Arg Arg Asn Thr Arg Met Pro Lys Tyr Ser
20 25 30
Lys Phe Thr Gln Gln Glu Leu Pro Ala Xaa Lys Pro Ile Leu Thr Pro
35 40 45
Lys Trp Val Val Ser
50

(2) INFORMATION FOR SEQ ID NO:1526:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..39
(D) OTHER INFORMATION: / Ceres Seq. ID 1500519
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1526:
Met Arg Pro Pro Gly Ala Arg Pro Gly Gly Thr Pro Gly Cys Pro Asn
1 5 10 15
Ile Pro Ser Ser His Ser Arg Ser Cys Pro Leu Xaa Ser Arg Phe Leu
20 25 30
Leu Gln Asn Gly Leu Ser Leu
35

(2) INFORMATION FOR SEQ ID NO:1527:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 535 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..535
(D) OTHER INFORMATION: / Ceres Seq. ID 1500539
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1527:
tgggatgaag ccgtgggttat gttaccgtga ctacgactgt aacttcaact ccgacatatt 60
cgttgagttt gctaccgata tcgcatcgaa aatgggtgat ggtccacgac gccatgccac 120
aggaacttca ccaattctgt tacttgcat ccaagcaaaa ggcacagctg gaatatgatc 180
gccggcaagc agaggccgca aattatgccg acggtcattg gaaaataaga gtaaaggacc 240
cgagattcaa aatttgcac gacaaattat gtaattggaa aagtatgctg cggcattggg 300
gcgaatcaaa ttggactgac tacgagtctt ttgttcccac cccaccagcc attaccgtag 360
accggagatc atcacttccc ggccataact tgtgacgcaa taattataca tacttattaa 420
tggatttcat gagttttttg gtttgaattg ttgctgagag attaggtgaa tatcagttgt 480
gtaactatat ctttttccta tagtttggtc aaattgaata aaacattttt ttgcg

(2) INFORMATION FOR SEQ ID NO:1528:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1500540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1528:

Gly Met Lys Pro Trp Leu Cys Tyr Arg Asp Tyr Asp Cys Asn Phe Asn
1 5 10 15
Ser Asp Ile Phe Val Glu Phe Ala Thr Asp Ile Ala Ser Lys Met Val
20 25 30
Asp Gly Pro Arg Arg His Ala Thr Gly Thr Ser Pro Ile Leu Leu Leu
35 40 45
Ala Ile Gln Ala Lys Gly Thr Ala Gly Ile
50 55

(2) INFORMATION FOR SEQ ID NO:1529:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1500541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1529:

Met Val His Asp Ala Met Pro Gln Glu Leu His Gln Phe Cys Tyr Leu
1 5 10 15
Arg Ser Lys Gln Lys Ala Gln Leu Glu Tyr Asp Arg Arg Gln Ala Glu
20 25 30
Ala Ala Asn Tyr Ala Asp Gly His Trp Lys Ile Arg Val Lys Asp Pro
35 40 45
Arg Phe Lys Ile Cys Ile Asp Lys Leu Cys Asn Trp Lys Ser Met Leu
50 55 60
Arg His Trp Gly Glu Ser Asn Trp Thr Asp Tyr Glu Ser Phe Val Pro
65 70 75 80
Thr Pro Pro Ala Ile Thr Val Asp Arg Arg Ser Ser Leu Pro Gly His
85 90 95
Asn Leu

(2) INFORMATION FOR SEQ ID NO:1530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1500542

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1530:

Met Pro Gln Glu Leu His Gln Phe Cys Tyr Leu Arg Ser Lys Gln Lys
1 5 10 15
Ala Gln Leu Glu Tyr Asp Arg Arg Gln Ala Glu Ala Ala Asn Tyr Ala
20 25 30
Asp Gly His Trp Lys Ile Arg Val Lys Asp Pro Arg Phe Lys Ile Cys
35 40 45
Ile Asp Lys Leu Cys Asn Trp Lys Ser Met Leu Arg His Trp Gly Glu
50 55 60
Ser Asn Trp Thr Asp Tyr Glu Ser Phe Val Pro Thr Pro Pro Ala Ile
65 70 75 80
Thr Val Asp Arg Arg Ser Ser Leu Pro Gly His Asn Leu
85 90

(2) INFORMATION FOR SEQ ID NO:1531:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1530 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1530
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500554
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1531:

```
atcgctcgtct tctattttttt cttcttttctt cgatttcata ccaaaacaag aactctctgt      60
tttcgacaaa aacgaaacct tgagatctat tttgattgac ttttaagaaa gagagagatc      120
tttcttagaa gattttgtct cgtcggcatt gaagatccag ggtttgtctt tcgaaattca      180
gagagaaaaat gggatgatgag gcagagatca aggaacattt aaagccacaa gcttcattctg      240
aaacaatgga caagaaacat aatgtgaaag ggaagaggtt atggcagaaa gtcaagtatc      300
aattgggtgga gtttcattca ttgcctgctt atttaagaga caatgagtac atcattggtc      360
attaccgatc cgaatggcgc atcaaacaga ttcttctcag catctttacc attcataatg      420
agactttgaa tgtttggacg cacttgattg ggtttttcct gtttttggcg ctactatat      480
acactgcaac gaaagtaccg agtgctgctg atcttcattc gcttcaacac cgtttaccgc      540
atttggttag gaaaacagat ctccacaaaac ttcattctga gctcatggct cgccttcctt      600
ctagtccatc tagttggcat gtgatggacc ttctttataa ctgtttgctt gaaagatttt      660
ctcatggcaa ctacactgac atgtgtgttc tgcattctgt gaggaagat cttgcaaaact      720
tgatagctcc tttgatcttc aggccaatta ctcgatggcc gttttatgca tttctaggtg      780
gtgctatgtt ctgtctatta gcaagcagca cgtgccacct cctctcatgt cactccgagc      840
gagtcctcta cataatgctt aggctttatt acgccggcat cgcagctcta atagcgactt      900
ccttctacc tccggtttat tactccttca tgtgtgatcc tttcttctgc aacctctact      960
taggattcat aaccatctta ggaatcgcca ctgtgcttgt ttctctctc cgggttttcc      1020
aaagcccgga gtttcgggtg gtgagggcgt ctctgttctt tggaatggga ttctctggct      1080
tagctccgat tcttcacaag ctgataatct tttgggacca acctgaagcc cttcacacga      1140
caggttatga gattttgatg gggttgcttt atgggttagg agctctgggt tatgcaacta      1200
ggatcccaga gagatggatg cggggtaaat tcgatatagc aggacatagc catcagttgt      1260
ttcatgttct ggttgttctg gtgcgttcac gcactataga gctgggctag tgtatcttaa      1320
gtggagagat atygaaggat gttgaagatg aagattgaag attagatgga atctttgaat      1380
cttgtttgta gtagcttcat ataaaagttg gattatgtaa agtcttatat gtaatcaaac      1440
gtttaattgt ttcctttatt caacaaagga tttatattgt taatccacat atgtattact      1500
ggttaaagaa gctgaaggat tcatattttt
```

(2) INFORMATION FOR SEQ ID NO:1532:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..373
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500555
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1532:

```
Met Gly Asp Glu Ala Glu Ile Lys Glu His Leu Lys Pro Gln Ala Ser
1           5           10           15
Ser Glu Thr Met Asp Lys Lys His Asn Val Lys Gly Lys Arg Leu Trp
20           25           30
Gln Lys Val Lys Tyr Gln Leu Val Glu Phe His Ser Leu Pro Ala Tyr
35           40           45
Leu Arg Asp Asn Glu Tyr Ile Ile Gly His Tyr Arg Ser Glu Trp Pro
50           55           60
Ile Lys Gln Ile Leu Leu Ser Ile Phe Thr Ile His Asn Glu Thr Leu
65           70           75           80
Asn Val Trp Thr His Leu Ile Gly Phe Phe Leu Phe Leu Ala Leu Thr
85           90           95
```

Ile	Tyr	Thr	Ala	Thr	Lys	Val	Pro	Ser	Val	Val	Asp	Leu	His	Ser	Leu
			100					105					110		
Gln	His	Arg	Leu	Pro	Asp	Leu	Leu	Arg	Lys	Thr	Asp	Leu	His	Lys	Leu
		115					120					125			
His	Ser	Glu	Leu	Met	Ala	Arg	Leu	Pro	Ser	Ser	Pro	Ser	Ser	Trp	His
	130					135					140				
Val	Met	Asp	Leu	Leu	Tyr	Asn	Cys	Leu	Pro	Glu	Arg	Phe	Ser	His	Gly
145					150					155					160
Asn	Tyr	Thr	Asp	Met	Cys	Val	Leu	His	Ser	Val	Arg	Glu	Asp	Leu	Ala
			165						170					175	
Asn	Leu	Ile	Ala	Pro	Leu	Ile	Phe	Arg	Pro	Ile	Thr	Arg	Trp	Pro	Phe
		180					185						190		
Tyr	Ala	Phe	Leu	Gly	Gly	Ala	Met	Phe	Cys	Leu	Leu	Ala	Ser	Ser	Thr
		195					200					205			
Cys	His	Leu	Leu	Ser	Cys	His	Ser	Glu	Arg	Val	Ser	Tyr	Ile	Met	Leu
	210					215					220				
Arg	Leu	Tyr	Tyr	Ala	Gly	Ile	Ala	Ala	Leu	Ile	Ala	Thr	Ser	Phe	Tyr
225					230					235					240
Pro	Pro	Val	Tyr	Tyr	Ser	Phe	Met	Cys	Asp	Pro	Phe	Phe	Cys	Asn	Leu
					245				250					255	
Tyr	Leu	Gly	Phe	Ile	Thr	Ile	Leu	Gly	Ile	Ala	Thr	Val	Leu	Val	Ser
		260						265					270		
Leu	Leu	Pro	Val	Phe	Gln	Ser	Pro	Glu	Phe	Arg	Val	Val	Arg	Ala	Ser
		275					280					285			
Leu	Phe	Phe	Gly	Met	Gly	Phe	Ser	Gly	Leu	Ala	Pro	Ile	Leu	His	Lys
	290					295				300					
Leu	Ile	Ile	Phe	Trp	Asp	Gln	Pro	Glu	Ala	Leu	His	Thr	Thr	Gly	Tyr
305					310					315					320
Glu	Ile	Leu	Met	Gly	Leu	Leu	Tyr	Gly	Leu	Gly	Ala	Leu	Val	Tyr	Ala
			325					330						335	
Thr	Arg	Ile	Pro	Glu	Arg	Trp	Met	Pro	Gly	Lys	Phe	Asp	Ile	Ala	Gly
		340					345						350		
His	Ser	His	Gln	Leu	Phe	His	Val	Leu	Val	Val	Leu	Val	Arg	Ser	Arg
		355					360						365		
Thr	Ile	Glu	Leu	Gly											
															370

(2) INFORMATION FOR SEQ ID NO:1533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..354

(D) OTHER INFORMATION: / Ceres Seq. ID 1500556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1533:

Met	Asp	Lys	Lys	His	Asn	Val	Lys	Gly	Lys	Arg	Leu	Trp	Gln	Lys	Val
1			5					10						15	
Lys	Tyr	Gln	Leu	Val	Glu	Phe	His	Ser	Leu	Pro	Ala	Tyr	Leu	Arg	Asp
		20						25					30		
Asn	Glu	Tyr	Ile	Ile	Gly	His	Tyr	Arg	Ser	Glu	Trp	Pro	Ile	Lys	Gln
		35				40						45			
Ile	Leu	Leu	Ser	Ile	Phe	Thr	Ile	His	Asn	Glu	Thr	Leu	Asn	Val	Trp
	50					55					60				
Thr	His	Leu	Ile	Gly	Phe	Phe	Leu	Phe	Leu	Ala	Leu	Thr	Ile	Tyr	Thr
65				70						75				80	
Ala	Thr	Lys	Val	Pro	Ser	Val	Val	Asp	Leu	His	Ser	Leu	Gln	His	Arg
			85					90					95		
Leu	Pro	Asp	Leu	Leu	Arg	Lys	Thr	Asp	Leu	His	Lys	Leu	His	Ser	Glu

		100				105					110				
Leu	Met	Ala	Arg	Leu	Pro	Ser	Ser	Pro	Ser	Ser	Trp	His	Val	Met	Asp
		115						120					125		
Leu	Leu	Tyr	Asn	Cys	Leu	Pro	Glu	Arg	Phe	Ser	His	Gly	Asn	Tyr	Thr
		130						135				140			
Asp	Met	Cys	Val	Leu	His	Ser	Val	Arg	Glu	Asp	Leu	Ala	Asn	Leu	Ile
		145					150				155				160
Ala	Pro	Leu	Ile	Phe	Arg	Pro	Ile	Thr	Arg	Trp	Pro	Phe	Tyr	Ala	Phe
				165						170				175	
Leu	Gly	Gly	Ala	Met	Phe	Cys	Leu	Leu	Ala	Ser	Ser	Thr	Cys	His	Leu
			180							185			190		
Leu	Ser	Cys	His	Ser	Glu	Arg	Val	Ser	Tyr	Ile	Met	Leu	Arg	Leu	Tyr
		195					200					205			
Tyr	Ala	Gly	Ile	Ala	Ala	Leu	Ile	Ala	Thr	Ser	Phe	Tyr	Pro	Pro	Val
		210					215					220			
Tyr	Tyr	Ser	Phe	Met	Cys	Asp	Pro	Phe	Phe	Cys	Asn	Leu	Tyr	Leu	Gly
		225				230					235				240
Phe	Ile	Thr	Ile	Leu	Gly	Ile	Ala	Thr	Val	Leu	Val	Ser	Leu	Leu	Pro
				245						250				255	
Val	Phe	Gln	Ser	Pro	Glu	Phe	Arg	Val	Val	Arg	Ala	Ser	Leu	Phe	Phe
			260					265					270		
Gly	Met	Gly	Phe	Ser	Gly	Leu	Ala	Pro	Ile	Leu	His	Lys	Leu	Ile	Ile
		275					280					285			
Phe	Trp	Asp	Gln	Pro	Glu	Ala	Leu	His	Thr	Thr	Gly	Tyr	Glu	Ile	Leu
		290				295					300				
Met	Gly	Leu	Leu	Tyr	Gly	Leu	Gly	Ala	Leu	Val	Tyr	Ala	Thr	Arg	Ile
		305				310					315				320
Pro	Glu	Arg	Trp	Met	Pro	Gly	Lys	Phe	Asp	Ile	Ala	Gly	His	Ser	His
				325					330					335	
Gln	Leu	Phe	His	Val	Leu	Val	Val	Leu	Val	Arg	Ser	Arg	Thr	Ile	Glu
			340					345					350		
Leu	Gly														

(2) INFORMATION FOR SEQ ID NO:1534:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..241

(D) OTHER INFORMATION: / Ceres Seq. ID 1500557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1534:

Met	Ala	Arg	Leu	Pro	Ser	Ser	Pro	Ser	Ser	Trp	His	Val	Met	Asp	Leu
1			5					10					15		
Leu	Tyr	Asn	Cys	Leu	Pro	Glu	Arg	Phe	Ser	His	Gly	Asn	Tyr	Thr	Asp
		20						25				30			
Met	Cys	Val	Leu	His	Ser	Val	Arg	Glu	Asp	Leu	Ala	Asn	Leu	Ile	Ala
		35					40				45				
Pro	Leu	Ile	Phe	Arg	Pro	Ile	Thr	Arg	Trp	Pro	Phe	Tyr	Ala	Phe	Leu
		50				55					60				
Gly	Gly	Ala	Met	Phe	Cys	Leu	Leu	Ala	Ser	Ser	Thr	Cys	His	Leu	Leu
				70					75					80	
Ser	Cys	His	Ser	Glu	Arg	Val	Ser	Tyr	Ile	Met	Leu	Arg	Leu	Tyr	Tyr
			85					90					95		
Ala	Gly	Ile	Ala	Ala	Leu	Ile	Ala	Thr	Ser	Phe	Tyr	Pro	Pro	Val	Tyr
			100					105				110			
Tyr	Ser	Phe	Met	Cys	Asp	Pro	Phe	Phe	Cys	Asn	Leu	Tyr	Leu	Gly	Phe
		115					120					125			

Ile	Thr	Ile	Leu	Gly	Ile	Ala	Thr	Val	Leu	Val	Ser	Leu	Leu	Pro	Val
130						135					140				
Phe	Gln	Ser	Pro	Glu	Phe	Arg	Val	Val	Arg	Ala	Ser	Leu	Phe	Phe	Gly
145					150					155					160
Met	Gly	Phe	Ser	Gly	Leu	Ala	Pro	Ile	Leu	His	Lys	Leu	Ile	Ile	Phe
				165					170						175
Trp	Asp	Gln	Pro	Glu	Ala	Leu	His	Thr	Thr	Gly	Tyr	Glu	Ile	Leu	Met
			180					185					190		
Gly	Leu	Leu	Tyr	Gly	Leu	Gly	Ala	Leu	Val	Tyr	Ala	Thr	Arg	Ile	Pro
			195				200					205			
Glu	Arg	Trp	Met	Pro	Gly	Lys	Phe	Asp	Ile	Ala	Gly	His	Ser	His	Gln
	210					215					220				
Leu	Phe	His	Val	Leu	Val	Val	Leu	Val	Arg	Ser	Arg	Thr	Ile	Glu	Leu
225					230					235					240
Gly															

(2) INFORMATION FOR SEQ ID NO:1535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..660
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1535:

atccaatatt	tctatggagt	catcttcttc	actccttcac	cactcttacc	tctcttacct	60
taatcaaaa	tttgaaaaa	gacctttgtt	ttcttatcca	ttaatgcaga	gttcgcgaaa	120
atgcaaaca	actcgcat	gttctaaca	gatgtatgtt	cccggtttg	gagaagcttc	180
accggaggct	aaggcagcga	agcatcttca	tgacttcttt	acttacgttg	cagtggaggat	240
agtgtctgct	cagcttgaga	gttataatcc	tgaggcttat	atggagttga	gagaattttt	300
agatacaaac	tctgtaagt	acggtgataa	attctgcgcc	actctcatgc	gtcgcctctc	360
acgtcacatg	aacttagccc	ttcgaatttt	agaggtacgg	tctgcttatt	gtaaaaacga	420
tttcgaatgg	gataatatga	agcgctcgc	cttcaagaac	gtagatgatt	ccaacacaag	480
actcatgcgc	gagtacgtct	tggagactag	ccatgtcgaa	accgattctg	ataagtgaag	540
ccgaatatct	cttcgaatca	cattcatata	tatagagtct	tgagagtata	cacacttgaa	600
accgtttgta	catacatata	cataccattg	tgctatgtta	ctcccagggt	ttgataacct	660

(2) INFORMATION FOR SEQ ID NO:1536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..178
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1536:

Ser	Asn	Ile	Ser	Met	Glu	Ser	Ser	Ser	Ser	Leu	Leu	His	His	Ser	Tyr
1				5					10					15	
Leu	Ser	Tyr	Leu	Asn	Pro	Lys	Phe	Gly	Lys	Arg	Pro	Leu	Val	Ser	Tyr
			20					25					30		
Pro	Leu	Met	Gln	Ser	Ser	Arg	Lys	Cys	Lys	Gln	Thr	Arg	Ile	Cys	Ser
			35				40					45			
Asn	Lys	Met	Tyr	Val	Pro	Gly	Phe	Gly	Glu	Ala	Ser	Pro	Glu	Ala	Lys
	50					55					60				
Ala	Ala	Lys	His	Leu	His	Asp	Phe	Phe	Thr	Tyr	Val	Ala	Val	Arg	Ile

65					70					75					80
Val	Ser	Ala	Gln	Leu	Glu	Ser	Tyr	Asn	Pro	Glu	Ala	Tyr	Met	Glu	Leu
				85					90					95	
Arg	Glu	Phe	Leu	Asp	Thr	Asn	Ser	Val	Ser	Asp	Gly	Asp	Lys	Phe	Cys
			100					105					110		
Ala	Thr	Leu	Met	Arg	Arg	Ser	Ser	Arg	His	Met	Asn	Leu	Ala	Leu	Arg
		115					120					125			
Ile	Leu	Glu	Val	Arg	Ser	Ala	Tyr	Cys	Lys	Asn	Asp	Phe	Glu	Trp	Asp
	130					135					140				
Asn	Met	Lys	Arg	Leu	Ala	Phe	Lys	Asn	Val	Asp	Asp	Ser	Asn	Thr	Arg
145				150						155					160
Leu	Met	Arg	Glu	Tyr	Val	Leu	Glu	Thr	Ser	His	Val	Glu	Thr	Asp	Ser
			165					170						175	

Asp Lys

(2) INFORMATION FOR SEQ ID NO:1537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500560

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1537:

Met	Glu	Ser	Ser	Ser	Ser	Leu	Leu	His	His	Ser	Tyr	Leu	Ser	Tyr	Leu
1				5					10					15	
Asn	Pro	Lys	Phe	Gly	Lys	Arg	Pro	Leu	Val	Ser	Tyr	Pro	Leu	Met	Gln
			20				25					30			
Ser	Ser	Arg	Lys	Cys	Lys	Gln	Thr	Arg	Ile	Cys	Ser	Asn	Lys	Met	Tyr
		35				40					45				
Val	Pro	Gly	Phe	Gly	Glu	Ala	Ser	Pro	Glu	Ala	Lys	Ala	Ala	Lys	His
	50					55				60					
Leu	His	Asp	Phe	Phe	Thr	Tyr	Val	Ala	Val	Arg	Ile	Val	Ser	Ala	Gln
65					70					75					80
Leu	Glu	Ser	Tyr	Asn	Pro	Glu	Ala	Tyr	Met	Glu	Leu	Arg	Glu	Phe	Leu
			85					90					95		
Asp	Thr	Asn	Ser	Val	Ser	Asp	Gly	Asp	Lys	Phe	Cys	Ala	Thr	Leu	Met
			100				105					110			
Arg	Arg	Ser	Ser	Arg	His	Met	Asn	Leu	Ala	Leu	Arg	Ile	Leu	Glu	Val
		115				120					125				
Arg	Ser	Ala	Tyr	Cys	Lys	Asn	Asp	Phe	Glu	Trp	Asp	Asn	Met	Lys	Arg
	130					135					140				
Leu	Ala	Phe	Lys	Asn	Val	Asp	Asp	Ser	Asn	Thr	Arg	Leu	Met	Arg	Glu
145				150						155					160
Tyr	Val	Leu	Glu	Thr	Ser	His	Val	Glu	Thr	Asp	Ser	Asp	Lys		
			165					170							

(2) INFORMATION FOR SEQ ID NO:1538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1538:

Met Gln Ser Ser Arg Lys Cys Lys Gln Thr Arg Ile Cys Ser Asn Lys
1 5 10 15
Met Tyr Val Pro Gly Phe Gly Glu Ala Ser Pro Glu Ala Lys Ala Ala
20 25 30
Lys His Leu His Asp Phe Phe Thr Tyr Val Ala Val Arg Ile Val Ser
35 40 45
Ala Gln Leu Glu Ser Tyr Asn Pro Glu Ala Tyr Met Glu Leu Arg Glu
50 55 60
Phe Leu Asp Thr Asn Ser Val Ser Asp Gly Asp Lys Phe Cys Ala Thr
65 70 75 80
Leu Met Arg Arg Ser Ser Arg His Met Asn Leu Ala Leu Arg Ile Leu
85 90 95
Glu Val Arg Ser Ala Tyr Cys Lys Asn Asp Phe Glu Trp Asp Asn Met
100 105 110
Lys Arg Leu Ala Phe Lys Asn Val Asp Asp Ser Asn Thr Arg Leu Met
115 120 125
Arg Glu Tyr Val Leu Glu Thr Ser His Val Glu Thr Asp Ser Asp Lys
130 135 140

(2) INFORMATION FOR SEQ ID NO:1539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1616
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1539:

atcgataacc	aaataaaaaa	tggcgatctc	tttcctctgt	gtttttctca	tcaccttcgt	60
ttcgtttaac	ttttttgcc	agaaaatcaa	acgatcaaaa	tggaatcttc	ctccaagccc	120
tccaagttt	ccggtcatcg	ggaacttaca	tcagattgga	gaattgcctc	acagggtcact	180
tcaacatctc	gccgaaagat	acggacctgt	gatgcttctt	cactttgggt	ttgtccctat	240
aactgtggtc	tcacgcgagag	aagccgctga	agaagtgcct	agaactcatg	acctagactg	300
ttgcagcagg	cctaagcttg	tcgggacaag	gttactctcg	gcgggatttt	aaagatatcg	360
gttttacgcc	atacggtaac	gaggtggaag	gcgcggcgta	aggtttgccc	tgcgtagagac	420
ttttctgttt	gaaaaaggtt	cagtccttta	ggcatatccg	agaggaagaa	tgtaactttc	480
tggtcaagca	actgtcggaa	tccgcggttg	atcgctctcc	ggtcgatttg	agcaaatccc	540
ttttctggct	aaccgctagt	atccttttta	gagttgcctt	aggacagaat	tttcacgaga	600
gcgattttat	cgataaagaa	aagatcgaag	agctcgtgtt	cgaagctgag	actgccctag	660
caagtttcac	ttgttctgat	ttcttccttg	ttgccggact	tggtatggctc	gttgattggg	720
tttcgggaca	acacaagaga	ctcaacgatg	ttttttacaa	gctcgatgct	ctgtttcaat	780
atgtcataga	tgatcattta	aatcctggaa	gatcaaaaga	gcacgaagac	atcatcgatt	840
caatgttgga	tgtgattcat	aaacaaggag	aggatagtcc	cttagagctc	acaatagatc	900
atatcaaggg	gtttctcgcg	aatatatttc	ttgcagggat	agacacaggg	gccatcacca	960
tgatatgggc	agtgcgggag	ctcgttaaaa	acccgaaact	gataaagaaa	gttcaaggcg	1020
atatccgaga	acaacttggc	agcaataagg	agagaatcac	cgaggaagat	atcgagaaa	1080
ttccttactt	gaagatggta	atcaaagaaa	cattcaggtt	acacccagca	gctcctctta	1140
tacttccaag	ggaaacaatg	gctcacatca	aagttcaagg	gtatgatatt	cctcccaaga	1200
ggaggatctt	ggtcaatggt	tcggcaatag	gaagagatcc	caaactctgg	acaaacccga	1260
aagagtttga	ccctgagagg	tttatggata	gctttgttga	ttatagggga	caacattacg	1320
agctcttacc	atttgggtcc	ggtcgaagga	tatgtcccgg	gatgccaatg	gggattgctg	1380
ccgtcgaatt	gggactcttg	aacttacttt	acttcttcga	ttggaagttg	cctgatggga	1440
tgacacataa	agatatcgat	actgaagaag	ctggtactct	tacaatagtc	aagaaagtac	1500
ctctcaagct	cgttccaggt	cgagttcagt	gatcagacca	aactccaaac	cttttgaata	1560
aatatatcat	gcaaatcatg	taagcttctc	tgatgatgta	tgaagtatat	ttttcc	

(2) INFORMATION FOR SEQ ID NO:1540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..229
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500563
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1540:

Met Leu Asp Val Ile His Lys Gln Gly Glu Asp Ser Ser Leu Glu Leu
1 5 10 15
Thr Ile Asp His Ile Lys Gly Phe Leu Ala Asn Ile Phe Leu Ala Gly
20 25 30
Ile Asp Thr Gly Ala Ile Thr Met Ile Trp Ala Val Thr Glu Leu Val
35 40 45
Lys Asn Pro Lys Leu Ile Lys Lys Val Gln Gly Asp Ile Arg Glu Gln
50 55 60
Leu Gly Ser Asn Lys Glu Arg Ile Thr Glu Glu Asp Ile Glu Lys Val
65 70 75 80
Pro Tyr Leu Lys Met Val Ile Lys Glu Thr Phe Arg Leu His Pro Ala
85 90 95
Ala Pro Leu Ile Leu Pro Arg Glu Thr Met Ala His Ile Lys Val Gln
100 105 110
Gly Tyr Asp Ile Pro Pro Lys Arg Arg Ile Leu Val Asn Val Ser Ala
115 120 125
Ile Gly Arg Asp Pro Lys Leu Trp Thr Asn Pro Lys Glu Phe Asp Pro
130 135 140
Glu Arg Phe Met Asp Ser Phe Val Asp Tyr Arg Gly Gln His Tyr Glu
145 150 155 160
Leu Leu Pro Phe Gly Ser Gly Arg Arg Ile Cys Pro Gly Met Pro Met
165 170 175
Gly Ile Ala Ala Val Glu Leu Gly Leu Asn Leu Leu Tyr Phe Phe
180 185 190
Asp Trp Lys Leu Pro Asp Gly Met Thr His Lys Asp Ile Asp Thr Glu
195 200 205
Glu Ala Gly Thr Leu Thr Ile Val Lys Lys Val Pro Leu Lys Leu Val
210 215 220
Pro Val Arg Val Gln
225

(2) INFORMATION FOR SEQ ID NO:1541:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..190
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500564
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1541:

Met Ile Trp Ala Val Thr Glu Leu Val Lys Asn Pro Lys Leu Ile Lys
1 5 10 15
Lys Val Gln Gly Asp Ile Arg Glu Gln Leu Gly Ser Asn Lys Glu Arg
20 25 30
Ile Thr Glu Glu Asp Ile Glu Lys Val Pro Tyr Leu Lys Met Val Ile
35 40 45
Lys Glu Thr Phe Arg Leu His Pro Ala Ala Pro Leu Ile Leu Pro Arg
50 55 60
Glu Thr Met Ala His Ile Lys Val Gln Gly Tyr Asp Ile Pro Pro Lys

65 70 75 80
Arg Arg Ile Leu Val Asn Val Ser Ala Ile Gly Arg Asp Pro Lys Leu
85 90 95
Trp Thr Asn Pro Lys Glu Phe Asp Pro Glu Arg Phe Met Asp Ser Phe
100 105 110
Val Asp Tyr Arg Gly Gln His Tyr Glu Leu Leu Pro Phe Gly Ser Gly
115 120 125
Arg Arg Ile Cys Pro Gly Met Pro Met Gly Ile Ala Ala Val Glu Leu
130 135 140
Gly Leu Leu Asn Leu Leu Tyr Phe Phe Asp Trp Lys Leu Pro Asp Gly
145 150 155 160
Met Thr His Lys Asp Ile Asp Thr Glu Glu Ala Gly Thr Leu Thr Ile
165 170 175
Val Lys Lys Val Pro Leu Lys Leu Val Pro Val Arg Val Gln
180 185 190

(2) INFORMATION FOR SEQ ID NO:1542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1542:

Met Val Ile Lys Glu Thr Phe Arg Leu His Pro Ala Ala Pro Leu Ile
1 5 10 15
Leu Pro Arg Glu Thr Met Ala His Ile Lys Val Gln Gly Tyr Asp Ile
20 25 30
Pro Pro Lys Arg Arg Ile Leu Val Asn Val Ser Ala Ile Gly Arg Asp
35 40 45
Pro Lys Leu Trp Thr Asn Pro Lys Glu Phe Asp Pro Glu Arg Phe Met
50 55 60
Asp Ser Phe Val Asp Tyr Arg Gly Gln His Tyr Glu Leu Leu Pro Phe
65 70 75 80
Gly Ser Gly Arg Arg Ile Cys Pro Gly Met Pro Met Gly Ile Ala Ala
85 90 95
Val Glu Leu Gly Leu Leu Asn Leu Leu Tyr Phe Phe Asp Trp Lys Leu
100 105 110
Pro Asp Gly Met Thr His Lys Asp Ile Asp Thr Glu Glu Ala Gly Thr
115 120 125
Leu Thr Ile Val Lys Lys Val Pro Leu Lys Leu Val Pro Val Arg Val
130 135 140
Gln
145

(2) INFORMATION FOR SEQ ID NO:1543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1928 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1928
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1543:

tttctctctt ttccatctcc acaaattcca aacatctctc tctctttctc tctcacacac 60
aaaattgcag aagaagaaga gtcattgaatg gtgaagaaag cttttagtaa gattgctctg 120

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tttttgttga gattgatcct tctggaagat atggaagata cgatgaaata cttggcaaag 180
gagcttcaaa gacagtatac agagcatttg atgagtatga aggtatagaa gtagcatgga 240
accaagtaaa gcttcgaaat ttcacaagga atcctgagga attagagaag tttttcagag 300
agattcatct tctcaagact ttgaatcatc aaaacattat gaaattctac acttcttggg 360
ttgatacca caatttatca atcaattttg tcactgaact cttcacctct ggtactctca 420
gacagtatag gttgagacat agaagagtga atattagagc agtgaagcaa tgggtgcaagc 480
agattttaaa agggcttctt tatttacata gtcgttctcc accaattata catagagatc 540
tcaaagtga taacattttc atcaatggaa accaaggtga agtcaagatc ggtgaccttg 600
gactcgctgc gattcttcgt aaatcacatg ccgttcgttg cgttggaacc cctgagttta 660
tgggtccaga agtgtatgat gaggaatata atgagttggt tgatgtatat gcttttggca 720
tgtgtgtggt ggagatgggt acttttgatt atccttacag tgaatgtact caccggcac 780
aaatctacaa gaaagttacc tcggggaaaa agcctgaagc tttttactta gtgaaggatc 840
ctgaggttcg tgagtttggt gagaagtgtt tagctaacgt gacgtgtagg ctaacggcat 900
tggagctttt acaagaccct tttctacaag atgataatat ggatggattt gttatgagac 960
ctattgatta ctacaatggt tatgatgaaa ctggtgtggt ccttagacat cctttgattg 1020
atgatcctct ttaccatgat cagtttgagt cgtcacagat atgtgagatc gatcttttcg 1080
ctaacgtaga tgaagatcat gtcgacattt cgattaaagg gaagagaaac ggtgatgatg 1140
ggatattctt gagacttaga atatctgatg ctgaaggacg gataaggaac atttacttcc 1200
cgtttgagac ggctattgat actgcatgga gtgtagcggg tgagatgggt tcagagctcg 1260
acataacgaa tcaagatggt gcgaaaaatcg cggagatgat cgatgcagag attgctgcat 1320
tgggtgcctga ttggaaaaat gatacagaaa gttcccaaaa tgtaaacaaac aacaagaaca 1380
acaacactgc aggatctgtg ggagagtgtg cttcaaacgg gtatatataa gagactgtat 1440
catcaggaga aaaatctcat cataatcatc atgagttcga tagttctgaa gacaagagct 1500
gttcttcggg tcacggtagg tttgcggata tgtgggggtt gcgagaatca tattctgatg 1560
atggagaaaa acagagctca aggaagggtt gaagtggacg gtggtcggag aatgagatga 1620
gacgagaact gagatggctt aaggcaaggc acaagattca acttatgaaa atgagaggtc 1680
aaacgatctg cgagacaccg atagagatct ctcttacacc gggaacttca gtttcgttac 1740
ctcttcttta cagggtata tcacttcctg tggatgccgt ggatatgtga cattattgta 1800
aagtctgatg atagttatca cttatatttg tatgtttcga catttttaac ttttgtttaag 1860
ttaaaggtta atgacatagt gtactttatt taaagagaag aagagtaaac gaaaaacata 1920
aattagtc
```

(2) INFORMATION FOR SEQ ID NO:1544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..595
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1544:

```
Ser Ser Ser Ile Ser Thr Asn Ser Lys His Leu Ser Leu Phe Leu
1          5          10          15
Ser His Thr Gln Asn Cys Arg Arg Arg Arg Val Met Asn Gly Glu Glu
20          25          30
Ser Phe Val Glu Asp Cys Ser Val Phe Val Glu Ile Asp Pro Ser Gly
35          40          45
Arg Tyr Gly Arg Tyr Asp Glu Ile Leu Gly Lys Gly Ala Ser Lys Thr
50          55          60
Val Tyr Arg Ala Phe Asp Glu Tyr Glu Gly Ile Glu Val Ala Trp Asn
65          70          75          80
Gln Val Lys Leu Arg Asn Phe Thr Arg Asn Pro Glu Glu Leu Glu Lys
85          90          95
Phe Phe Arg Glu Ile His Leu Leu Lys Thr Leu Asn His Gln Asn Ile
100         105         110
Met Lys Phe Tyr Thr Ser Trp Val Asp Thr Asn Asn Leu Ser Ile Asn
115         120         125
Phe Val Thr Glu Leu Phe Thr Ser Gly Thr Leu Arg Gln Tyr Arg Leu
130         135         140
```

Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	Val	Lys	Gln	Trp	Cys	Lys	Gln
145					150					155					160
Ile	Leu	Lys	Gly	Leu	Leu	Tyr	Leu	His	Ser	Arg	Ser	Pro	Pro	Ile	Ile
				165					170					175	
His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	Phe	Ile	Asn	Gly	Asn	Gln	Gly
			180					185					190		
Glu	Val	Lys	Ile	Gly	Asp	Leu	Gly	Leu	Ala	Ala	Ile	Leu	Arg	Lys	Ser
		195					200					205			
His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	Glu	Phe	Met	Ala	Pro	Glu	Val
	210					215					220				
Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	Asp	Val	Tyr	Ala	Phe	Gly	Met
225					230					235					240
Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	Tyr	Pro	Tyr	Ser	Glu	Cys	Thr
				245					250					255	
His	Pro	Ala	Gln	Ile	Tyr	Lys	Lys	Val	Thr	Ser	Gly	Lys	Lys	Pro	Glu
			260					265					270		
Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	Val	Arg	Glu	Phe	Val	Glu	Lys
		275					280					285			
Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	Thr	Ala	Leu	Glu	Leu	Leu	Gln
		290				295					300				
Asp	Pro	Phe	Leu	Gln	Asp	Asn	Met	Asp	Gly	Phe	Val	Met	Arg	Pro	
305					310				315					320	
Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly	Val	Phe	Leu	Arg	His
				325					330					335	
Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	Asp	Gln	Phe	Glu	Ser	Ser	Gln
			340					345					350		
Ile	Cys	Glu	Ile	Asp	Leu	Phe	Ala	Asn	Asp	Asp	Glu	Asp	His	Val	Asp
		355					360					365			
Ile	Ser	Ile	Lys	Gly	Lys	Arg	Asn	Gly	Asp	Asp	Gly	Ile	Phe	Leu	Arg
	370					375					380				
Leu	Arg	Ile	Ser	Asp	Ala	Glu	Gly	Arg	Ile	Arg	Asn	Ile	Tyr	Phe	Pro
				390						395					400
Phe	Glu	Thr	Ala	Ile	Asp	Thr	Ala	Trp	Ser	Val	Ala	Val	Glu	Met	Val
				405					410					415	
Ser	Glu	Leu	Asp	Ile	Thr	Asn	Gln	Asp	Val	Ala	Lys	Ile	Ala	Glu	Met
			420					425					430		
Ile	Asp	Ala	Glu	Ile	Ala	Ala	Leu	Val	Pro	Asp	Trp	Lys	Asn	Asp	Thr
		435					440					445			
Glu	Ser	Ser	Gln	Asn	Val	Asn	Asn	Asn	Lys	Asn	Asn	Asn	Thr	Ala	Gly
	450					455					460				
Phe	Cys	Gly	Glu	Cys	Ala	Ser	Asn	Gly	Tyr	Ile	Gln	Glu	Thr	Val	Ser
				470					475						480
Ser	Gly	Glu	Lys	Ser	His	His	Asn	His	His	Glu	Phe	Asp	Ser	Ser	Glu
				485					490					495	
Asp	Lys	Ser	Cys	Ser	Ser	Val	His	Gly	Arg	Phe	Ala	Asp	Met	Trp	Gly
			500					505					510		
Leu	Arg	Glu	Ser	Tyr	Ser	Asp	Asp	Gly	Glu	Lys	Gln	Ser	Ser	Arg	Lys
		515					520					525			
Val	Arg	Ser	Gly	Arg	Trp	Ser	Glu	Asn	Glu	Met	Arg	Arg	Glu	Leu	Arg
		530				535					540				
Trp	Leu	Lys	Ala	Arg	His	Lys	Ile	Gln	Leu	Met	Lys	Met	Arg	Gly	Gln
				550					555						560
Thr	Ile	Cys	Glu	Thr	Pro	Ile	Glu	Ile	Ser	Leu	Thr	Pro	Gly	Thr	Ser
				565					570					575	
Val	Ser	Leu	Pro	Leu	Leu	Tyr	Arg	Ala	Ile	Ser	Leu	Pro	Val	Asp	Ala
			580					585					590		
Val	Asp	Met													
		595													

(2) INFORMATION FOR SEQ ID NO:1545:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 568 amino acids

```

      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..568
      (D) OTHER INFORMATION: / Ceres Seq. ID 1500616
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1545:

```

Met 1	Asn	Gly	Glu	Glu 5	Ser	Phe	Val	Glu	Asp 10	Cys	Ser	Val	Phe	Val 15	Glu
Ile	Asp	Pro	Ser 20	Gly	Arg	Tyr	Gly	Arg 25	Tyr	Asp	Glu	Ile	Leu 30	Gly	Lys
Gly	Ala	Ser 35	Lys	Thr	Val	Tyr	Arg 40	Ala	Phe	Asp	Glu 45	Tyr	Glu	Gly	Ile
Glu	Val 50	Ala	Trp	Asn	Gln	Val 55	Lys	Leu	Arg	Asn 60	Phe	Thr	Arg	Asn	Pro
Glu 65	Glu	Leu	Glu	Lys 70	Phe	Phe	Arg	Glu	Ile	His 75	Leu	Leu	Lys	Thr	Leu 80
Asn	His	Gln	Asn 85	Met	Lys	Phe	Tyr	Thr 90	Ser	Trp	Val	Asp	Thr 95	Asn	
Asn	Leu	Ser 100	Ile	Asn	Phe	Val	Thr	Glu 105	Leu	Phe	Thr	Ser	Gly 110	Thr	Leu
Arg	Gln	Tyr 115	Arg	Leu	Arg	His	Arg 120	Arg	Val	Asn	Ile	Arg	Ala 125	Val	Lys
Gln	Trp 130	Cys	Lys	Gln	Ile	Leu 135	Lys	Gly	Leu	Leu	Tyr 140	Leu	His	Ser	Arg
Ser 145	Pro	Pro	Ile	Ile 150	His	Arg	Asp	Leu	Lys	Cys 155	Asp	Asn	Ile	Phe	Ile 160
Asn	Gly	Asn	Gln 165	Gly	Glu	Val	Lys	Ile	Gly 170	Asp	Leu	Gly	Leu 175	Ala	Ala
Ile	Leu	Arg 180	Lys	Ser	His	Ala	Val	Arg 185	Cys	Val	Gly	Thr	Pro 190	Glu	Phe
Met	Ala 195	Pro	Glu	Val	Tyr	Asp	Glu 200	Glu	Tyr	Asn	Glu	Leu	Val 205	Asp	Val
Tyr	Ala 210	Phe	Gly	Met	Cys	Val 215	Leu	Glu	Met	Val	Thr 220	Phe	Asp	Tyr	Pro
Tyr 225	Ser	Glu	Cys	Thr 230	His	Pro	Ala	Gln	Ile	Tyr 235	Lys	Lys	Val	Thr	Ser 240
Gly	Lys	Lys	Pro 245	Glu	Ala	Phe	Tyr	Leu	Val 250	Lys	Asp	Pro	Glu	Val 255	Arg
Glu	Phe	Val 260	Glu	Lys	Cys	Leu	Ala 265	Asn	Val	Thr	Cys	Arg	Leu 270	Thr	Ala
Leu	Glu 275	Leu	Leu	Gln	Asp	Pro	Phe 280	Leu	Gln	Asp	Asp	Asn	Met 285	Asp	Gly
Phe	Val 290	Met	Arg	Pro	Ile	Asp 295	Tyr	Tyr	Asn	Gly	Tyr 300	Asp	Glu	Thr	Gly
Val 305	Phe	Leu	Arg	His 310	Pro	Leu	Ile	Asp	Asp	Pro 315	Leu	Tyr	His	Asp	Gln 320
Phe	Glu	Ser	Ser 325	Gln	Ile	Cys	Glu	Ile	Asp 330	Leu	Phe	Ala	Asn 335	Asp	Asp
Glu	Asp	His 340	Val	Asp	Ile	Ser	Ile	Lys 345	Gly	Lys	Arg	Asn	Gly 350	Asp	Asp
Gly	Ile 355	Phe	Leu	Arg	Leu	Arg	Ile 360	Ser	Asp	Ala	Glu	Gly 365	Arg	Ile	Arg
Asn	Ile 370	Tyr	Phe	Pro	Phe	Glu 375	Thr	Ala	Ile	Asp 380	Thr	Ala	Trp	Ser	Val
Ala 385	Val	Glu	Met	Val 390	Ser	Glu	Leu	Asp	Ile	Thr 395	Asn	Gln	Asp	Val	Ala 400
Lys	Ile	Ala	Glu 405	Met	Ile	Asp	Ala	Glu	Ile 410	Ala	Ala	Leu	Val 415	Pro	Asp

Trp	Lys	Asn	Asp	Thr	Glu	Ser	Ser	Gln	Asn	Val	Asn	Asn	Asn	Lys	Asn
			420					425					430		
Asn	Asn	Thr	Ala	Gly	Phe	Cys	Gly	Glu	Cys	Ala	Ser	Asn	Gly	Tyr	Ile
		435					440					445			
Gln	Glu	Thr	Val	Ser	Ser	Gly	Glu	Lys	Ser	His	His	Asn	His	His	Glu
	450					455					460				
Phe	Asp	Ser	Ser	Glu	Asp	Lys	Ser	Cys	Ser	Ser	Val	His	Gly	Arg	Phe
465					470					475					480
Ala	Asp	Met	Trp	Gly	Leu	Arg	Glu	Ser	Tyr	Ser	Asp	Asp	Gly	Glu	Lys
				485					490					495	
Gln	Ser	Ser	Arg	Lys	Val	Arg	Ser	Gly	Arg	Trp	Ser	Glu	Asn	Glu	Met
			500					505					510		
Arg	Arg	Glu	Leu	Arg	Trp	Leu	Lys	Ala	Arg	His	Lys	Ile	Gln	Leu	Met
		515					520					525			
Lys	Met	Arg	Gly	Gln	Thr	Ile	Cys	Glu	Thr	Pro	Ile	Glu	Ile	Ser	Leu
	530					535					540				
Thr	Pro	Gly	Thr	Ser	Val	Ser	Leu	Pro	Leu	Leu	Tyr	Arg	Ala	Ile	Ser
545					550					555					560
Leu	Pro	Val	Asp	Ala	Val	Asp	Met								
					565										

(2) INFORMATION FOR SEQ ID NO:1546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..483

(D) OTHER INFORMATION: / Ceres Seq. ID 1500617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1546:

Met	Lys	Phe	Tyr	Thr	Ser	Trp	Val	Asp	Thr	Asn	Asn	Leu	Ser	Ile	Asn
1				5				10						15	
Phe	Val	Thr	Glu	Leu	Phe	Thr	Ser	Gly	Thr	Leu	Arg	Gln	Tyr	Arg	Leu
			20					25					30		
Arg	His	Arg	Arg	Val	Asn	Ile	Arg	Ala	Val	Lys	Gln	Trp	Cys	Lys	Gln
			35				40					45			
Ile	Leu	Lys	Gly	Leu	Leu	Tyr	Leu	His	Ser	Arg	Ser	Pro	Pro	Ile	Ile
	50					55				60					
His	Arg	Asp	Leu	Lys	Cys	Asp	Asn	Ile	Phe	Ile	Asn	Gly	Asn	Gln	Gly
65				70					75					80	
Glu	Val	Lys	Ile	Gly	Asp	Leu	Gly	Leu	Ala	Ala	Ile	Leu	Arg	Lys	Ser
			85					90						95	
His	Ala	Val	Arg	Cys	Val	Gly	Thr	Pro	Glu	Phe	Met	Ala	Pro	Glu	Val
			100					105					110		
Tyr	Asp	Glu	Glu	Tyr	Asn	Glu	Leu	Val	Asp	Val	Tyr	Ala	Phe	Gly	Met
	115						120					125			
Cys	Val	Leu	Glu	Met	Val	Thr	Phe	Asp	Tyr	Pro	Tyr	Ser	Glu	Cys	Thr
	130					135					140				
His	Pro	Ala	Gln	Ile	Tyr	Lys	Lys	Val	Thr	Ser	Gly	Lys	Lys	Pro	Glu
145				150					155					160	
Ala	Phe	Tyr	Leu	Val	Lys	Asp	Pro	Glu	Val	Arg	Glu	Phe	Val	Glu	Lys
			165					170						175	
Cys	Leu	Ala	Asn	Val	Thr	Cys	Arg	Leu	Thr	Ala	Leu	Glu	Leu	Leu	Gln
			180					185					190		
Asp	Pro	Phe	Leu	Gln	Asp	Asp	Asn	Met	Asp	Gly	Phe	Val	Met	Arg	Pro
	195						200					205			
Ile	Asp	Tyr	Tyr	Asn	Gly	Tyr	Asp	Glu	Thr	Gly	Val	Phe	Leu	Arg	His
210					215						220				
Pro	Leu	Ile	Asp	Asp	Pro	Leu	Tyr	His	Asp	Gln	Phe	Glu	Ser	Ser	Gln

225 230 235 240
Ile Cys Glu Ile Asp Leu Phe Ala Asn Asp Asp Glu Asp His Val Asp
245 250 255
Ile Ser Ile Lys Gly Lys Arg Asn Gly Asp Asp Gly Ile Phe Leu Arg
260 265 270
Leu Arg Ile Ser Asp Ala Glu Gly Arg Ile Arg Asn Ile Tyr Phe Pro
275 280 285
Phe Glu Thr Ala Ile Asp Thr Ala Trp Ser Val Ala Val Glu Met Val
290 295 300
Ser Glu Leu Asp Ile Thr Asn Gln Asp Val Ala Lys Ile Ala Glu Met
305 310 315 320
Ile Asp Ala Glu Ile Ala Ala Leu Val Pro Asp Trp Lys Asn Asp Thr
325 330 335
Glu Ser Ser Gln Asn Val Asn Asn Asn Lys Asn Asn Asn Thr Ala Gly
340 345 350
Phe Cys Gly Glu Cys Ala Ser Asn Gly Tyr Ile Gln Glu Thr Val Ser
355 360 365
Ser Gly Glu Lys Ser His His Asn His His Glu Phe Asp Ser Ser Glu
370 375 380
Asp Lys Ser Cys Ser Ser Val His Gly Arg Phe Ala Asp Met Trp Gly
385 390 395 400
Leu Arg Glu Ser Tyr Ser Asp Asp Gly Glu Lys Gln Ser Ser Arg Lys
405 410 415
Val Arg Ser Gly Arg Trp Ser Glu Asn Glu Met Arg Arg Glu Leu Arg
420 425 430
Trp Leu Lys Ala Arg His Lys Ile Gln Leu Met Lys Met Arg Gly Gln
435 440 445
Thr Ile Cys Glu Thr Pro Ile Glu Ile Ser Leu Thr Pro Gly Thr Ser
450 455 460
Val Ser Leu Pro Leu Leu Tyr Arg Ala Ile Ser Leu Pro Val Asp Ala
465 470 475 480
Val Asp Met

(2) INFORMATION FOR SEQ ID NO:1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1512
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1547:

attctgaata	agatcaagaa	tttacagggt	ctctcttctc	tctctctcaa	gttctgtttt	60
gtttatacaa	attacaactt	tagtttcgta	aataggtact	cattagttga	tcattgctct	120
ctatgtcttg	ctatgcaatt	caataggcta	gtgtatcacc	aatcacagat	ccgggatccc	180
ggcttagtaa	acattataaa	gcttgcata	acactttatt	tggatttgga	tttagtaaaa	240
aaattcattt	tacagtattt	gaaaaaatac	aaaatggcga	aaatctaccg	gaagttgaca	300
ggctacgggtg	gtgaaggagg	gcgtgaatgg	gacgatgatg	tatatgaggg	tgtaagaaaa	360
gtgtatgtag	gacaagatat	caatcgtatc	acttacgtca	aattcgagta	tgtgaaggaa	420
gacggccaag	tagtaacaac	tgaatatggg	aaaatcattc	aacaacccaa	agagtttgta	480
cttcaatatc	cggacgaaca	tatcatagcg	gtggaaggaa	actatcgcg	agtggctcta	540
tgtgccacag	aggtgatcac	aaacctcgct	ttcaagacct	caaagggtag	aaagtcacca	600
ctgtttggct	caaacttgct	tggaattacg	accggtacaa	agttcgttat	tgaggatgga	660
ggaaagaaga	tcgtagggtt	tcatggacgg	tcgggtaatg	ctctcgacgc	gcttgagggt	720
tactttgtac	atggctctct	aacaacgtct	ccgcctgttt	acaagctgga	tgcccaagggt	780
ggtacagacg	ggcgtgtttg	ggatgatggt	tcttacgacg	gcgttaaatac	gctgcgtatt	840
ggtcaagata	attctcgtat	tacttattta	gagttcgagt	acgagaaaag	cggtaaagta	900
gagacatgtc	gccatggggg	gaaacaagaa	agatcactga	agtttgagct	taaccgggat	960

gaatacatca	aatcggtgga	agcaacctat	gataaacgg	acattttccg	caatgtcgtc	1020
attacatcgc	ttmcatttga	aacatcgaag	gggagmacgt	cattctctgg	gtataaggga	1080
ggtaagaagt	ttaagctaga	gcaaaagggt	cgtaggcttg	tcgggttcca	tggaaggaa	1140
ggttcagcta	ttgatgccct	tgagcatat	tttgaccta	ttcctactcc	gactcctata	1200
attccagaag	aaactaccag	caataggcgg	cagcggagga	gttgcattgg	atgatgggtg	1260
ctacgatggg	gtaaggaaga	tacttgtagg	acaaggtaac	gatgggtgag	cctttgtcaa	1320
gtttgaatac	aataaaggaa	aagatcttgt	atctggagat	gaccatggga	agatgacatt	1380
actcggaact	gaagagtttg	tgcttgaaga	tggtgaatat	ctcacggcca	tagatggcta	1440
ttacgataag	attttcggag	tcgagacacc	aatgattatc	tgtcttcagt	ttaagacgaa	1500
caaaaggag tc						

(2) INFORMATION FOR SEQ ID NO:1548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..417

(D) OTHER INFORMATION: / Ceres Seq. ID 1500619

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1548:

Ile	Leu	Asn	Lys	Ile	Lys	Asn	Leu	Gln	Val	Leu	Ser	Ser	Leu	Ser	Leu
1			5					10						15	
Lys	Phe	Cys	Phe	Val	Tyr	Thr	Asn	Tyr	Asn	Phe	Ser	Phe	Val	Asn	Arg
			20					25					30		
Tyr	Ser	Leu	Val	Asp	His	Cys	Ser	Leu	Cys	Leu	Ala	Met	Gln	Phe	Asn
			35					40				45			
Arg	Leu	Val	Tyr	His	Gln	Ser	Gln	Ile	Arg	Asp	Pro	Gly	Leu	Val	Asn
			50				55				60				
Ile	Ile	Lys	Leu	Ala	Tyr	Thr	Leu	Tyr	Leu	Asp	Leu	Asp	Leu	Val	Lys
65							70			75				80	
Lys	Phe	Ile	Leu	Gln	Tyr	Leu	Lys	Lys	Tyr	Lys	Met	Ala	Lys	Ile	Tyr
			85							90				95	
Arg	Lys	Leu	Thr	Gly	Tyr	Gly	Gly	Glu	Gly	Gly	Arg	Glu	Trp	Asp	Asp
			100					105					110		
Asp	Val	Tyr	Glu	Gly	Val	Arg	Lys	Val	Tyr	Val	Gly	Gln	Asp	Ile	Asn
			115				120					125			
Arg	Ile	Thr	Tyr	Val	Lys	Phe	Glu	Tyr	Val	Lys	Glu	Asp	Gly	Gln	Val
			130				135					140			
Val	Thr	Thr	Glu	Tyr	Gly	Lys	Ile	Ile	Gln	Gln	Pro	Lys	Glu	Phe	Val
145						150				155				160	
Leu	Gln	Tyr	Pro	Asp	Glu	His	Ile	Ile	Ala	Val	Glu	Gly	Asn	Tyr	Arg
			165						170					175	
Gly	Val	Ala	Leu	Cys	Ala	Thr	Glu	Val	Ile	Thr	Asn	Leu	Val	Phe	Lys
			180					185					190		
Thr	Ser	Lys	Gly	Arg	Lys	Ser	Pro	Leu	Phe	Gly	Pro	Asn	Leu	Leu	Gly
			195				200					205			
Ile	Thr	Thr	Gly	Thr	Lys	Phe	Val	Ile	Glu	Asp	Gly	Gly	Lys	Lys	Ile
			210				215				220				
Val	Gly	Phe	His	Gly	Arg	Ser	Gly	Asn	Ala	Leu	Asp	Ala	Leu	Gly	Val
225					230				235					240	
Tyr	Phe	Val	His	Gly	Ser	Leu	Thr	Thr	Ser	Pro	Pro	Val	Tyr	Lys	Leu
			245						250					255	
Asp	Ala	Gln	Gly	Gly	Thr	Asp	Gly	Arg	Val	Trp	Asp	Asp	Gly	Ser	Tyr
			260					265					270		
Asp	Gly	Val	Lys	Ser	Leu	Arg	Ile	Gly	Gln	Asp	Asn	Ser	Arg	Ile	Thr
			275				280					285			
Tyr	Leu	Glu	Phe	Glu	Tyr	Glu	Lys	Gly	Gly	Lys	Leu	Glu	Thr	Cys	Arg
			290				295				300				
His	Gly	Val	Lys	Gln	Glu	Arg	Ser	Leu	Lys	Phe	Glu	Leu	Asn	Pro	Asp

305					310					315					320
Glu	Tyr	Ile	Lys	Ser	Val	Glu	Ala	Thr	Tyr	Asp	Lys	Pro	Asp	Ile	Phe
				325					330					335	
Arg	Asn	Val	Val	Ile	Thr	Ser	Leu	Xaa	Phe	Glu	Thr	Ser	Lys	Gly	Xaa
			340					345					350		
Thr	Ser	Phe	Ser	Gly	Tyr	Lys	Gly	Gly	Lys	Lys	Phe	Lys	Leu	Glu	Gln
		355					360					365			
Lys	Gly	Arg	Arg	Leu	Val	Gly	Phe	His	Gly	Lys	Glu	Gly	Ser	Ala	Ile
	370					375					380				
Asp	Ala	Leu	Gly	Ala	Tyr	Phe	Ala	Pro	Ile	Pro	Thr	Pro	Thr	Pro	Ile
385					390					395					400
Ile	Pro	Glu	Glu	Thr	Thr	Ser	Asn	Arg	Arg	Gln	Arg	Arg	Ser	Cys	Met
				405					410					415	
Gly															

(2) INFORMATION FOR SEQ ID NO:1549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 373 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..373

(D) OTHER INFORMATION: / Ceres Seq. ID 1500620

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1549:

Met	Gln	Phe	Asn	Arg	Leu	Val	Tyr	His	Gln	Ser	Gln	Ile	Arg	Asp	Pro
1				5					10					15	
Gly	Leu	Val	Asn	Ile	Ile	Lys	Leu	Ala	Tyr	Thr	Leu	Tyr	Leu	Asp	Leu
			20					25					30		
Asp	Leu	Val	Lys	Lys	Phe	Ile	Leu	Gln	Tyr	Leu	Lys	Lys	Tyr	Lys	Met
		35					40					45			
Ala	Lys	Ile	Tyr	Arg	Lys	Leu	Thr	Gly	Tyr	Gly	Gly	Glu	Gly	Gly	Arg
	50					55					60				
Glu	Trp	Asp	Asp	Asp	Val	Tyr	Glu	Gly	Val	Arg	Lys	Val	Tyr	Val	Gly
65					70					75					80
Gln	Asp	Ile	Asn	Arg	Ile	Thr	Tyr	Val	Lys	Phe	Glu	Tyr	Val	Lys	Glu
			85						90					95	
Asp	Gly	Gln	Val	Val	Thr	Thr	Glu	Tyr	Gly	Lys	Ile	Ile	Gln	Gln	Pro
			100					105					110		
Lys	Glu	Phe	Val	Leu	Gln	Tyr	Pro	Asp	Glu	His	Ile	Ile	Ala	Val	Glu
		115					120					125			
Gly	Asn	Tyr	Arg	Gly	Val	Ala	Leu	Cys	Ala	Thr	Glu	Val	Ile	Thr	Asn
	130					135					140				
Leu	Val	Phe	Lys	Thr	Ser	Lys	Gly	Arg	Lys	Ser	Pro	Leu	Phe	Gly	Pro
145					150					155					160
Asn	Leu	Leu	Gly	Ile	Thr	Thr	Gly	Thr	Lys	Phe	Val	Ile	Glu	Asp	Gly
			165						170					175	
Gly	Lys	Lys	Ile	Val	Gly	Phe	His	Gly	Arg	Ser	Gly	Asn	Ala	Leu	Asp
		180						185					190		
Ala	Leu	Gly	Val	Tyr	Phe	Val	His	Gly	Ser	Leu	Thr	Thr	Ser	Pro	Pro
		195					200					205			
Val	Tyr	Lys	Leu	Asp	Ala	Gln	Gly	Gly	Thr	Asp	Gly	Arg	Val	Trp	Asp
	210					215					220				
Asp	Gly	Ser	Tyr	Asp	Gly	Val	Lys	Ser	Leu	Arg	Ile	Gly	Gln	Asp	Asn
225					230					235					240
Ser	Arg	Ile	Thr	Tyr	Leu	Glu	Phe	Glu	Tyr	Glu	Lys	Gly	Gly	Lys	Leu
			245						250					255	
Glu	Thr	Cys	Arg	His	Gly	Val	Lys	Gln	Glu	Arg	Ser	Leu	Lys	Phe	Glu
			260					265						270	

Leu Asn Pro Asp Glu Tyr Ile Lys Ser Val Glu Ala Thr Tyr Asp Lys
275 280 285
Pro Asp Ile Phe Arg Asn Val Val Ile Thr Ser Leu Xaa Phe Glu Thr
290 295 300
Ser Lys Gly Xaa Thr Ser Phe Ser Gly Tyr Lys Gly Gly Lys Lys Phe
305 310 315 320
Lys Leu Glu Gln Lys Gly Arg Arg Leu Val Gly Phe His Gly Lys Glu
325 330 335
Gly Ser Ala Ile Asp Ala Leu Gly Ala Tyr Phe Ala Pro Ile Pro Thr
340 345 350
Pro Thr Pro Ile Ile Pro Glu Glu Thr Thr Ser Asn Arg Arg Gln Arg
355 360 365
Arg Ser Cys Met Gly
370

(2) INFORMATION FOR SEQ ID NO:1550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..326

(D) OTHER INFORMATION: / Ceres Seq. ID 1500621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1550:

Met Ala Lys Ile Tyr Arg Lys Leu Thr Gly Tyr Gly Gly Glu Gly Gly
1 5 10 15
Arg Glu Trp Asp Asp Val Tyr Glu Gly Val Arg Lys Val Tyr Val
20 25 30
Gly Gln Asp Ile Asn Arg Ile Thr Tyr Val Lys Phe Glu Tyr Val Lys
35 40 45
Glu Asp Gly Gln Val Val Thr Thr Glu Tyr Gly Lys Ile Ile Gln Gln
50 55 60
Pro Lys Glu Phe Val Leu Gln Tyr Pro Asp Glu His Ile Ile Ala Val
65 70 75 80
Glu Gly Asn Tyr Arg Gly Val Ala Leu Cys Ala Thr Glu Val Ile Thr
85 90 95
Asn Leu Val Phe Lys Thr Ser Lys Gly Arg Lys Ser Pro Leu Phe Gly
100 105 110
Pro Asn Leu Leu Gly Ile Thr Thr Gly Thr Lys Phe Val Ile Glu Asp
115 120 125
Gly Gly Lys Lys Ile Val Gly Phe His Gly Arg Ser Gly Asn Ala Leu
130 135 140
Asp Ala Leu Gly Val Tyr Phe Val His Gly Ser Leu Thr Thr Ser Pro
145 150 155 160
Pro Val Tyr Lys Leu Asp Ala Gln Gly Gly Thr Asp Gly Arg Val Trp
165 170 175
Asp Asp Gly Ser Tyr Asp Gly Val Lys Ser Leu Arg Ile Gly Gln Asp
180 185 190
Asn Ser Arg Ile Thr Tyr Leu Glu Phe Glu Tyr Glu Lys Gly Gly Lys
195 200 205
Leu Glu Thr Cys Arg His Gly Val Lys Gln Glu Arg Ser Leu Lys Phe
210 215 220
Glu Leu Asn Pro Asp Glu Tyr Ile Lys Ser Val Glu Ala Thr Tyr Asp
225 230 235 240
Lys Pro Asp Ile Phe Arg Asn Val Val Ile Thr Ser Leu Xaa Phe Glu
245 250 255
Thr Ser Lys Gly Xaa Thr Ser Phe Ser Gly Tyr Lys Gly Gly Lys Lys
260 265 270
Phe Lys Leu Glu Gln Lys Gly Arg Arg Leu Val Gly Phe His Gly Lys

	275					280						285					
Glu	Gly	Ser	Ala	Ile	Asp	Ala	Leu	Gly	Ala	Tyr	Phe	Ala	Pro	Ile	Pro		
	290					295					300						
Thr	Pro	Thr	Pro	Ile	Ile	Pro	Glu	Glu	Thr	Thr	Ser	Asn	Arg	Arg	Gln		
305					310					315					320		
Arg	Arg	Ser	Cys	Met	Gly												
				325													

(2) INFORMATION FOR SEQ ID NO:1551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 721 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..721

(D) OTHER INFORMATION: / Ceres Seq. ID 1500622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1551:

aacttaaact	cttttagtaa	caatggtttc	ttcttcttta	accaagcttg	tgttcttttg	60
ttgtctcctc	ctgctcacat	tcacggacaa	ccttggtggt	ggaaaatctg	gcaaagtga	120
gctcaatcct	tactacgaat	cactttgtcc	cggttgtcag	gaattcatcg	tcgatgacct	180
aggtaaaatc	tttgactacg	atctctacac	aatcactgat	ctcaagctgt	ttccatttgg	240
taatgccgaa	ctctccgata	atctgactgt	cacttgccag	catggtgaag	aggaatgcaa	300
actaaacgcc	cttgaagctt	gcgcattaag	aacttggccc	gatcagaaat	cacaatactc	360
gttcatacgg	tgcgtcgaaa	gcgatacgaa	aggctgggaa	tcatgtgtta	aaaactctgg	420
acgtgagaaa	gacgcaagt	aagaagactg	ataattctga	agctatttgg	gtaaatacca	480
attctcttca	tctttacttg	aggtttta	ttcttttgatg	ttcttttttt	ctttcttagt	540
tcttatgggt	attgttggtta	ttagtgtgtg	gttggtgttg	ttggtgatgt	tggtgttcta	600
atcatctctt	gtttctttta	ctctggtctt	gattatttga	ataaaggata	tctagagatt	660
gtgttggtg	tgtttttgta	ataattagag	tttgataaaa	graaatwaaa	tatttaaggt	720

(2) INFORMATION FOR SEQ ID NO:1552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1500623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1552:

Met	Val	Ser	Ser	Ser	Leu	Thr	Lys	Leu	Val	Phe	Phe	Gly	Cys	Leu	Leu		
1				5					10					15			
Leu	Leu	Thr	Phe	Thr	Asp	Asn	Leu	Val	Ala	Gly	Lys	Ser	Gly	Lys	Val		
			20					25					30				
Lys	Leu	Asn	Leu	Tyr	Tyr	Glu	Ser	Leu	Cys	Pro	Gly	Cys	Gln	Glu	Phe		
		35					40					45					
Ile	Val	Asp	Asp	Leu	Gly	Lys	Ile	Phe	Asp	Tyr	Asp	Leu	Tyr	Thr	Ile		
	50					55				60							
Thr	Asp	Leu	Lys	Leu	Phe	Pro	Phe	Gly	Asn	Ala	Glu	Leu	Ser	Asp	Asn		
65				70					75					80			
Leu	Thr	Val	Thr	Cys	Gln	His	Gly	Glu	Glu	Cys	Lys	Leu	Asn	Ala			
			85					90					95				
Leu	Glu	Ala	Cys	Ala	Leu	Arg	Thr	Trp	Pro	Asp	Gln	Lys	Ser	Gln	Tyr		
		100					105					110					
Ser	Phe	Ile	Arg	Cys	Val	Glu	Ser	Asp	Thr	Lys	Gly	Trp	Glu	Ser	Cys		
	115					120					125						
Val	Lys	Asn	Ser	Gly	Arg	Glu	Lys	Asp	Ala	Ser	Glu	Glu	Asp				

130 135 140

(2) INFORMATION FOR SEQ ID NO:1553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 605 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..605

(D) OTHER INFORMATION: / Ceres Seq. ID 1500633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1553:

gcaccccttt	tattgtagcg	acgcaagaag	aagcagctat	agcgtacgat	atcgcagcta	60
tcgagtaccg	tggactcaac	gccgttacta	acttcgacat	cagccgttat	ctgaaactcc	120
cgggtgccgga	gaaccctatc	gataccgcga	ataatctcct	cgagagtccg	cattctgatc	180
ttagcccat	tataaaacct	aaccacgagt	ctgacttatc	acagagtcaa	tcttcgtcag	240
aggacaacga	tgatcggaaa	acaaagctct	tgaagtcgtc	accttttagtg	gcagaggagg	300
taatcggacc	atcgacgcca	cctgagattg	ctccgcctcg	tcggagcttc	ccggaagata	360
tccagacgta	tttcgggtgt	caaaactccg	gcaagttaac	ggcggaggaa	gatgatgtta	420
tcttcgggtga	tttagattct	ttccttacgc	ctgatttcta	cagcgagtta	aatgattgct	480
aaagtgttgt	tcttctgata	agttttgttt	tttagttgtt	cagaatctcg	gttgtgaaaa	540
tcaacattga	cacatcgatt	attctttctt	gtgacaatct	tatataataa	agtttgaatc	600
ttttt						

(2) INFORMATION FOR SEQ ID NO:1554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1500634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1554:

Thr	Pro	Phe	Ile	Val	Ala	Thr	Gln	Glu	Glu	Ala	Ala	Ile	Ala	Tyr	Asp	
1				5					10					15		
Ile	Ala	Ala	Ile	Glu	Tyr	Arg	Gly	Leu	Asn	Ala	Val	Thr	Asn	Phe	Asp	
				20				25					30			
Ile	Ser	Arg	Tyr	Leu	Lys	Leu	Pro	Val	Pro	Glu	Asn	Pro	Ile	Asp	Thr	
				35				40				45				
Ala	Asn	Asn	Leu	Leu	Glu	Ser	Pro	His	Ser	Asp	Leu	Ser	Pro	Phe	Ile	
				50				55			60					
Lys	Pro	Asn	His	Glu	Ser	Asp	Leu	Ser	Gln	Ser	Gln	Ser	Ser	Ser	Glu	
65				70					75					80		
Asp	Asn	Asp	Asp	Arg	Lys	Thr	Lys	Leu	Leu	Lys	Ser	Ser	Pro	Leu	Val	
				85				90					95			
Ala	Glu	Glu	Val	Ile	Gly	Pro	Ser	Thr	Pro	Pro	Glu	Ile	Ala	Pro	Pro	
				100				105					110			
Arg	Arg	Ser	Phe	Pro	Glu	Asp	Ile	Gln	Thr	Tyr	Phe	Gly	Cys	Gln	Asn	
				115				120				125				
Ser	Gly	Lys	Leu	Thr	Ala	Glu	Glu	Asp	Asp	Val	Ile	Phe	Gly	Asp	Leu	
				130				135				140				
Asp	Ser	Phe	Leu	Thr	Pro	Asp	Phe	Tyr	Ser	Glu	Leu	Asn	Asp	Cys		
145				150						155						

(2) INFORMATION FOR SEQ ID NO:1555:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1393 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1393
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1555:

```
aagccataga tattgacgaa atacactttt tgtctttttg ttgctgtgca acgtcataga      60
tctaactccg gaagaagaag aagatgagtg acgaaacgac gtcattctccg tccccagctc      120
cggcgaaagaa gaagcagaat ctgggatgga tggagtggtat gaggggatgg agcagtggtt      180
tcggggagat tctcttccag aggatcacag ctctctcattt ggagaatcct ctctctcttc      240
cttccgtcaa cgacctcact tgcgttgta cttggtccac cagcggcatt ggccgtgaaa      300
ccgcgaggca gcttgccagaa gctggtgctc atgttggtgat ggccgtaagg aacacaaagg      360
cggctcagga gctgatactg caatggcaga acgaatggtc tggtaaagggt ctcccactca      420
atattgaggc aatggagatt gatctactct cactggattc tgtcgcgaga tttgctgagg      480
ctttcaacgc tcggttagga cctttgcatg ttctgattaa caatgctggg atgtttgcta      540
tgggagaggc gcaaaaattc tcagaggaag gatatgagca gcacatgcaa gtgaatcatt      600
tagctccagc gctgctttca gtacttcttt tgccgtctct gatccgaggc tctcctagcc      660
gaatcattaa tgtgaattcc gttatgcata gtgtcggttt tgttgacccg gatgacatga      720
atgttggttc tggtagacgt aagtactcaa gccttatagg atactcaagc agcaagcttg      780
cccagattat gtttagtagc attcttttca aaaagcttcc tctggaaaca ggagtcagcg      840
tcgtatgtct atccccctggt gttgtcctaa caaatgttgc cagggatcta tccaggattc      900
ttcaagctct ttacgcagtg ataccttatt tcatattttc accccaagaa ggttgtagaa      960
gttctctatt ctcggccaca gatcctcaga ttccagagta ctgggaaaca ctaaaaaacg     1020
atgattggcc tgtttgccc ttcattctctc aagattgccg ccctgcaa at ccttccgaag     1080
aagcacacaa cacagaaact gcacagagag tgtggaaaaa gacgttagag ctggtgggtc     1140
ttcctctcga tgcagttgag aagctcatag aaggggaaaa tatccaatgc cggtatggag     1200
cacaacacga atagtctttc aaaattacca caggttaagt gacccattac agatcaaagg     1260
gtaggtaatt gagaaaatat cttttttttt tgtttccttg tattaatcta cacgatacag     1320
tggggaatgg atccccccagg catgtagttt gcttgagaat gtttgattgt tggataaaaag     1380
tcaagcttta gct
```

(2) INFORMATION FOR SEQ ID NO:1556:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..376
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1556:

```
Met Ser Asp Glu Thr Ser Ser Pro Ser Pro Ala Pro Ala Lys Lys
1      5      10      15
Lys Gln Asn Leu Gly Trp Met Glu Trp Met Arg Gly Trp Ser Ser Val
20      25      30
Phe Gly Glu Ile Leu Phe Gln Arg Ile Thr Ala Ser His Leu Glu Asn
35      40      45
Pro Leu Pro Leu Pro Ser Val Asn Asp Leu Thr Cys Val Val Thr Gly
50      55      60
Ser Thr Ser Gly Ile Gly Arg Glu Thr Ala Arg Gln Leu Ala Glu Ala
65      70      75      80
Gly Ala His Val Val Met Ala Val Arg Asn Thr Lys Ala Ala Gln Glu
85      90      95
Leu Ile Leu Gln Trp Gln Asn Glu Trp Ser Gly Lys Gly Leu Pro Leu
100      105      110
Asn Ile Glu Ala Met Glu Ile Asp Leu Leu Ser Leu Asp Ser Val Ala
115      120      125
Arg Phe Ala Glu Ala Phe Asn Ala Arg Leu Gly Pro Leu His Val Leu
130      135      140
```

Ile Asn Asn Ala Gly Met Phe Ala Met Gly Glu Ala Gln Lys Phe Ser
145 150 155 160
Glu Glu Gly Tyr Glu Gln His Met Gln Val Asn His Leu Ala Pro Ala
165 170 175
Leu Leu Ser Val Leu Leu Leu Pro Ser Leu Ile Arg Gly Ser Pro Ser
180 185 190
Arg Ile Ile Asn Val Asn Ser Val Met His Ser Val Gly Phe Val Asp
195 200 205
Pro Asp Asp Met Asn Val Val Ser Gly Arg Arg Lys Tyr Ser Ser Leu
210 215 220
Ile Gly Tyr Ser Ser Ser Lys Leu Ala Gln Ile Met Phe Ser Ser Ile
225 230 235 240
Leu Phe Lys Lys Leu Pro Leu Glu Thr Gly Val Ser Val Val Cys Leu
245 250 255
Ser Pro Gly Val Val Leu Thr Asn Val Ala Arg Asp Leu Ser Arg Ile
260 265 270
Leu Gln Ala Leu Tyr Ala Val Ile Pro Tyr Phe Ile Phe Ser Pro Gln
275 280 285
Glu Gly Cys Arg Ser Ser Leu Phe Ser Ala Thr Asp Pro Gln Ile Pro
290 295 300
Glu Tyr Trp Glu Thr Leu Lys Asn Asp Asp Trp Pro Val Cys Pro Phe
305 310 315 320
Ile Ser Gln Asp Cys Arg Pro Ala Asn Pro Ser Glu Glu Ala His Asn
325 330 335
Thr Glu Thr Ala Gln Arg Val Trp Lys Lys Thr Leu Glu Leu Val Gly
340 345 350
Leu Pro Leu Asp Ala Val Glu Lys Leu Ile Glu Gly Glu Asn Ile Gln
355 360 365
Cys Arg Tyr Gly Ala Gln His Glu
370 375

(2) INFORMATION FOR SEQ ID NO:1557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..354
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500647

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1557:

Met Glu Trp Met Arg Gly Trp Ser Ser Val Phe Gly Glu Ile Leu Phe
1 5 10 15
Gln Arg Ile Thr Ala Ser His Leu Glu Asn Pro Leu Pro Leu Pro Ser
20 25 30
Val Asn Asp Leu Thr Cys Val Val Thr Gly Ser Thr Ser Gly Ile Gly
35 40 45
Arg Glu Thr Ala Arg Gln Leu Ala Glu Ala Gly Ala His Val Val Met
50 55 60
Ala Val Arg Asn Thr Lys Ala Ala Gln Glu Leu Ile Leu Gln Trp Gln
65 70 75 80
Asn Glu Trp Ser Gly Lys Gly Leu Pro Leu Asn Ile Glu Ala Met Glu
85 90 95
Ile Asp Leu Leu Ser Leu Asp Ser Val Ala Arg Phe Ala Glu Ala Phe
100 105 110
Asn Ala Arg Leu Gly Pro Leu His Val Leu Ile Asn Asn Ala Gly Met
115 120 125
Phe Ala Met Gly Glu Ala Gln Lys Phe Ser Glu Glu Gly Tyr Glu Gln
130 135 140
His Met Gln Val Asn His Leu Ala Pro Ala Leu Leu Ser Val Leu Leu

145					150					155				160	
Leu	Pro	Ser	Leu	Ile	Arg	Gly	Ser	Pro	Ser	Arg	Ile	Ile	Asn	Val	Asn
				165					170					175	
Ser	Val	Met	His	Ser	Val	Gly	Phe	Val	Asp	Pro	Asp	Asp	Met	Asn	Val
			180					185					190		
Val	Ser	Gly	Arg	Arg	Lys	Tyr	Ser	Ser	Leu	Ile	Gly	Tyr	Ser	Ser	Ser
		195					200					205			
Lys	Leu	Ala	Gln	Ile	Met	Phe	Ser	Ser	Ile	Leu	Phe	Lys	Lys	Leu	Pro
	210					215					220				
Leu	Glu	Thr	Gly	Val	Ser	Val	Val	Cys	Leu	Ser	Pro	Gly	Val	Val	Leu
225					230				235					240	
Thr	Asn	Val	Ala	Arg	Asp	Leu	Ser	Arg	Ile	Leu	Gln	Ala	Leu	Tyr	Ala
			245						250					255	
Val	Ile	Pro	Tyr	Phe	Ile	Phe	Ser	Pro	Gln	Glu	Gly	Cys	Arg	Ser	Ser
		260					265						270		
Leu	Phe	Ser	Ala	Thr	Asp	Pro	Gln	Ile	Pro	Glu	Tyr	Trp	Glu	Thr	Leu
	275					280						285			
Lys	Asn	Asp	Asp	Trp	Pro	Val	Cys	Pro	Phe	Ile	Ser	Gln	Asp	Cys	Arg
	290					295					300				
Pro	Ala	Asn	Pro	Ser	Glu	Glu	Ala	His	Asn	Thr	Glu	Thr	Ala	Gln	Arg
305					310				315					320	
Val	Trp	Lys	Lys	Thr	Leu	Glu	Leu	Val	Gly	Leu	Pro	Leu	Asp	Ala	Val
			325						330					335	
Glu	Lys	Leu	Ile	Glu	Gly	Glu	Asn	Ile	Gln	Cys	Arg	Tyr	Gly	Ala	Gln
			340				345						350		
His	Glu														

(2) INFORMATION FOR SEQ ID NO:1558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..351
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1558:

Met	Arg	Gly	Trp	Ser	Ser	Val	Phe	Gly	Glu	Ile	Leu	Phe	Gln	Arg	Ile
1				5				10					15		
Thr	Ala	Ser	His	Leu	Glu	Asn	Pro	Leu	Pro	Leu	Pro	Ser	Val	Asn	Asp
			20					25					30		
Leu	Thr	Cys	Val	Val	Thr	Gly	Ser	Thr	Ser	Gly	Ile	Gly	Arg	Glu	Thr
		35				40						45			
Ala	Arg	Gln	Leu	Ala	Glu	Ala	Gly	Ala	His	Val	Val	Met	Ala	Val	Arg
	50					55					60				
Asn	Thr	Lys	Ala	Ala	Gln	Glu	Leu	Ile	Leu	Gln	Trp	Gln	Asn	Glu	Trp
65					70					75				80	
Ser	Gly	Lys	Gly	Leu	Pro	Leu	Asn	Ile	Glu	Ala	Met	Glu	Ile	Asp	Leu
			85					90					95		
Leu	Ser	Leu	Asp	Ser	Val	Ala	Arg	Phe	Ala	Glu	Ala	Phe	Asn	Ala	Arg
		100						105					110		
Leu	Gly	Pro	Leu	His	Val	Leu	Ile	Asn	Asn	Ala	Gly	Met	Phe	Ala	Met
		115					120					125			
Gly	Glu	Ala	Gln	Lys	Phe	Ser	Glu	Glu	Gly	Tyr	Glu	Gln	His	Met	Gln
	130					135					140				
Val	Asn	His	Leu	Ala	Pro	Ala	Leu	Leu	Ser	Val	Leu	Leu	Leu	Pro	Ser
145					150					155				160	
Leu	Ile	Arg	Gly	Ser	Pro	Ser	Arg	Ile	Ile	Asn	Val	Asn	Ser	Val	Met
			165						170					175	

His Ser Val Gly Phe Val Asp Pro Asp Asp Met Asn Val Val Ser Gly
180 185 190
Arg Arg Lys Tyr Ser Ser Leu Ile Gly Tyr Ser Ser Ser Lys Leu Ala
195 200 205
Gln Ile Met Phe Ser Ser Ile Leu Phe Lys Lys Leu Pro Leu Glu Thr
210 215 220
Gly Val Ser Val Val Cys Leu Ser Pro Gly Val Val Leu Thr Asn Val
225 230 235 240
Ala Arg Asp Leu Ser Arg Ile Leu Gln Ala Leu Tyr Ala Val Ile Pro
245 250 255
Tyr Phe Ile Phe Ser Pro Gln Glu Gly Cys Arg Ser Ser Leu Phe Ser
260 265 270
Ala Thr Asp Pro Gln Ile Pro Glu Tyr Trp Glu Thr Leu Lys Asn Asp
275 280 285
Asp Trp Pro Val Cys Pro Phe Ile Ser Gln Asp Cys Arg Pro Ala Asn
290 295 300
Pro Ser Glu Glu Ala His Asn Thr Glu Thr Ala Gln Arg Val Trp Lys
305 310 315 320
Lys Thr Leu Glu Leu Val Gly Leu Pro Leu Asp Ala Val Glu Lys Leu
325 330 335
Ile Glu Gly Glu Asn Ile Gln Cys Arg Tyr Gly Ala Gln His Glu
340 345 350

(2) INFORMATION FOR SEQ ID NO:1559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1272
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1559:

atagtaaacc	tattagccct	gtctttgctc	ttgaagcaac	ttcctccagg	agggttggtt	60
ycaaagctgc	tgctgggtgtg	tcaggtgact	tacctgagag	tactcctaag	gaacttagtc	120
agtatgagaa	gattattgag	cttttgacaa	ccctttttcc	actttgggtt	attttgggaa	180
cacttgttgg	catcttcaag	ccatccttgg	ttacatgggt	ggaaacagat	ctctttactc	240
taggtcttgg	atcttcttatg	ctttccatgg	gtttgactct	tacgtttgaa	gatttcagaa	300
gatgtttacg	taatccatgg	acggtgggtg	ttggttttct	tgctcaatat	atgatcaagc	360
caattctagg	ttttctcatt	gcaatgactc	ttaagctttc	ggcacctctt	gcgactggcc	420
ttatcctagt	ctcatgctgc	cctggaggac	aggcgtcaaa	cgttgctact	tacatttcca	480
aggggaatgt	agcgctctct	gtactcatga	caacgtgttc	aaccattggg	gctattataa	540
tgactcctct	tcttactaag	cttcttgctg	gtcagcttgt	tcccgttgac	gctgctggac	600
ttgctcttag	tacgttccaa	gtagtgttgg	ttcctaccat	aattggagtt	ctggcaaatg	660
agttctttcc	taaattttacg	tctaagatca	taacagtgac	gcctctaate	ggagtcattc	720
tgactactct	gctctgtgcc	agccctattg	gacaagttgc	agatgttttg	aaaacccaag	780
gagctcaact	tatactcccg	gtggcactcc	ttcatgctgc	agcctttgct	attggctatt	840
ggatttcaaa	gttttctttc	ggcgagtcca	cttcgcgtac	catttctata	gaatgtggaa	900
tgcaaagttc	agcgctcggg	ttcttgcttg	cacaaaagca	tttcacaaac	cctctagttg	960
ctgttccttc	tgcagtcagt	gttgtctgta	tggcgcttgg	cgggagcggc	ctggccgtgt	1020
tctggagaaa	cctaccgatt	ccggcagatg	acaaggatga	cttcaaagag	taaatagaagt	1080
aggaaaggct	gtttgcatct	tctccaaacg	atgtgattgt	tttgttgtaa	tgtagtaaaa	1140
cattacaaaa	tttgtgttga	aaaacatgaa	acaaaatgtg	tttaagagac	atagaaacaa	1200
ggcggtgcat	gatgacaact	ttgtggtcaa	cctttttttt	atttctcaat	taatggacaa	1260
atcttttttg	gc					

(2) INFORMATION FOR SEQ ID NO:1560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..356
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1560:

Ser	Lys	Pro	Ile	Ser	Pro	Val	Phe	Ala	Leu	Glu	Ala	Thr	Ser	Ser	Arg
1				5					10					15	
Arg	Val	Val	Cys	Lys	Ala	Ala	Ala	Gly	Val	Ser	Gly	Asp	Leu	Pro	Glu
		20						25					30		
Ser	Thr	Pro	Lys	Glu	Leu	Ser	Gln	Tyr	Glu	Lys	Ile	Ile	Glu	Leu	Leu
		35				40						45			
Thr	Thr	Leu	Phe	Pro	Leu	Trp	Val	Ile	Leu	Gly	Thr	Leu	Val	Gly	Ile
	50				55						60				
Phe	Lys	Pro	Ser	Leu	Val	Thr	Trp	Leu	Glu	Thr	Asp	Leu	Phe	Thr	Leu
65				70						75					80
Gly	Leu	Gly	Phe	Leu	Met	Leu	Ser	Met	Gly	Leu	Thr	Leu	Thr	Phe	Glu
			85						90					95	
Asp	Phe	Arg	Arg	Cys	Leu	Arg	Asn	Pro	Trp	Thr	Val	Gly	Val	Gly	Phe
			100					105					110		
Leu	Ala	Gln	Tyr	Met	Ile	Lys	Pro	Ile	Leu	Gly	Phe	Leu	Ile	Ala	Met
		115					120						125		
Thr	Leu	Lys	Leu	Ser	Ala	Pro	Leu	Ala	Thr	Gly	Leu	Ile	Leu	Val	Ser
	130					135						140			
Cys	Cys	Pro	Gly	Gly	Gln	Ala	Ser	Asn	Val	Ala	Thr	Tyr	Ile	Ser	Lys
145					150					155					160
Gly	Asn	Val	Ala	Leu	Ser	Val	Leu	Met	Thr	Thr	Cys	Ser	Thr	Ile	Gly
			165						170					175	
Ala	Ile	Ile	Met	Thr	Pro	Leu	Leu	Thr	Lys	Leu	Leu	Ala	Gly	Gln	Leu
			180					185					190		
Val	Pro	Val	Asp	Ala	Ala	Gly	Leu	Ala	Leu	Ser	Thr	Phe	Gln	Val	Val
		195					200						205		
Leu	Val	Pro	Thr	Ile	Ile	Gly	Val	Leu	Ala	Asn	Glu	Phe	Phe	Pro	Lys
	210					215							220		
Phe	Thr	Ser	Lys	Ile	Ile	Thr	Val	Thr	Pro	Leu	Ile	Gly	Val	Ile	Leu
225					230					235					240
Thr	Thr	Leu	Leu	Cys	Ala	Ser	Pro	Ile	Gly	Gln	Val	Ala	Asp	Val	Leu
			245						250					255	
Lys	Thr	Gln	Gly	Ala	Gln	Leu	Ile	Leu	Pro	Val	Ala	Leu	Leu	His	Ala
			260					265						270	
Ala	Ala	Phe	Ala	Ile	Gly	Tyr	Trp	Ile	Ser	Lys	Phe	Ser	Phe	Gly	Glu
		275					280						285		
Ser	Thr	Ser	Arg	Thr	Ile	Ser	Ile	Glu	Cys	Gly	Met	Gln	Ser	Ser	Ala
	290					295					300				
Leu	Gly	Phe	Leu	Leu	Ala	Gln	Lys	His	Phe	Thr	Asn	Pro	Leu	Val	Ala
305					310					315					320
Val	Pro	Ser	Ala	Val	Ser	Val	Val	Cys	Met	Ala	Leu	Gly	Gly	Ser	Gly
			325						330					335	
Leu	Ala	Val	Phe	Trp	Arg	Asn	Leu	Pro	Ile	Pro	Ala	Asp	Asp	Lys	Asp
			340				345						350		
Asp	Phe	Lys	Glu												
		355													

(2) INFORMATION FOR SEQ ID NO:1561:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 271 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..271

(D) OTHER INFORMATION: / Ceres Seq. ID 1500651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1561:

Met	Leu	Ser	Met	Gly	Leu	Thr	Leu	Thr	Phe	Glu	Asp	Phe	Arg	Arg	Cys
1			5						10					15	
Leu	Arg	Asn	Pro	Trp	Thr	Val	Gly	Val	Gly	Phe	Leu	Ala	Gln	Tyr	Met
			20					25					30		
Ile	Lys	Pro	Ile	Leu	Gly	Phe	Leu	Ile	Ala	Met	Thr	Leu	Lys	Leu	Ser
		35					40					45			
Ala	Pro	Leu	Ala	Thr	Gly	Leu	Ile	Leu	Val	Ser	Cys	Cys	Pro	Gly	Gly
	50					55					60				
Gln	Ala	Ser	Asn	Val	Ala	Thr	Tyr	Ile	Ser	Lys	Gly	Asn	Val	Ala	Leu
65					70					75					80
Ser	Val	Leu	Met	Thr	Thr	Cys	Ser	Thr	Ile	Gly	Ala	Ile	Ile	Met	Thr
			85						90					95	
Pro	Leu	Leu	Thr	Lys	Leu	Leu	Ala	Gly	Gln	Leu	Val	Pro	Val	Asp	Ala
			100					105					110		
Ala	Gly	Leu	Ala	Leu	Ser	Thr	Phe	Gln	Val	Val	Leu	Val	Pro	Thr	Ile
		115					120					125			
Ile	Gly	Val	Leu	Ala	Asn	Glu	Phe	Phe	Pro	Lys	Phe	Thr	Ser	Lys	Ile
	130					135					140				
Ile	Thr	Val	Thr	Pro	Leu	Ile	Gly	Val	Ile	Leu	Thr	Thr	Leu	Leu	Cys
145					150					155					160
Ala	Ser	Pro	Ile	Gly	Gln	Val	Ala	Asp	Val	Leu	Lys	Thr	Gln	Gly	Ala
			165					170						175	
Gln	Leu	Ile	Leu	Pro	Val	Ala	Leu	Leu	His	Ala	Ala	Ala	Phe	Ala	Ile
		180						185					190		
Gly	Tyr	Trp	Ile	Ser	Lys	Phe	Ser	Phe	Gly	Glu	Ser	Thr	Ser	Arg	Thr
		195					200					205			
Ile	Ser	Ile	Glu	Cys	Gly	Met	Gln	Ser	Ser	Ala	Leu	Gly	Phe	Leu	Leu
	210					215					220				
Ala	Gln	Lys	His	Phe	Thr	Asn	Pro	Leu	Val	Ala	Val	Pro	Ser	Ala	Val
225					230					235					240
Ser	Val	Val	Cys	Met	Ala	Leu	Gly	Gly	Ser	Gly	Leu	Ala	Val	Phe	Trp
			245						250					255	
Arg	Asn	Leu	Pro	Ile	Pro	Ala	Asp	Asp	Lys	Asp	Asp	Phe	Lys	Glu	
		260					265						270		

(2) INFORMATION FOR SEQ ID NO:1562:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..268

(D) OTHER INFORMATION: / Ceres Seq. ID 1500652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1562:

Met	Gly	Leu	Thr	Leu	Thr	Phe	Glu	Asp	Phe	Arg	Arg	Cys	Leu	Arg	Asn
1				5					10					15	
Pro	Trp	Thr	Val	Gly	Val	Gly	Phe	Leu	Ala	Gln	Tyr	Met	Ile	Lys	Pro
			20					25					30		
Ile	Leu	Gly	Phe	Leu	Ile	Ala	Met	Thr	Leu	Lys	Leu	Ser	Ala	Pro	Leu
		35					40					45			
Ala	Thr	Gly	Leu	Ile	Leu	Val	Ser	Cys	Cys	Pro	Gly	Gly	Gln	Ala	Ser
	50					55					60				
Asn	Val	Ala	Thr	Tyr	Ile	Ser	Lys	Gly	Asn	Val	Ala	Leu	Ser	Val	Leu
65					70				75						80
Met	Thr	Thr	Cys	Ser	Thr	Ile	Gly	Ala	Ile	Ile	Met	Thr	Pro	Leu	Leu

	85		90		95										
Thr	Lys	Leu	Leu	Ala	Gly	Gln	Leu	Val	Pro	Val	Asp	Ala	Ala	Gly	Leu
		100						105					110		
Ala	Leu	Ser	Thr	Phe	Gln	Val	Val	Leu	Val	Pro	Thr	Ile	Ile	Gly	Val
		115						120				125			
Leu	Ala	Asn	Glu	Phe	Phe	Pro	Lys	Phe	Thr	Ser	Lys	Ile	Ile	Thr	Val
	130					135					140				
Thr	Pro	Leu	Ile	Gly	Val	Ile	Leu	Thr	Thr	Leu	Leu	Cys	Ala	Ser	Pro
145					150					155					160
Ile	Gly	Gln	Val	Ala	Asp	Val	Leu	Lys	Thr	Gln	Gly	Ala	Gln	Leu	Ile
				165					170					175	
Leu	Pro	Val	Ala	Leu	Leu	His	Ala	Ala	Ala	Phe	Ala	Ile	Gly	Tyr	Trp
		180						185					190		
Ile	Ser	Lys	Phe	Ser	Phe	Gly	Glu	Ser	Thr	Ser	Arg	Thr	Ile	Ser	Ile
	195					200					205				
Glu	Cys	Gly	Met	Gln	Ser	Ser	Ala	Leu	Gly	Phe	Leu	Leu	Ala	Gln	Lys
	210					215				220					
His	Phe	Thr	Asn	Pro	Leu	Val	Ala	Val	Pro	Ser	Ala	Val	Ser	Val	Val
225					230					235					240
Cys	Met	Ala	Leu	Gly	Gly	Ser	Gly	Leu	Ala	Val	Phe	Trp	Arg	Asn	Leu
			245						250					255	
Pro	Ile	Pro	Ala	Asp	Asp	Lys	Asp	Asp	Phe	Lys	Glu				
		260				265									

(2) INFORMATION FOR SEQ ID NO:1563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1563:

gagactgaag	atattttaac	tttttgattt	ttgaagcaca	gagtgcctgat	gatcgggtgaa	60
gcctaaggaa	ggatttttaga	aagcaactga	gaacaaacct	tatccggttac	agtgggcaatg	120
gaggacaaat	cgccgacgtt	accgatttct	gaagatttat	cccggaaaaat	aatctctctt	180
gccgccggtg	aagctcatat	gatcgctctg	accggcgatg	gatgtgtgta	ctcatggggga	240
agaggaatgt	ttgggcgtct	tggtacgggt	aaggaatcgg	acgagcttgt	tccagttcga	300
gtcgaagtgc	agttcccaaa	tcaagcggaa	ggagaacgga	ttcgaatcat	tggtgttgct	360
gctggtgctt	atcacagtct	cgctgtctca	gatgatggct	cggtttggtg	ttgggggttat	420
aacatttatg	gtcaacttgg	ttttgatggg	gaaaactcct	tggcaccatg	tttgggtcaaa	480
aatttgtttg	aacaagaagc	atctagttct	tctct			

(2) INFORMATION FOR SEQ ID NO:1564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1564:

Met	Glu	Asp	Lys	Ser	Pro	Thr	Leu	Pro	Ile	Ser	Glu	Asp	Leu	Ser	Arg
1				5				10					15		
Lys	Ile	Ile	Ser	Leu	Ala	Ala	Gly	Glu	Ala	His	Thr	Ile	Ala	Leu	Thr
			20					25					30		
Gly	Asp	Gly	Cys	Val	Tyr	Ser	Trp	Gly	Arg	Gly	Met	Phe	Gly	Arg	Leu

[illegible]

(2) INFORMATION FOR SEQ ID NO:1565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..99
(D) OTHER INFORMATION: / Ceres Seq. ID 1500655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1565:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..89
(D) OTHER INFORMATION: / Ceres Seq. ID 1500656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1566:

Met	Phe	Gly	Arg	Leu	Gly	Thr	Gly	Lys	Glu	Ser	Asp	Glu	Leu	Val	Pro
1				5					10					15	
Val	Arg	Val	Glu	Phe	Glu	Phe	Pro	Asn	Gln	Ala	Glu	Gly	Glu	Arg	Ile
			20					25					30		
Arg	Ile	Ile	Gly	Val	Ala	Ala	Gly	Ala	Tyr	His	Ser	Leu	Ala	Val	Ser
			35				40					45			
Asp	Asp	Gly	Ser	Val	Trp	Cys	Trp	Gly	Tyr	Asn	Ile	Tyr	Gly	Gln	Leu
	50					55				60					
Gly	Phe	Asp	Gly	Glu	Asn	Ser	Leu	Ala	Pro	Cys	Leu	Val	Lys	Asn	Leu
65					70					75					80

Phe Glu Gln Glu Ala Ser Ser Ser Ser
85

(2) INFORMATION FOR SEQ ID NO:1567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500661

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1567:

aaaaacccta	gaaaacctct	ggagctatgg	agatgatgca	ggattcgttc	caagtccata	60
ggattccaca	atcgaagtat	gtcgatggag	ttagatggct	tccacaagct	tctgctttga	120
atcgtttctt	cgcaacagcg	tcctatgacg	cggattgtga	ttcttcatca	atcgagatcc	180
aatcgctcga	cccaaaccct	agagggaatc	acaacacgaa	cccgttaatc	gagtcgttat	240
cttcatggac	ttcaccttct	cgcgtttcgt	ctctagaagt	cgcgggaaac	ggcgggtggtg	300
gcggttcatt	caaaccaatg	gtttcagcag	ctacgtcttc	tggttctctt	cacgttctga	360
tgattgattt	ggtggaagga	gctgcgattg	aagaggttta	cgcggcggaa	gggggagagg	420
tttcatrgtg	ggacgcgtgg	aaggtgtgga	ttggagagag	ggaggagaat	gtgttactgt	480
tggtgaagat	gggagagtga	atgtagtgaa	gattgtgaat	ggtgaagggt	taaggatatag	540
aaaggtcttt	gatgggaatg	gattggtggc	ttatagagct	gtgaaatggg	cttctccgac	600
tgagtttggt	actggaggat	atggttttgg	tttgcaattg	tgggatcaga	ggaagtcttg	660
tgaagctggt	tcacaactca	aagggaactg	gtttcaaggc	aaaacttctg	caattgtcca	720
ctccattgac	attcatccat	ctcgggaagca	cacttgcat	gcgggagggt	cttcagggtac	780
tgtatttgct	tgggatcttc	ggtggccaca	gcaaccatt	gttctttctg	gggttgaggc	840
aagtgagaat	ataaacaatc	ctctgtctga	aagtgaggt	tgggaagttc	agtatgactc	900
atacacaaaa	tccaacgtct	catactcaag	gattctccct	gttatgacct	gctctgaaga	960
tggaatccct	ggtatcatag	aacaagggga	agaaccaatc	gagcttcttg	ctgaaccttg	1020
tgccattaac	agttttgaca	tcgacaggca	aaatccacag	gatgtgat	gtagcttgga	1080
gtgggaatca	atagcagttt	tctcaaggcc	ttagtataat	atggaactgt	gcacgggtatg	1140
ctatgttttc	ttctgcgagc	tacaacgaag	aaattgagga	aggtagtgat	agatgatgag	1200
agacaagttt	aaggaagagg	gtgtggaatg	tgtttataag	tttcattata	acaagatctt	1260
aaaatacatt	ctgcacaaac	agagttttgt	attcatctta	aagttagtgt	gatcttgaag	1320
atttgc						

(2) INFORMATION FOR SEQ ID NO:1568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..157
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1568:

Met	Glu	Met	Met	Gln	Asp	Ser	Phe	Gln	Val	His	Arg	Ile	Pro	Gln	Ser	
1				5					10					15		
Lys	Tyr	Val	Asp	Gly	Val	Arg	Trp	Leu	Pro	Gln	Ala	Ser	Ala	Leu	Asn	
			20					25					30			
Arg	Phe	Phe	Ala	Thr	Ala	Ser	Tyr	Asp	Ala	Asp	Cys	Asp	Ser	Ser	Ser	
			35				40				45					
Ile	Glu	Ile	Gln	Ser	Leu	Asp	Pro	Asn	Pro	Arg	Gly	Asn	His	Asn	Thr	
			50			55				60						
Asn	Pro	Leu	Ile	Glu	Ser	Leu	Ser	Ser	Trp	Thr	Ser	Pro	Ser	Arg	Val	
65					70				75					80		
Ser	Ser	Leu	Glu	Val	Ala	Gly	Asn	Gly	Gly	Gly	Gly	Ser	Phe	Lys		
			85					90					95			

Pro Met Val Ser Ala Ala Thr Ser Ser Gly Ser Leu His Val Leu Met
100 105 110
Ile Asp Leu Val Glu Gly Ala Ala Ile Glu Glu Val Tyr Ala Ala Glu
115 120 125
Gly Gly Glu Val Ser Xaa Trp Asp Ala Trp Lys Val Trp Ile Gly Glu
130 135 140
Arg Glu Glu Asn Val Leu Leu Leu Val Lys Met Gly Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:1569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1500663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1569:

Met Met Gln Asp Ser Phe Gln Val His Arg Ile Pro Gln Ser Lys Tyr
1 5 10 15
Val Asp Gly Val Arg Trp Leu Pro Gln Ala Ser Ala Leu Asn Arg Phe
20 25 30
Phe Ala Thr Ala Ser Tyr Asp Ala Asp Cys Asp Ser Ser Ile Glu
35 40 45
Ile Gln Ser Leu Asp Pro Asn Pro Arg Gly Asn His Asn Thr Asn Pro
50 55 60
Leu Ile Glu Ser Leu Ser Ser Trp Thr Ser Pro Ser Arg Val Ser Ser
65 70 75 80
Leu Glu Val Ala Gly Asn Gly Gly Gly Gly Gly Ser Phe Lys Pro Met
85 90 95
Val Ser Ala Ala Thr Ser Ser Gly Ser Leu His Val Leu Met Ile Asp
100 105 110
Leu Val Glu Gly Ala Ala Ile Glu Glu Val Tyr Ala Ala Glu Gly Gly
115 120 125
Glu Val Ser Xaa Trp Asp Ala Trp Lys Val Trp Ile Gly Glu Arg Glu
130 135 140
Glu Asn Val Leu Leu Leu Val Lys Met Gly Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:1570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1500664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1570:

Met Gln Asp Ser Phe Gln Val His Arg Ile Pro Gln Ser Lys Tyr Val
1 5 10 15
Asp Gly Val Arg Trp Leu Pro Gln Ala Ser Ala Leu Asn Arg Phe Phe
20 25 30
Ala Thr Ala Ser Tyr Asp Ala Asp Cys Asp Ser Ser Ser Ile Glu Ile
35 40 45
Gln Ser Leu Asp Pro Asn Pro Arg Gly Asn His Asn Thr Asn Pro Leu
50 55 60
Ile Glu Ser Leu Ser Ser Trp Thr Ser Pro Ser Arg Val Ser Ser Leu

[illegible]

(2) INFORMATION FOR SEQ ID NO:1571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..542
(D) OTHER INFORMATION: / Ceres Seq. ID 1500665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1571:

acataagtct	ctctctttaca	ttttgaaacc	ctaattttctc	aaaataaatg	tctgaagttg	60
agtaccggtg	ctttgtctggc	ggccttgcct	gggccaccaa	tgatgaagat	cttcaaagga	120
cgttctcaca	gttcggcgac	gttatcgatt	ctaagatcat	taacgaccgc	gagagtggaa	180
gatcaagggg	attcggattg	gtcaccttca	aggacgagaa	agccattgag	gatgctgattg	240
aagagatgaa	cggtaaatgc	ctcagtgac	gtgtcatcac	cgtgaacgag	gctcagtcga	300
gaggtagcgg	cgggtgatgg	gaaagttacg	gaggcggtgg	tggcggttgg	taatcaaaaga	360
tagagttggt	tgcgtgctgc	tgcctctgtt	ttggtttaga	tttggaattt	tgtcaccact	420
tcttggtttg	ttatcgttcg	tttggtttac	ttttttgatg	aaacagtttc	gtttaagtct	480
tctttgtctg	gatcgaaatg	ttaattcgcg	tgttgtttac	taaattttata	acgttttcctt	540
tt						

(2) INFORMATION FOR SEQ ID NO:1572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..101
(D) OTHER INFORMATION: / Ceres Seq. ID 1500666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1572:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..931
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1573:

aagatgggga	cgaaattgag	ctggatatag	aagctgtcga	caatgagact	ctatgggagc	60
ttgatcggtt	tgtgacgaac	tacaagaaga	tggctagcaa	aatcaagcgc	caagggttta	120
tcaggaacgt	gtcaactcca	cttaggaaca	tggcttcggt	agcagaaatg	ggtagtgcg	180
agaagagAAC	aaggagagga	gatgcagggg	aagaggatgt	tgacattgga	gaggacatac	240
caatcgaaga	ttatccatct	stagagatcg	aaagagatgg	gtactgcagt	tgacagtgc	300
gctagtagtg	gttctagttc	ttcaggcagt	tccagttcta	gtggtggtag	ttcctcgtct	360
agtgattcag	ggtcagggtg	gagttcatca	ggtagtgtat	ctgatgcaga	tagtggtcaa	420
tcgccatttg	tggaagcaaa	agaagcccaa	tgtaaaatc	atttggaat	ttaacggtg	480
attctgtcct	gaagtactag	gaacgtttag	ctgaggggtg	aaagggagga	atgaagggga	540
aaactgaagg	aaaggatttg	ttttttcttt	cgatgataaa	cttaggaagc	agatgtagtt	600
agaaagamaa	aatgtaatat	gtagatagaa	agagaatgct	agtttaagca	agaagaagag	660
ttcgttattt	aatacctttt	acatttagga	gttggttagt	gtatttgtga	gatgctgaac	720
agaggggtgag	agtgagtggg	taggtactgt	aggagaagaa	gaagaagaaa	agagtccttt	780
taggttctat	gactttat	atttttcttt	gttagtagtg	ttaaagagtc	tggttggtg	840
aggaaaaatg	gtgatagaag	agaagaaaga	aatcaatgca	atgtatcaga	tgtaaagtgt	900
tgcatatta	aaaaagaaaa	gttgattttc	c			

(2) INFORMATION FOR SEQ ID NO:1574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1574:

Asp	Gly	Asp	Glu	Ile	Glu	Leu	Asp	Ile	Glu	Ala	Val	Asp	Asn	Glu	Thr
1			5						10					15	
Leu	Trp	Glu	Leu	Asp	Arg	Phe	Val	Thr	Asn	Tyr	Lys	Lys	Met	Ala	Ser
			20					25					30		
Lys	Ile	Lys	Arg	Gln	Gly	Phe	Ile	Arg	Asn	Val	Ser	Thr	Pro	Leu	Arg
			35				40					45			
Asn	Met	Ala	Ser	Val	Ala	Glu	Met	Gly	Ser	Ala	Glu	Lys	Arg	Thr	Arg
			50				55				60				
Arg	Gly	Asp	Ala	Gly	Glu	Glu	Asp	Val	Asp	Ile	Gly	Glu	Asp	Ile	Pro
							70			75				80	
Ile	Glu	Asp	Tyr	Pro	Ser	Xaa	Glu	Ile	Glu	Arg	Asp	Gly	Tyr	Cys	Ser
							85			90				95	
Cys	Ser	Cys	Cys												

(2) INFORMATION FOR SEQ ID NO:1575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1500669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1575:

```
Met Ala Ser Lys Ile Lys Arg Gln Gly Phe Ile Arg Asn Val Ser Thr
1          5          10          15
Pro Leu Arg Asn Met Ala Ser Val Ala Glu Met Gly Ser Ala Glu Lys
          20          25          30
Arg Thr Arg Arg Gly Asp Ala Gly Glu Glu Asp Val Asp Ile Gly Glu
          35          40          45
Asp Ile Pro Ile Glu Asp Tyr Pro Ser Xaa Glu Ile Glu Arg Asp Gly
          50          55          60
Tyr Cys Ser Cys Ser Cys Cys
65          70
```

(2) INFORMATION FOR SEQ ID NO:1576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1500670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1576:

```
Met Gly Thr Ala Val Ala Ala Ala Ser Ser Gly Ser Ser Ser Ser
1          5          10          15
Gly Ser Ser Ser Ser Ser Gly Gly Ser Ser Ser Ser Ser Asp Ser Gly
          20          25          30
Ser Gly Gly Ser Ser Ser Gly Ser Asp Ser Asp Ala Asp Ser Val Gln
          35          40          45
Ser Pro Phe Val Glu Ala Lys Glu Ala Gln Cys
50          55
```

(2) INFORMATION FOR SEQ ID NO:1577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1506 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1506

(D) OTHER INFORMATION: / Ceres Seq. ID 1500675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1577:

```
accgagaaat gggatcggtca gccaatacag aaaccaacgg caacgcaccg ccaccgtcgt      60
cgaatcaaaa gcctccgggt acgaacggcg ttgatgggtc tcatcctcct cctcctcctt      120
taactcctga tcaagctatt atagagtcgg atccgtcgaa gaagaggaaa atggggatgc      180
ttcctctaga agtgggtact cgtgtgatgt gtcggtggag agacgggaaa caccatccgg      240
tgaaagtaat tgagcgccgg cggataycat aacggcgggtc aaaatgatta cgagtattac      300
gttcattaca ctgagtttaa taggaggctg gatgaatgga ctgagctgga ccaactggac      360
cttgattcag tagagtgcgc tgtagatgaa aaattggaag acaaggtaac aagcttgaag      420
gatgacacgt caccagaaga ggaagatcga taggacaca tatagagggt catgaagagc      480
tggatgcagc aagtttgcgt gaacatgaag agttcacgaa agtgaagaac atatcaacaa      540
ttgagcttgg aaaatatgag attgagactt ggtacttctc cccttttccg ccagaataca      600
atgactgtgt gaagctcttt ttttgtgagt ttgacctgaa cttcatgaaa cgcaaagagc      660
agcttcaaag gcatatgagr aagtgtgacc tgaagcacc acctgggtgat gaaatttacc      720
gaagtggtag cttgtcaatg tttgaggtag atggcaaaaa gaacaagggt tatgcacaga      780
atctctgcta cctggcaaa ttatttcttg accacaaaac tctttactac gatgttgatt      840
tgtttctatt ctacgttctt tgccaatgtg atgaccgagg atgccacatg gttgggtact      900
tttcaaagga gaagcattcg gaagaagcat acaacttagc ttgcattcta accctgcctt      960
```


catatcaaag	aaaaggctat	ggaaagttct	taatagcctt	ttcctatgaa	ctgtcaaaga	1020
aagagggaaa	agttgggaca	ccggraaaga	cccttgtcgg	atctaggcctt	actaagctac	1080
agaggttatt	ggactcgtgt	tctattagaa	atcttgaaaa	aacataaggg	aaacatttct	1140
atcaaggagc	tgagcgacgt	gacagcaatc	aaagcggaag	atatattaag	cacacttcag	1200
agcctagaac	tgatacagta	caggaaagga	cagcatgtga	tctgtgcgga	tccaaagggt	1260
ctggaccgac	atctgaaagc	tgcaggccga	ggtggtcctg	atgtagatgc	tagcaaactg	1320
atttgacac	cttacaagga	ccagagttaa	gagtaagtac	actcctcctg	tgccattgga	1380
tttgatttga	gtgtgtaagt	aaggggctgt	cttattctcc	tgaaatgtaa	gtgtacttta	1440
cttgtaaagt	ttgaaatcgt	acttggaatg	gtgtttgttt	acaactnctt	ataatgagga	1500
aatttg						

(2) INFORMATION FOR SEQ ID NO:1578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..225

(D) OTHER INFORMATION: / Ceres Seq. ID 1500676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1578:

Met	Arg	Thr	His	Ile	Glu	Gly	His	Glu	Leu	Asp	Ala	Ala	Ser	Leu
1			5					10					15	
Arg	Glu	His	Glu	Glu	Phe	Thr	Lys	Val	Lys	Asn	Ile	Ser	Thr	Ile
			20					25				30		
Leu	Gly	Lys	Tyr	Glu	Ile	Glu	Thr	Trp	Tyr	Phe	Ser	Pro	Phe	Pro
			35				40				45			
Glu	Tyr	Asn	Asp	Cys	Val	Lys	Leu	Phe	Phe	Cys	Glu	Phe	Cys	Leu
			50			55				60				Asn
Phe	Met	Lys	Arg	Lys	Glu	Gln	Leu	Gln	Arg	His	Met	Xaa	Lys	Cys
65					70				75					80
Leu	Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg	Ser	Gly	Thr	Leu
			85						90					95
Met	Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Val	Tyr	Ala	Gln	Asn
			100					105					110	Leu
Cys	Tyr	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys	Thr	Leu	Tyr	Tyr
			115				120					125		Asp
Val	Asp	Leu	Phe	Leu	Phe	Tyr	Val	Leu	Cys	Glu	Cys	Asp	Arg	Gly
			130			135				140				
Cys	His	Met	Val	Gly	Tyr	Phe	Ser	Lys	Glu	Lys	His	Ser	Glu	Glu
145					150				155					160
Tyr	Asn	Leu	Ala	Cys	Ile	Leu	Thr	Leu	Pro	Ser	Tyr	Gln	Arg	Lys
			165						170				175	Gly
Tyr	Gly	Lys	Phe	Leu	Ile	Ala	Phe	Ser	Tyr	Glu	Leu	Ser	Lys	Lys
			180				185					190		Glu
Gly	Lys	Val	Gly	Thr	Pro	Xaa	Lys	Thr	Leu	Val	Gly	Ser	Arg	Leu
			195				200					205		Thr
Lys	Leu	Gln	Arg	Leu	Leu	Asp	Ser	Cys	Ser	Ile	Arg	Asn	Leu	Glu
			210			215					220			Lys
Thr														
225														

(2) INFORMATION FOR SEQ ID NO:1579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1500677

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1579:

Met	Lys	Arg	Lys	Glu	Gln	Leu	Gln	Arg	His	Met	Xaa	Lys	Cys	Asp	Leu
1			5					10						15	
Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg	Ser	Gly	Thr	Leu	Ser	Met
			20					25					30		
Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Val	Tyr	Ala	Gln	Asn	Leu	Cys
		35					40					45			
Tyr	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys	Thr	Leu	Tyr	Tyr	Asp	Val
	50					55					60				
Asp	Leu	Phe	Leu	Phe	Tyr	Val	Leu	Cys	Glu	Cys	Asp	Asp	Arg	Gly	Cys
65					70				75					80	
His	Met	Val	Gly	Tyr	Phe	Ser	Lys	Glu	Lys	His	Ser	Glu	Glu	Ala	Tyr
			85					90						95	
Asn	Leu	Ala	Cys	Ile	Leu	Thr	Leu	Pro	Ser	Tyr	Gln	Arg	Lys	Gly	Tyr
			100					105					110		
Gly	Lys	Phe	Leu	Ile	Ala	Phe	Ser	Tyr	Glu	Leu	Ser	Lys	Lys	Glu	Gly
		115					120					125			
Lys	Val	Gly	Thr	Pro	Xaa	Lys	Thr	Leu	Val	Gly	Ser	Arg	Leu	Thr	Lys
	130					135					140				
Leu	Gln	Arg	Leu	Leu	Asp	Ser	Cys	Ser	Ile	Arg	Asn	Leu	Glu	Lys	Thr
145					150					155					160

(2) INFORMATION FOR SEQ ID NO:1580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..150

(D) OTHER INFORMATION: / Ceres Seq. ID 1500678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1580:

Met	Xaa	Lys	Cys	Asp	Leu	Lys	His	Pro	Pro	Gly	Asp	Glu	Ile	Tyr	Arg
1			5					10						15	
Ser	Gly	Thr	Leu	Ser	Met	Phe	Glu	Val	Asp	Gly	Lys	Lys	Asn	Lys	Val
			20					25					30		
Tyr	Ala	Gln	Asn	Leu	Cys	Tyr	Leu	Ala	Lys	Leu	Phe	Leu	Asp	His	Lys
		35					40					45			
Thr	Leu	Tyr	Tyr	Asp	Val	Asp	Leu	Phe	Leu	Phe	Tyr	Val	Leu	Cys	Glu
	50					55					60				
Cys	Asp	Asp	Arg	Gly	Cys	His	Met	Val	Gly	Tyr	Phe	Ser	Lys	Glu	Lys
65					70				75					80	
His	Ser	Glu	Glu	Ala	Tyr	Asn	Leu	Ala	Cys	Ile	Leu	Thr	Leu	Pro	Ser
			85					90						95	
Tyr	Gln	Arg	Lys	Gly	Tyr	Gly	Lys	Phe	Leu	Ile	Ala	Phe	Ser	Tyr	Glu
			100				105						110		
Leu	Ser	Lys	Lys	Glu	Gly	Lys	Val	Gly	Thr	Pro	Xaa	Lys	Thr	Leu	Val
		115					120					125			
Gly	Ser	Arg	Leu	Thr	Lys	Leu	Gln	Arg	Leu	Leu	Asp	Ser	Cys	Ser	Ile
	130					135					140				
Arg	Asn	Leu	Glu	Lys	Thr										
145					150										

(2) INFORMATION FOR SEQ ID NO:1581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 889 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..889
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500679

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1581:

aaaacgaact agagacagtt tgattcgaaa atcttgctcg	aaaatggagg atatcgtcga	60
ccaagaatta agcaattact gggaacctag ctccttgctc	caaaacgaat acttcgaata	120
cgacagctgg ccttttgaag aagccatttc tgggtcgat	gattcgagtt cgccggatgg	180
agctgcttcg tcgccggctt ctaagaatat tgtgtcggag	agaaacagaa gacagaaact	240
taaccagaga ctcttcgctc ttcgatcagt tgttcccaat	atcactaaga tggataaagc	300
ctcaataatc aaagatgcta ttagttacat agaaggatta	caatatgaag aaaagaagct	360
cgaagctgag atcagagaaac ttgaatctac accaaagagt	agccttagtt tcagcaaagg	420
atcttgatcg tgatttactt gttcctgtca catccaagaa	gatgaagcag cttgattctg	480
gttcttccac ttctctcatc gaagttctcg aattgaaggt	aacattcatg ggagagagga	540
caatggtggt gagtgttaaca tgtaataaga ggacagatac	aatggtgaaa ctgtgtgaag	600
tctttgagtc attgaatctc aaaatcctca cttccaatct	cacctctttc tctggcatga	660
tcttccacac tgtctttatt gaggcggatg aagaagaaca	agaggtgttg cggttaaaaa	720
tagaaacagg aataggagct tataatgaaa ctcaaagccc	tactttgagc atcgactctc	780
tttactaata atactttttt tcttcctttt ttggttcatt	ttggcttctc tctttacaat	840
aatgtatgtc tctcttttca tttttatgat ctcctacgtt	tgtttgctc	

(2) INFORMATION FOR SEQ ID NO:1582:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..141
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1582:

Lys Arg Thr Arg Asp Ser Leu Ile Arg Lys Ser Cys Arg Lys Met Glu	
1	5 10 15
Asp Ile Val Asp Gln Glu Leu Ser Asn Tyr Trp Glu Pro Ser Ser Leu	
20	25 30
Leu Gln Asn Glu Tyr Phe Glu Tyr Asp Ser Trp Pro Leu Glu Glu Ala	
35	40 45
Ile Ser Gly Ser Tyr Asp Ser Ser Ser Pro Asp Gly Ala Ala Ser Ser	
50	55 60
Pro Ala Ser Lys Asn Ile Val Ser Glu Arg Asn Arg Arg Gln Lys Leu	
65	70 75 80
Asn Gln Arg Leu Phe Ala Leu Arg Ser Val Val Pro Asn Ile Thr Lys	
85	90 95
Met Asp Lys Ala Ser Ile Ile Lys Asp Ala Ile Ser Tyr Ile Glu Gly	
100	105 110
Leu Gln Tyr Glu Glu Lys Lys Leu Glu Ala Glu Ile Arg Glu Leu Glu	
115	120 125
Ser Thr Pro Lys Ser Ser Leu Ser Phe Ser Lys Gly Phe	
130	135 140

(2) INFORMATION FOR SEQ ID NO:1583:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1500681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1583:

```
Met Glu Asp Ile Val Asp Gln Glu Leu Ser Asn Tyr Trp Glu Pro Ser
1          5          10          15
Ser Leu Leu Gln Asn Glu Tyr Phe Glu Tyr Asp Ser Trp Pro Leu Glu
          20          25          30
Glu Ala Ile Ser Gly Ser Tyr Asp Ser Ser Ser Pro Asp Gly Ala Ala
          35          40          45
Ser Ser Pro Ala Ser Lys Asn Ile Val Ser Glu Arg Asn Arg Arg Gln
          50          55          60
Lys Leu Asn Gln Arg Leu Phe Ala Leu Arg Ser Val Val Pro Asn Ile
65          70          75          80
Thr Lys Met Asp Lys Ala Ser Ile Ile Lys Asp Ala Ile Ser Tyr Ile
          85          90          95
Glu Gly Leu Gln Tyr Glu Glu Lys Lys Leu Glu Ala Glu Ile Arg Glu
          100          105          110
Leu Glu Ser Thr Pro Lys Ser Ser Leu Ser Phe Ser Lys Gly Phe
          115          120          125
```

(2) INFORMATION FOR SEQ ID NO:1584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1500682

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1584:

```
Met Lys Lys Arg Ser Ser Lys Leu Arg Ser Glu Asn Leu Asn Leu His
1          5          10          15
Gln Arg Val Ala Leu Val Ser Ala Lys Asp Phe Asp Arg Asp Leu Leu
          20          25          30
Val Pro Val Thr Ser Lys Lys Met Lys Gln Leu Asp Ser Gly Ser Ser
          35          40          45
Thr Ser Leu Ile Glu Val Leu Glu Leu Lys Val Thr Phe Met Gly Glu
          50          55          60
Arg Thr Met Val Val Ser Val Thr Cys Asn Lys Arg Thr Asp Thr Met
65          70          75          80
Val Lys Leu Cys Glu Val Phe Glu Ser Leu Asn Leu Lys Ile Leu Thr
          85          90          95
Ser Asn Leu Thr Ser Phe Ser Gly Met Ile Phe His Thr Val Phe Ile
          100          105          110
Glu Ala Asp Glu Glu Glu Gln Glu Val Leu Arg Leu Lys Ile Glu Thr
          115          120          125
Gly Ile Gly Ala Tyr Asn Glu Thr Gln Ser Pro Thr Leu Ser Ile Asp
          130          135          140
Ser Leu Tyr
145
```

(2) INFORMATION FOR SEQ ID NO:1585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 672 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(D) OTHER INFORMATION: / Ceres Seq. ID 1500683

(X1) SEQUENCE ALIGNMENT: SEQ ID NO:1000						
acccaaaaaaa	acaaaacaaa	aaattatat	caagagaaaa	aggaaaaaat	gaatttcac	60
tccgatcagg	taaagaaact	ctcaagctca	acaccagagg	agccagacca	caacaagcca	120
gtcgaaggaa	ccgaaacagc	tacaagacca	gctaccaacg	ccgagctcat	ggcaagtgcc	180
aagggttgtag	ctgaagctgc	tcaagccgca	gctcgtaacg	aatcagacaa	actcgacaag	240
ggtaaaagctg	ccggagcctc	tgctgatatc	ttagacgctg	ccgagaaata	cggtaaagttc	300
gatgaaaaga	ctgagcactg	tcagtacctc	gacaaggctg	agaagtattc	caacgactac	360
gagtcgtcac	actccaccgg	tgctgggtgg	cctcctcctc	cgacgagtca	ggctgagcca	420
gcaagtcagc	ctgagccggc	ggctaagaaa	gacgatgaag	agtctggtgg	tgggcttgga	480
ggttatgccca	agatggctca	aggtttcttg	aagtgatattg	atctttaatt	gttggttcac	540
attttcgtaa	tgataaatta	aataactagt	atcgtttgtg	actagtttat	gttgcttcgt	600
ttatgtttat	ggggagtgc	gagtgagtgt	aataacttct	ggtgatcatg	aatctaattc	660
atctttgttg	tg					

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1586:

(2) INFORMATION FOR SEQ ID NO:1587:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1500685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1587:

Met Asn Phe Ile Ser Asp Gln Val Lys Lys Leu Ser Ser Ser Thr Pro
1 5 10 15
Glu Glu Pro Asp His Asn Lys Pro Val Glu Gly Thr Glu Thr Ala Thr
20 25 30
Arg Pro Ala Thr Asn Ala Glu Leu Met Ala Ser Ala Lys Val Val Ala
35 40 45
Glu Ala Ala Gln Ala Ala Ala Arg Asn Glu Ser Asp Lys Leu Asp Lys
50 55 60
Gly Lys Val Ala Gly Ala Ser Ala Asp Ile Leu Asp Ala Ala Glu Lys
65 70 75 80
Tyr Gly Lys Phe Asp Glu Lys Ser Ser Thr Gly Gln Tyr Leu Asp Lys
85 90 95
Ala Glu Lys Tyr Leu Asn Asp Tyr Glu Ser Ser His Ser Thr Gly Ala
100 105 110
Gly Gly Pro Pro Pro Thr Ser Gln Ala Glu Pro Ala Ser Gln Pro
115 120 125
Glu Pro Ala Ala Lys Lys Asp Asp Glu Glu Ser Gly Gly Gly Leu Gly
130 135 140
Gly Tyr Ala Lys Met Ala Gln Gly Phe Leu Lys
145 150 155

(2) INFORMATION FOR SEQ ID NO:1588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1500686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1588:

Met Ala Ser Ala Lys Val Val Ala Glu Ala Ala Gln Ala Ala Ala Arg
1 5 10 15
Asn Glu Ser Asp Lys Leu Asp Lys Gly Lys Val Ala Gly Ala Ser Ala
20 25 30
Asp Ile Leu Asp Ala Ala Glu Lys Tyr Gly Lys Phe Asp Glu Lys Ser
35 40 45
Ser Thr Gly Gln Tyr Leu Asp Lys Ala Glu Lys Tyr Leu Asn Asp Tyr
50 55 60
Glu Ser Ser His Ser Thr Gly Ala Gly Gly Pro Pro Pro Pro Thr Ser
65 70 75 80
Gln Ala Glu Pro Ala Ser Gln Pro Glu Pro Ala Ala Lys Lys Asp Asp
85 90 95
Glu Glu Ser Gly Gly Gly Leu Gly Gly Tyr Ala Lys Met Ala Gln Gly
100 105 110
Phe Leu Lys
115

(2) INFORMATION FOR SEQ ID NO:1589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1057

(D) OTHER INFORMATION: / Ceres Seq. ID 1500687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1589:

aagcttttctt cttgttccta catacccatc ttccctcacc tacatcaaac ctaggggttc

ttaactatat	caacaacata	tataaattta	tatataggtt	gtgatctatt	gaagatcata	120
aagatcaaaa	ggagagaggt	attaaaaaat	gatgtgtagt	cgaggccatt	ggagacctgc	180
agaagacgag	aagctaaag	aactcgtcga	acaatttggt	cctcataatt	ggaacgccat	240
agctcagaag	ctctctggtc	gactctggtaa	gagttgtaga	ttgagatggt	ttaatcaatt	300
ggatcctagg	attaaccgaa	accctttcac	ggaggaagaa	gaagaaaggc	ttttagcgtc	360
tcatcggatc	catgggaaca	gatggctctg	gatcgttaga	ttttttcccg	gtcgaactga	420
taacgctggt	aaaaaccatt	ggcacgtcat	catggctcgt	cgtggccgag	aacggtccaa	480
gtcccggtcca	cgaggctctg	gcatatgag	cacggtggct	gcgactggga	tgattggtta	540
ttataaagac	tgcgataagg	agcaagatt	ggcaaccaca	accgctatca	attttcttaa	600
tcaattctct	catattaatc	attttcaagt	cctcaaagag	ttcttgaccg	taaagatcgg	660
gttcagaaat	agtactactc	caatacaaga	aggagcaata	gaccaaacta	aacgaccgat	720
ggagtctctac	aattttcttc	aagtaaacac	ggattcgaag	atacacgaat	tgatagataa	780
ttcaagaaaa	gacgaagaag	aagatgtcga	tcaaaacaac	cgaattccta	acgagaattg	840
tgttccattt	ttcgactttt	tgctctgttg	aaactctgcc	tctcagggtt	tatgttaatt	900
tgctccgtacc	acatgtacta	taaggtggac	catatgttaa	ttaaagataa	tgtagaaagt	960
actaatcaat	tagagctctt	gtttgagcca	aatgtgaaaa	ttagttaaagc	catcccaaac	1020
atgttcttgt	ataacaaata	taaggttgtta	cttttcc			

(2) INFORMATION FOR SEQ ID NO:1590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1500688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1590:

Met 1	Met	Cys	Ser	Arg 5	Gly	His	Trp	Arg	Pro 10	Ala	Glu	Asp	Glu	Lys 15	Leu
Arg	Glu	Leu	Val 20	Glu	Gln	Phe	Gly	Pro 25	His	Asn	Trp	Asn	Ala 30	Ile	Ala
Gln	Lys	Leu	Ser 35	Gly	Arg	Ser	Gly 40	Lys	Ser	Cys	Arg	Leu 45	Trp	Phe	
Asn	Gln 50	Leu	Asp	Pro	Arg	Ile 55	Asn	Arg	Asn	Pro	Phe 60	Thr	Glu	Glu	Glu
Glu 65	Glu	Arg	Leu	Leu	Ala 70	Ser	His	Arg	Ile	His 75	Gly	Asn	Arg	Trp	Ser 80
Val	Ile	Ala	Arg	Phe 85	Phe	Pro	Gly	Arg	Thr 90	Asp	Asn	Ala	Val	Lys 95	Asn
His	Trp	His	Val 100	Ile	Met	Ala	Arg	Arg 105	Gly	Arg	Glu	Arg	Ser 110	Lys	Leu
Arg	Pro	Arg	Gly 115	Leu	Gly	His	Asp 120	Gly	Thr	Val	Ala	Ala 125	Thr	Gly	Met
Ile	Gly 130	Asn	Tyr	Lys	Asp	Cys 135	Asp	Lys	Glu	Arg	Arg 140	Leu	Ala	Thr	Thr
Thr 145	Ala	Ile	Asn	Phe 150	Pro	Tyr	Gln	Phe	Ser	His 155	Ile	Asn	His	Phe	Gln 160
Val	Leu	Lys	Glu	Phe 165	Leu	Thr	Val	Lys	Ile 170	Gly	Phe	Arg	Asn	Ser 175	Thr
Thr	Pro	Ile	Gln 180	Glu	Gly	Ala	Ile	Asp 185	Gln	Thr	Lys	Arg	Pro 190	Met	Glu
Phe	Tyr	Asn 195	Phe	Leu	Gln	Val	Asn 200	Thr	Asp	Ser	Lys	Ile 205	His	Glu	Leu
Ile	Asp 210	Asn	Ser	Arg	Lys	Asp 215	Glu	Glu	Glu	Asp	Val 220	Asp	Gln	Asn	Asn
Arg 225	Ile	Pro	Asn	Glu	Asn 230	Cys	Val	Pro	Phe	Phe 235	Asp	Phe	Leu	Ser	Val 240
Gly	Asn	Ser	Ala	Ser 245	Gln	Gly	Leu	Cys							

(2) INFORMATION FOR SEQ ID NO:1591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..248
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1591:

Met Cys Ser Arg Gly His Trp Arg Pro Ala Glu Asp Glu Lys Leu Arg
1 5 10 15
Glu Leu Val Glu Gln Phe Gly Pro His Asn Trp Asn Ala Ile Ala Gln
20 25 30
Lys Leu Ser Gly Arg Ser Gly Lys Ser Cys Arg Leu Arg Trp Phe Asn
35 40 45
Gln Leu Asp Pro Arg Ile Asn Arg Asn Pro Phe Thr Glu Glu Glu Glu
50 55 60
Glu Arg Leu Leu Ala Ser His Arg Ile His Gly Asn Arg Trp Ser Val
65 70 75 80
Ile Ala Arg Phe Phe Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His
85 90 95
Trp His Val Ile Met Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu Arg
100 105 110
Pro Arg Gly Leu Gly His Asp Gly Thr Val Ala Ala Thr Gly Met Ile
115 120 125
Gly Asn Tyr Lys Asp Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr Thr
130 135 140
Ala Ile Asn Phe Pro Tyr Gln Phe Ser His Ile Asn His Phe Gln Val
145 150 155 160
Leu Lys Glu Phe Leu Thr Val Lys Ile Gly Phe Arg Asn Ser Thr Thr
165 170 175
Pro Ile Gln Glu Gly Ala Ile Asp Gln Thr Lys Arg Pro Met Glu Phe
180 185 190
Tyr Asn Phe Leu Gln Val Asn Thr Asp Ser Lys Ile His Glu Leu Ile
195 200 205
Asp Asn Ser Arg Lys Asp Glu Glu Glu Asp Val Asp Gln Asn Asn Arg
210 215 220
Ile Pro Asn Glu Asn Cys Val Pro Phe Phe Asp Phe Leu Ser Val Gly
225 230 235 240
Asn Ser Ala Ser Gln Gly Leu Cys
245

(2) INFORMATION FOR SEQ ID NO:1592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1592:

Met Ala Arg Arg Gly Arg Glu Arg Ser Lys Leu Arg Pro Arg Gly Leu
1 5 10 15
Gly His Asp Gly Thr Val Ala Ala Thr Gly Met Ile Gly Asn Tyr Lys
20 25 30
Asp Cys Asp Lys Glu Arg Arg Leu Ala Thr Thr Thr Ala Ile Asn Phe

35 40 45
Pro Tyr Gln Phe Ser His Ile Asn His Phe Gln Val Leu Lys Glu Phe
50 55 60
Leu Thr Val Lys Ile Gly Phe Arg Asn Ser Thr Thr Pro Ile Gln Glu
65 70 75 80
Gly Ala Ile Asp Gln Thr Lys Arg Pro Met Glu Phe Tyr Asn Phe Leu
85 90 95
Gln Val Asn Thr Asp Ser Lys Ile His Glu Leu Ile Asp Asn Ser Arg
100 105 110
Lys Asp Glu Glu Asp Val Asp Gln Asn Asn Arg Ile Pro Asn Glu
115 120 125
Asn Cys Val Pro Phe Phe Asp Phe Leu Ser Val Gly Asn Ser Ala Ser
130 135 140
Gln Gly Leu Cys
145

(2) INFORMATION FOR SEQ ID NO:1593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..546
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1593:

agtaattttc agtcggcgtc cttcttttgt ctgaaccacc ggaggagctc gatccattga	60
ttagaagatg acaactccac aagtgaagac cggtttgttc gttgggttga acaagggaca	120
tggtgttacc agacgtgaat tagctcctcg tctcgttct cgcaaaggaa aaacgagcaa	180
gaggacaatc tttatcagaa acttgataaa ggaagttgct ggtcaagctc cctatgagaa	240
gagaatcact gagcttttga aggttgctaa gaggaagttg ggaaccacaca agagagccaa	300
gcgaaagaga gaggagatgt ccagtgttct ccgcaagatg aggtctggcg gtggtggtgc	360
aactgagaag aagaagtga cgtcatctta agtttggtgaa tcgctcgtaa agagttatgg	420
tttcttggtg caaaatcggtt attatgattc ctaagcttct cgtattatgt tttgttagaa	480
tatcggactt aaagagagtt ttgtctgaga ccagtgactc tgscttttaa ctatttgcct	540
cttttg	

(2) INFORMATION FOR SEQ ID NO:1594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1594:

Met Thr Thr Pro Gln Val Lys Thr Gly Leu Phe Val Gly Leu Asn Lys	
1 5 10 15	
Gly His Val Val Thr Arg Arg Glu Leu Ala Pro Arg Pro Arg Ser Arg	
20 25 30	
Lys Gly Lys Thr Ser Lys Arg Thr Ile Phe Ile Arg Asn Leu Ile Lys	
35 40 45	
Glu Val Ala Gly Gln Ala Pro Tyr Glu Lys Arg Ile Thr Glu Leu Leu	
50 55 60	
Lys Val Ala Lys Arg Lys Leu Gly Thr His Lys Arg Ala Lys Arg Lys	
65 70 75 80	
Arg Glu Glu Met Ser Ser Val Leu Arg Lys Met Arg Ser Gly Gly Gly	
85 90 95	

Gly Ala Thr Glu Lys Lys Lys
100

(2) INFORMATION FOR SEQ ID NO:1595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..702
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1595:

tcttttgcgt	gactgtcaaa	tctcattctt	ctctttcttc	tctctctcca	agagaaagaa	60
aatctgagtt	tccgagaaaa	taaaatctca	agagttaaaa	agaaagaaac	ttttgtcgaa	120
gagattccaa	tcggtgatct	ttgtctttct	tttctctaga	aaatctctgt	tgctctatat	180
atatccatat	agatgctcta	agactatagt	tggtgttgca	gataataatg	gagggagaca	240
caatatctag	gatgatggga	agtggagttc	aaatggatgg	gaagattctt	caaacgtttg	300
agaaaagttt	tgttcaagtg	caaaacatat	tggaaccaca	cagattgctt	ataaacgaga	360
taaacccaaa	ccatgagttc	aaaatcccgg	acaacctcgg	acgaaacgtc	ggtttgatcc	420
gagaattgaa	caataacgtg	agaagggttg	ctcatcttta	tgctgatctt	tccaacaact	480
tctccaaatc	catggaagct	tcttctgaag	gagactcatc	agaaggacga	ggtaacagaa	540
gaatcaggcc	tgcttaatta	agaatcaggg	ttgtttcttc	aaaattagct	tcgaaattag	600
cttttaatgt	gggctaattc	cctttctcaa	gtgattggcg	ataaatgttt	taaagcagaa	660
atggtgattg	taattgaaaa	atatgttcaa	tactattatt	tg		

(2) INFORMATION FOR SEQ ID NO:1596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1596:

Met	Glu	Gly	Asp	Thr	Ile	Ser	Arg	Met	Met	Gly	Ser	Gly	Val	Gln	Met
1				5				10						15	
Asp	Gly	Lys	Ile	Leu	Gln	Thr	Phe	Glu	Lys	Ser	Phe	Val	Gln	Val	Gln
			20					25					30		
Asn	Ile	Leu	Asp	His	Asn	Arg	Leu	Leu	Ile	Asn	Glu	Ile	Asn	Gln	Asn
			35				40					45			
His	Glu	Ser	Lys	Ile	Pro	Asp	Asn	Leu	Gly	Arg	Asn	Val	Gly	Leu	Ile
			50				55				60				
Arg	Glu	Leu	Asn	Asn	Asn	Val	Arg	Arg	Val	Ala	His	Leu	Tyr	Val	Asp
65					70					75				80	
Leu	Ser	Asn	Asn	Phe	Ser	Lys	Ser	Met	Glu	Ala	Ser	Ser	Glu	Gly	Asp
			85						90					95	
Ser	Ser	Glu	Gly	Arg	Gly	Asn	Arg	Arg	Ile	Arg	Pro	Ala			
			100					105							

(2) INFORMATION FOR SEQ ID NO:1597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1500697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1597:

```
Met Met Gly Ser Gly Val Gln Met Asp Gly Lys Ile Leu Gln Thr Phe
1      5      10      15
Glu Lys Ser Phe Val Gln Val Gln Asn Ile Leu Asp His Asn Arg Leu
20      25      30
Leu Ile Asn Glu Ile Asn Gln Asn His Glu Ser Lys Ile Pro Asp Asn
35      40      45
Leu Gly Arg Asn Val Gly Leu Ile Arg Glu Leu Asn Asn Val Arg
50      55      60
Arg Val Ala His Leu Tyr Val Asp Leu Ser Asn Asn Phe Ser Lys Ser
65      70      75      80
Met Glu Ala Ser Ser Glu Gly Asp Ser Ser Glu Gly Arg Gly Asn Arg
85      90      95
Arg Ile Arg Pro Ala
100
```

(2) INFORMATION FOR SEQ ID NO:1598:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1500698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1598:

```
Met Gly Ser Gly Val Gln Met Asp Gly Lys Ile Leu Gln Thr Phe Glu
1      5      10      15
Lys Ser Phe Val Gln Val Gln Asn Ile Leu Asp His Asn Arg Leu Leu
20      25      30
Ile Asn Glu Ile Asn Gln Asn His Glu Ser Lys Ile Pro Asp Asn Leu
35      40      45
Gly Arg Asn Val Gly Leu Ile Arg Glu Leu Asn Asn Asn Val Arg Arg
50      55      60
Val Ala His Leu Tyr Val Asp Leu Ser Asn Asn Phe Ser Lys Ser Met
65      70      75      80
Glu Ala Ser Ser Glu Gly Asp Ser Ser Glu Gly Arg Gly Asn Arg Arg
85      90      95
Ile Arg Pro Ala
100
```

(2) INFORMATION FOR SEQ ID NO:1599:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1422 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1422

(D) OTHER INFORMATION: / Ceres Seq. ID 1500703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1599:

```
ammaacaaag tctctctccc tctcctattc aactttttca gttactttac tccgttcatc 60
ttttattttt ctttctgctg attctcatca atactacaaa aatatatact tctatatatc 120
gtgcagaggt tacatgcatt gtrcaatttt gttgtscbga gaaacaagcg gatcagagac 180
aaaatcagag tcggtttcct gctttttgat tctcttttat taatcagcaa agatcgattc 240
cacttctcct ctctctctct ctctctctct gttctttaat ttagagagaa aaaataagca 300
ttcttccttc tctgttttcg agcgggaaat tctggagatg gctatacaag cgcagttgaa 360
```

(2) INFORMATION FOR SEQ ID NO:1600:

(A) LENGTH: 265 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..265

(D) OTHER INFORMATION: / Ceres Seq. ID 1500704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1600:

Met	Ala	Ile	Gln	Ala	Gln	Leu	Asn	Tyr	Asn	Ala	Pro	Asn	Ala	Asn	Gln
1				5					10					15	
Ile	Gly	Phe	Gly	Gly	Ser	Glu	Phe	Ser	Leu	Ile	Asn	Asn	Asn	Gly	Val
			20					25					30		
Ile	Gly	Ile	Gly	Asn	Asp	Gln	Ser	Tyr	Leu	Val	Asn	Asn	Leu	Gln	Leu
			35				40					45			
Gln	Lys	Asp	Phe	Asn	Gln	His	Ala	Leu	Phe	His	His	Gln	His	His	Gln
	50					55				60					
Gln	Gln	Gln	Ser	Pro	Ser	Gln	Ser	Phe	Leu	Ala	Gln	Met	Glu	Lys	
65					70					75				80	
Gln	Lys	Gln	Glu	Ile	Asp	Gln	Phe	Ile	Lys	Ile	Gln	Asn	Glu	Arg	Leu
				85					90				95		
Arg	Tyr	Val	Leu	Gln	Glu	Gln	Arg	Lys	Arg	Glu	Met	Glu	Met	Ile	Leu
			100					105					110		
Arg	Lys	Met	Glu	Ser	Lys	Ala	Leu	Leu	Leu	Met	Ser	Gln	Lys	Glu	Glu
			115				120					125			
Glu	Met	Ser	Lys	Ala	Leu	Asn	Lys	Asn	Met	Glu	Leu	Glu	Asp	Leu	Leu
						135				140					
Arg	Lys	Met	Glu	Met	Glu	Asn	Gln	Thr	Trp	Gln	Arg	Met	Ala	Arg	Glu
145					150					155					160
Asn	Glu	Ala	Ile	Val	Gln	Thr	Leu	Asn	Thr	Thr	Leu	Glu	Gln	Val	Arg
				165					170					175	
Glu	Arg	Ala	Ala	Thr	Cys	Tyr	Asp	Ala	Gly	Glu	Ala	Glu	Val	Glu	Asp
			180					185					190		
Glu	Gly	Ser	Phe	Cys	Gly	Xaa	Glu	Gly	Asp	Gly	Asn	Ser	Leu	Pro	Ala
			195				200					205			
Lys	Lys	Met	Lys	Met	Ser	Ser	Cys	Cys	Cys	Asn	Cys	Gly	Ser	Asn	Gly
	210					215				220					
Val	Thr	Xaa	Val	Leu	Phe	Xaa	Pro	Phe	Arg	His	Leu	Cys	Cys	Cys	Met
225					230					235					240
Asp	Xaa	Glu	Xaa	Gly	Leu	Xaa	Leu	Cys	Pro	Ile	Cys	Asn	Thr	Pro	Lys

245 250 255
Lys Ser Arg Ile Glu Ala Leu Ile Xaa
260 265
(2) INFORMATION FOR SEQ ID NO:1601:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 188 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..188
(D) OTHER INFORMATION: / Ceres Seq. ID 1500705
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1601:
Met Glu Lys Gln Lys Gln Glu Ile Asp Gln Phe Ile Lys Ile Gln Asn
1 5 10 15
Glu Arg Leu Arg Tyr Val Leu Gln Glu Gln Arg Lys Arg Glu Met Glu
20 25 30
Met Ile Leu Arg Lys Met Glu Ser Lys Ala Leu Leu Leu Met Ser Gln
35 40 45
Lys Glu Glu Glu Met Ser Lys Ala Leu Asn Lys Asn Met Glu Leu Glu
50 55 60
Asp Leu Leu Arg Lys Met Glu Met Glu Asn Gln Thr Trp Gln Arg Met
65 70 75 80
Ala Arg Glu Asn Glu Ala Ile Val Gln Thr Leu Asn Thr Thr Leu Glu
85 90 95
Gln Val Arg Glu Arg Ala Ala Thr Cys Tyr Asp Ala Gly Glu Ala Glu
100 105 110
Val Glu Asp Glu Gly Ser Phe Cys Gly Xaa Glu Gly Asp Gly Asn Ser
115 120 125
Leu Pro Ala Lys Lys Met Lys Met Ser Ser Cys Cys Cys Asn Cys Gly
130 135 140
Ser Asn Gly Val Thr Xaa Val Leu Phe Xaa Pro Phe Arg His Leu Cys
145 150 155 160
Cys Cys Met Asp Xaa Glu Xaa Gly Leu Xaa Leu Cys Pro Ile Cys Asn
165 170 175
Thr Pro Lys Lys Ser Arg Ile Glu Ala Leu Ile Xaa
180 185

(2) INFORMATION FOR SEQ ID NO:1602:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..158
(D) OTHER INFORMATION: / Ceres Seq. ID 1500706
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1602:
Met Glu Met Ile Leu Arg Lys Met Glu Ser Lys Ala Leu Leu Leu Met
1 5 10 15
Ser Gln Lys Glu Glu Glu Met Ser Lys Ala Leu Asn Lys Asn Met Glu
20 25 30
Leu Glu Asp Leu Leu Arg Lys Met Glu Met Glu Asn Gln Thr Trp Gln
35 40 45
Arg Met Ala Arg Glu Asn Glu Ala Ile Val Gln Thr Leu Asn Thr Thr
50 55 60
Leu Glu Gln Val Arg Glu Arg Ala Ala Thr Cys Tyr Asp Ala Gly Glu
65 70 75 80

Ala Glu Val Glu Asp Glu Gly Ser Phe Cys Gly Xaa Glu Gly Asp Gly
85 90 95
Asn Ser Leu Pro Ala Lys Lys Met Lys Met Ser Ser Cys Cys Cys Asn
100 105 110
Cys Gly Ser Asn Gly Val Thr Xaa Val Leu Phe Xaa Pro Phe Arg His
115 120 125
Leu Cys Cys Cys Met Asp Xaa Glu Xaa Gly Leu Xaa Leu Cys Pro Ile
130 135 140
Cys Asn Thr Pro Lys Lys Ser Arg Ile Glu Ala Leu Ile Xaa
145 150 155

(2) INFORMATION FOR SEQ ID NO:1603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1188
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500707

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1603:

```
atcattctcg gtttaactga aacacataat aaaacaaaga gaaagagata taatatgggt      60
gggtgggcaa tcgcagtaca cggtggtgcc ggtatcgacc ctaatcttcc ggcagagaga      120
caagaagagg cgaaacagct ttttaactcgt tgtctcaacc tcggcataat agctttgcgt      180
tccaatgttt ccgccattga cgtcgttgag ctcgctcatta gagaattgga gacggatcct      240
ctgtttaatt caggccgtgg atcttctttg acggagaaaag gaacgggtga gatggaagct      300
agcattatgg acggtagcaa gagacgatgc ggtgccgttt cggggataac caccgtgaaa      360
aatcctatat ctcttgctcg tctcgctcatg gacaaatctc cccactctta ccttgctttc      420
tcaggtgcag aggatttcgc ccgcaaacag ggagttgaaa ttgtggacaa cgagtacttt      480
gtcacggacg acaacgtagg aatgctcaag ttggccaagg aagctaactc catcttgttt      540
gattaccgga ttccgccgat gggatgtgcc ggcgcagctg cgaccgacag tccaatccaa      600
atgaacggtc ttccgatcag catttacgca ccgggagaca gtcgggtgcg ttgtggttga      660
cgggaaagga cattgtgccg ccgggacatc cacgggtggt ttaatgaaca agatgatggg      720
aaggattggt gactcgccgc tgataggagc cgggacgtat gcgtcggagt tttgtggtgt      780
gtcgtgtacc ggagaaggag aagccattat aagagcaacc ctagctcgtg atgtgtcagc      840
tgttatggag tataaaggac ttaacctcca agaagcgggt gattacgtca tcaagcatcg      900
acttgacgaa gggttcgtg gactcattgc tgtctcgaat aaaggagagg tggtttgtgg      960
ttttaactct aatgggatgt tcaggggatg tgcaactgag gatggattca tggacgttgc      1020
tatttgggag tgagaaatat tttagattaa gaaaatgtct tactagtatt taatcagtca      1080
tcgctctatt aatttggtta ttcattatca taaagctgga gtagtaaatt tagttctgtc      1140
gttatcacca gtcctatatt gatttgtgtt taatgcggtt tcaaattgg
```

(2) INFORMATION FOR SEQ ID NO:1604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..219
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500708

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1604:

Ile Ile Leu Gly Leu Thr Glu Thr His Asn Lys Thr Lys Arg Lys Arg
1 5 10 15
Tyr Asn Met Gly Gly Trp Ala Ile Ala Val His Gly Gly Ala Gly Ile
20 25 30
Asp Pro Asn Leu Pro Ala Glu Arg Gln Glu Glu Ala Lys Gln Leu Leu
35 40 45
Thr Arg Cys Leu Asn Leu Gly Ile Ile Ala Leu Arg Ser Asn Val Ser

50	55	60
Ala Ile Asp Val Val Glu Leu Val Ile Arg Glu Leu Glu Thr Asp Pro		
65	70	75
Leu Phe Asn Ser Gly Arg Gly Ser Ser Leu Thr Glu Lys Gly Thr Val		80
	85	90
Glu Met Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala		95
	100	105
Val Ser Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu		110
	115	120
Val Met Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu		125
	130	135
Asp Phe Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe		140
145	150	155
Val Thr Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn		160
	165	170
Ser Ile Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala		175
	180	185
Ala Ala Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile		190
	195	200
Tyr Ala Pro Gly Asp Ser Arg Val Arg Cys Gly		205
210	215	

(2) INFORMATION FOR SEQ ID NO:1605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..201

(D) OTHER INFORMATION: / Ceres Seq. ID 1500709

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1605:

Met Gly Gly Trp Ala Ile Ala Val His Gly Gly Ala Gly Ile Asp Pro		
1	5	10
Asn Leu Pro Ala Glu Arg Gln Glu Glu Ala Lys Gln Leu Leu Thr Arg		15
	20	25
Cys Leu Asn Leu Gly Ile Ile Ala Leu Arg Ser Asn Val Ser Ala Ile		30
	35	40
Asp Val Val Glu Leu Val Ile Arg Glu Leu Glu Thr Asp Pro Leu Phe		45
	50	55
Asn Ser Gly Arg Gly Ser Ser Leu Thr Glu Lys Gly Thr Val Glu Met		60
65	70	75
Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala Val Ser		80
	85	90
Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu Val Met		95
	100	105
Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu Asp Phe		110
	115	120
Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe Val Thr		125
	130	135
Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn Ser Ile		140
145	150	155
Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala Ala		160
	165	170
Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr Ala		175
	180	185
Pro Gly Asp Ser Arg Val Arg Cys Gly		190
	195	200

(2) INFORMATION FOR SEQ ID NO:1606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..122
(D) OTHER INFORMATION: / Ceres Seq. ID 1500710
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1606:
Met Glu Ala Ser Ile Met Asp Gly Thr Lys Arg Arg Cys Gly Ala Val
1 5 10 15
Ser Gly Ile Thr Thr Val Lys Asn Pro Ile Ser Leu Ala Arg Leu Val
20 25 30
Met Asp Lys Ser Pro His Ser Tyr Leu Ala Phe Ser Gly Ala Glu Asp
35 40 45
Phe Ala Arg Lys Gln Gly Val Glu Ile Val Asp Asn Glu Tyr Phe Val
50 55 60
Thr Asp Asp Asn Val Gly Met Leu Lys Leu Ala Lys Glu Ala Asn Ser
65 70 75 80
Ile Leu Phe Asp Tyr Arg Ile Pro Pro Met Gly Cys Ala Gly Ala Ala
85 90 95
Ala Thr Asp Ser Pro Ile Gln Met Asn Gly Leu Pro Ile Ser Ile Tyr
100 105 110
Ala Pro Gly Asp Ser Arg Val Arg Cys Gly
115 120

(2) INFORMATION FOR SEQ ID NO:1607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..868
(D) OTHER INFORMATION: / Ceres Seq. ID 1500719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1607:

aatcacttgt taattctaag cttcttctct ttccaaaaat ggcgtcatca tcggcttttag	60
ctctcaggag acttctctct tcttccaccg tcgccgtccc tcgcgcctta agagccgttc	120
gtccggtgtc tgcttcttct cgcctcttca ataccaacgc cgccagaaac tatgaagacg	180
gtgtcgatag gaaccatcac tcaaaccgac atgtttctcg ccacggcggc gatttcttct	240
cagatatact cgatccgttt actccaacga gaagcttgag ccagatgctg aatttcatgg	300
accaggtaag cgaaatccct ttggtatcag ctactcgtgg aatgggagct tctggagtta	360
gacgtgggtg gaacgtgaaa gagaaagacg acgcgttgca tctaaggata gatatgccgg	420
gactaagcag agaggatgtg aaattggctt tggaacagaa cacattggtg attagaggag	480
aaggggaaac agaggaggga gaagatgttt ctggagatgg acggagggtt acgagtagga	540
ttgagttacc ggagaaagta tacaagactg atgagattaa ggcggaaatg aagaatggtg	600
tgttgaaagt ggtgattcca aagattaaag aggatgagcg taacaatatt cgtcacataa	660
acgttgacta gagtgtttta ttttggtatt tttgagatgg aatggaagta agtgagtga	720
tttgatgaact ttaaggtgtc ctttggtgaa tcaaggagaa tgacatttcc cacggtccta	780
tgtgttcggg attttgactt ttttcgttac atcaatgatc tatgtacgtt tgactacttt	840
catatcatag gttcggattt tgtttccc	

(2) INFORMATION FOR SEQ ID NO:1608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..222

(D) OTHER INFORMATION: / Ceres Seq. ID 1500720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1608:

Ser	Leu	Val	Asn	Ser	Lys	Leu	Leu	Leu	Phe	Pro	Lys	Met	Ala	Ser	Ser
1			5						10					15	
Ser	Ala	Leu	Ala	Leu	Arg	Arg	Leu	Leu	Ser	Ser	Ser	Thr	Val	Ala	Val
			20					25					30		
Pro	Arg	Ala	Leu	Arg	Ala	Val	Arg	Pro	Val	Ser	Ala	Ser	Ser	Arg	Leu
			35				40					45			
Phe	Asn	Thr	Asn	Ala	Ala	Arg	Asn	Tyr	Glu	Asp	Gly	Val	Asp	Arg	Asn
	50					55					60				
His	His	Ser	Asn	Arg	His	Val	Ser	Arg	His	Gly	Gly	Asp	Phe	Phe	Ser
65					70					75				80	
Asp	Ile	Leu	Asp	Pro	Phe	Thr	Pro	Thr	Arg	Ser	Leu	Ser	Gln	Met	Leu
				85					90					95	
Asn	Phe	Met	Asp	Gln	Val	Ser	Glu	Ile	Pro	Leu	Val	Ser	Ala	Thr	Arg
			100					105					110		
Gly	Met	Gly	Ala	Ser	Gly	Val	Arg	Arg	Gly	Trp	Asn	Val	Lys	Glu	Lys
			115				120					125			
Asp	Asp	Ala	Leu	His	Leu	Arg	Ile	Asp	Met	Pro	Gly	Leu	Ser	Arg	Glu
	130					135					140				
Asp	Val	Lys	Leu	Ala	Leu	Glu	Gln	Asn	Thr	Leu	Val	Ile	Arg	Gly	Glu
145					150					155					160
Gly	Glu	Thr	Glu	Glu	Gly	Glu	Asp	Val	Ser	Gly	Asp	Gly	Arg	Arg	Phe
			165				170						175		
Thr	Ser	Arg	Ile	Glu	Leu	Pro	Glu	Lys	Val	Tyr	Lys	Thr	Asp	Glu	Ile
			180				185						190		
Lys	Ala	Glu	Met	Lys	Asn	Gly	Val	Leu	Lys	Val	Val	Ile	Pro	Lys	Ile
			195				200					205			
Lys	Glu	Asp	Glu	Arg	Asn	Asn	Ile	Arg	His	Ile	Asn	Val	Asp		
	210				215						220				

(2) INFORMATION FOR SEQ ID NO:1609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..210

(D) OTHER INFORMATION: / Ceres Seq. ID 1500721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1609:

Met	Ala	Ser	Ser	Ser	Ala	Leu	Ala	Leu	Arg	Arg	Leu	Leu	Ser	Ser	Ser
1				5					10					15	
Thr	Val	Ala	Val	Pro	Arg	Ala	Leu	Arg	Ala	Val	Arg	Pro	Val	Ser	Ala
			20					25					30		
Ser	Ser	Arg	Leu	Phe	Asn	Thr	Asn	Ala	Ala	Arg	Asn	Tyr	Glu	Asp	Gly
			35				40					45			
Val	Asp	Arg	Asn	His	His	Ser	Asn	Arg	His	Val	Ser	Arg	His	Gly	Gly
	50				55					60					
Asp	Phe	Phe	Ser	Asp	Ile	Leu	Asp	Pro	Phe	Thr	Pro	Thr	Arg	Ser	Leu
65					70					75				80	
Ser	Gln	Met	Leu	Asn	Phe	Met	Asp	Gln	Val	Ser	Glu	Ile	Pro	Leu	Val
				85					90					95	
Ser	Ala	Thr	Arg	Gly	Met	Gly	Ala	Ser	Gly	Val	Arg	Arg	Gly	Trp	Asn
			100				105						110		
Val	Lys	Glu	Lys	Asp	Asp	Ala	Leu	His	Leu	Arg	Ile	Asp	Met	Pro	Gly
			115				120					125			
Leu	Ser	Arg	Glu	Asp	Val	Lys	Leu	Ala	Leu	Glu	Gln	Asn	Thr	Leu	Val

130 135 140
Ile Arg Gly Glu Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp
145 150 155 160
Gly Arg Arg Phe Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys
165 170 175
Thr Asp Glu Ile Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val
180 185 190
Ile Pro Lys Ile Lys Glu Asp Glu Arg Asn Asn Ile Arg His Ile Asn
195 200 205
Val Asp
210

(2) INFORMATION FOR SEQ ID NO:1610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1500722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1610:

Met Leu Asn Phe Met Asp Gln Val Ser Glu Ile Pro Leu Val Ser Ala
1 5 10 15
Thr Arg Gly Met Gly Ala Ser Gly Val Arg Arg Gly Trp Asn Val Lys
20 25 30
Glu Lys Asp Asp Ala Leu His Leu Arg Ile Asp Met Pro Gly Leu Ser
35 40 45
Arg Glu Asp Val Lys Leu Ala Leu Glu Gln Asn Thr Leu Val Ile Arg
50 55 60
Gly Glu Gly Glu Thr Glu Glu Gly Glu Asp Val Ser Gly Asp Gly Arg
65 70 75 80
Arg Phe Thr Ser Arg Ile Glu Leu Pro Glu Lys Val Tyr Lys Thr Asp
85 90 95
Glu Ile Lys Ala Glu Met Lys Asn Gly Val Leu Lys Val Val Ile Pro
100 105 110
Lys Ile Lys Glu Asp Glu Arg Asn Ile Arg His Ile Asn Val Asp
115 120 125

(2) INFORMATION FOR SEQ ID NO:1611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 763 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..763

(D) OTHER INFORMATION: / Ceres Seq. ID 1500734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1611:

ctgttttttg tctctcgcac tcacaagtct cacataatcg aaagctcgca gaagtcaaga 60
ggaagaagat gagtggtaga gtgacaatgc acagtgtctt cgtctacggc agtctcatgg 120
cggacgacgt cgttcgtctc ctctcaccac gtatccctca aaccgcttcc gcaaccctcc 180
ctgaktkatt cagcatcaaa ggctcgtgtt atccggcgat tataccagct aagtcttgat 240
aaagtctctg gaaaggtgtt atttggaatc acagatgatg aacttaatgt tttagatgag 300
tttgaggatg ttgagtatga aagagagaat gttcaagttt tgtaaacaga tagttcagac 360
gagaaactgc aaacaaaaac ctacgttttg gccaaagaaag atgatcctga cctatacggg 420
acatgggatt tcgaggaatg gaagcaactt cacatggaag gtttcttgaa gatgactaaa 480

gaatttgctg aagagttgaa tttaccgaaa tccgagatat gactcgccgc tacattcggg 540
tcagtaaatg aaatctggta tagtttcctc aatgaattgg tcaatatatt cttggtgttc 600
tctctaggaa gggtagatt cttcttcatt aatacacata catgaggggg atttgggggtt 660
ttgtgggtatt acttaattca actgataagg aataagaaaa cagctacata ttcttgtgcg 720
gtatgttatt atacaatata catatagaca tgtgttttagc ttc

(2) INFORMATION FOR SEQ ID NO:1612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1500735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1612:

Val Phe Gly Leu Ser His Ser Gln Val Ser His Asn Arg Lys Leu Ala
1 5 10 15
Glu Val Lys Arg Lys Lys Met Ser Gly Thr Val Thr Met His Ser Val
20 25 30
Phe Val Tyr Gly Ser Leu Met Ala Asp Asp Val Val Arg Leu Leu Leu
35 40 45
Asn Arg Ile Pro Gln Thr Ala Ser Ala Thr Leu Pro Xaa Xaa Phe Ser
50 55 60
Ile Lys Gly Arg Val Tyr Pro Ala Ile Ile Pro Ala Lys Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:1613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1500736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1613:

Met Ser Gly Thr Val Thr Met His Ser Val Phe Val Tyr Gly Ser Leu
1 5 10 15
Met Ala Asp Asp Val Val Arg Leu Leu Asn Arg Ile Pro Gln Thr
20 25 30
Ala Ser Ala Thr Leu Pro Xaa Xaa Phe Ser Ile Lys Gly Arg Val Tyr
35 40 45
Pro Ala Ile Ile Pro Ala Lys Ser
50 55

(2) INFORMATION FOR SEQ ID NO:1614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1500737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1614:

Met His Ser Val Phe Val Tyr Gly Ser Leu Met Ala Asp Asp Val Val
1 5 10 15

Arg Leu Leu Leu Asn Arg Ile Pro Gln Thr Ala Ser Ala Thr Leu Pro
20 25 30
Xaa Xaa Phe Ser Ile Lys Gly Arg Val Tyr Pro Ala Ile Ile Pro Ala
35 40 45
Lys Ser
50

(2) INFORMATION FOR SEQ ID NO:1615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..846
(D) OTHER INFORMATION: / Ceres Seq. ID 1500742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1615:

atcctgatcg	ggaaacccaa	aacgagtgg	cgaatagttt	ccgactgatt	cttccgaggg	60
ttgaagctca	atagctatgg	cttctctttc	agtctcttcc	tcttcaacca	tcacgatttc	120
aagagctcct	ccttctcgac	tagcctccgc	ctccgcctct	tctccgtcgt	gcatttcact	180
tcccacactt	ccgattcagt	ctcatacccg	tgccgctaaa	gccactgctt	actgtcggaa	240
gattgtgagg	aacggttgta	cgagagctac	tactgaagtt	ggtgaagctc	ctgccactac	300
taccgaagct	gagactactg	agttacctga	aatcgtcaag	actgctcaag	aagcttgga	360
gaaagtggat	gacaagtacg	ctattggttc	tcttgccctt	gctagtgtag	tggctctttg	420
gggttctgct	ggaatgawtt	csgcaatcga	taggcttcca	ttggttcctg	gtgttcttga	480
acttgtaggc	atcgggttaca	caggatgggt	cacttacaag	aacctgggtc	tcaaaccaga	540
cagggaggct	ttgtttgaga	aggtaagag	cacatacaaa	gacatattag	ggagcagctg	600
aatcaaagga	ggaagaagaa	gaagaagagc	ctttttgagg	ccattcatga	attggaatga	660
aggatatcaa	aagaatctaa	cacaaaggcc	acgtccttcc	ttcaatcttt	ccttcttcta	720
actaaataat	tttcatcctt	tctctctctc	tgtctctggg	cttttttagc	tcaaagtatc	780
atccatttat	gtcaaagtgt	tgtaaattcc	tcaagactat	atatgagatg	ttttgtttca	840
ttttcc						

(2) INFORMATION FOR SEQ ID NO:1616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..174
(D) OTHER INFORMATION: / Ceres Seq. ID 1500743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1616:

Met	Ala	Ser	Leu	Ser	Val	Ser	Ser	Ser	Ser	Thr	Ile	Ile	Asp	Ser	Arg	
1				5					10					15		
Ala	Pro	Pro	Ser	Arg	Leu	Ala	Ser	Ala	Ser	Ser	Pro	Ser	Cys			
			20					25				30				
Ile	Ser	Leu	Pro	Thr	Leu	Pro	Ile	Gln	Ser	His	Thr	Arg	Ala	Ala	Lys	
		35				40					45					
Ala	Thr	Ala	Tyr	Cys	Arg	Lys	Ile	Val	Arg	Asn	Val	Val	Thr	Arg	Ala	
	50					55				60						
Thr	Thr	Glu	Val	Gly	Glu	Ala	Pro	Ala	Thr	Thr	Glu	Ala	Glu	Thr		
65					70				75					80		
Thr	Glu	Leu	Pro	Glu	Ile	Val	Lys	Thr	Ala	Gln	Glu	Ala	Trp	Glu	Lys	
			85					90					95			
Val	Asp	Asp	Lys	Tyr	Ala	Ile	Gly	Ser	Leu	Ala	Phe	Ala	Ser	Val	Val	
			100					105					110			
Ala	Leu	Trp	Gly	Ser	Ala	Gly	Met	Xaa	Xaa	Ala	Ile	Asp	Arg	Leu	Pro	
		115					120						125			

Leu Val Pro Gly Val Leu Glu Leu Val Gly Ile Gly Tyr Thr Gly Trp
130 135 140
Phe Thr Tyr Lys Asn Leu Val Phe Lys Pro Asp Arg Glu Ala Leu Phe
145 150 155 160
Glu Lys Val Lys Ser Thr Tyr Lys Asp Ile Leu Gly Ser Ser
165 170

(2) INFORMATION FOR SEQ ID NO:1617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..621
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1617:

aaatcaaaac acaacattaa aagctttggc gattttttctc tctgattcaa tcttttcata	60
gttttctaagc tctcagattc ttgaagaagc catggctcgt acgaagcaaa ccgcgagaaa	120
atcacacgga ggaaaagctc cgacgaagca gctcgtctacc aaggcggcaa ggaaatctgc	180
accgactacc ggaggagtca agaaacctca ccgtttccgt cctggaaccg tcgctcttcg	240
tgagattcgt aaataccaaa agagcacaga gttggtgaac cgtaaacttc cattccaacg	300
tcttgttcgt gaaatcgctc aagatttcaa gacggatctg agattccaaa gccatgcagt	360
gtagctctt caagaagctg cggaggcata tttggttggt ttgtttgaag acacaaatct	420
ctgtgccatt catgcaaaga gggttaccat tatgcctaaa gatgttcaat tggcaagaag	480
gattcgtgca gagcgtgctt agaaattaga atttaatcca ttcatatgaa ctagtatttt	540
tttttttcta ttagggtttt cgattgtttt tgctttggtt ctttttaaca aaaatacatt	600
atgtcacatt ctctttgaga g	

(2) INFORMATION FOR SEQ ID NO:1618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1618:

Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser His Gly Gly Lys Ala	
1 5 10 15	
Pro Thr Lys Gln Leu Ala Thr Lys Ala Ala Arg Lys Ser Ala Pro Thr	
20 25 30	
Thr Gly Gly Val Lys Lys Pro His Arg Phe Arg Pro Gly Thr Val Ala	
35 40 45	
Leu Arg Glu Ile Arg Lys Tyr Gln Lys Ser Thr Glu Leu Leu Asn Arg	
50 55 60	
Lys Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Ala Gln Asp Phe Lys	
65 70 75 80	
Thr Asp Leu Arg Phe Gln Ser His Ala Val Leu Ala Leu Gln Glu Ala	
85 90 95	
Ala Glu Ala Tyr Leu Val Gly Leu Phe Glu Asp Thr Asn Leu Cys Ala	
100 105 110	
Ile His Ala Lys Arg Val Thr Ile Met Pro Lys Asp Val Gln Leu Ala	
115 120 125	
Arg Arg Ile Arg Ala Glu Arg Ala	
130 135	

(2) INFORMATION FOR SEQ ID NO:1619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1795
(D) OTHER INFORMATION: / Ceres Seq. ID 1500758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1619:

```
agagatcaag agagagatat ggagagaact ttgcttcaat ggagactatt gcctcttctc      60
gcactcatcg ttgctctttt ctcccttctt ttcgcttctc ctcgctcttt acaggggaat      120
aataagtgtg gtcttcttcc tcatgatcat tactggatct caagtaaacg catcgtcaca      180
cctaattgtc tcatctctgg ttctgtggag gtgaaggagg gaattattgt gtcgggtggg      240
aaggaagtgt attggcataa gagtcaaagg agtcgagtga aagtgattga ttatggagaa      300
gctgtcctca tgccctggtc cattgatgtg catgttcatc ttgatgatcc tggaagaagt      360
gaatgggaag gttttccttc tggaactaag gctgctgctg ctgggggaat aactacattg      420
gttgacatgc ccttaaacag tttcccttca actgtatctc ctgaaacttt gaaactcaag      480
attgaagctg cgaaaaacag aatacatgtt gatgttgggt tctggggagg tctggtacct      540
gacaatgcac tcaactcaag tgctcttgag tctctcttag atgctggagt tcttgggtctc      600
aagtccttta tgtgcccttc aggaatcaac gattttccaa tgacaaacat cactcatata      660
aaggaaggac tatctgtatt agctaaatac aaacgaccat tgcttgtaca cgcagagatc      720
gagagagact tagagattga agatggtagt gaaaatgatc ctcgttctta tctgacttat      780
ttaaaaaacca ggcctacttc atgggaggag ggagcaatca gaaacctatt atcggttact      840
gaaaacacaa gaattggtgg ttctgcagaa ggagctcatc ttcattattgt acatttatct      900
gatgccagtt ctcccttgga tttgataaag gaagcaaaaag gcaaaggaga cagtgttact      960
gttgaaacat gtccacatta cctagctttc tcagccgaag agattccaga aggtgatact      1020
cgtttcaaag gctcccctcc tatacgtgag gcggcaataa gagaaaaatt gtgggaagct      1080
ttgatggaag gagacattga tatgctgagc tctgatcatt cacctacaaa gcctgaactc      1140
aaacttatga gtgatggcaa cttcttgaaa gcttgggggt ggatatcttc tttacagttt      1200
gttcttccta tcacatgggc ttatggaaaa aagtatggag taacgctcga gcaggtaact      1260
tcttgggtga gtgataggcc ttccaaactc gctcgactac actctaaggg agcggttacg      1320
gttggaatac acgcagatct tgttgtgtgg gaacctgaag ccgaatttga tgtagatgaa      1380
gatcatccaa ttcacttcaa acaccctagt atctcagctt atttgggaag aagattatca      1440
ggcaaagtgg tttcgacatt tgtgagaggg aacttggttt ttggagaagg caagcatgct      1500
tctgatgctt gcgggtctct gcaacttgca actacttaac ttaaaaaggg atttaaaaga      1560
tcttgatctg caccatttaa acaaatgtaa atatgcgatt aagagttgct ctcattgttc      1620
aagatggttg atgtaatgag tgagtctttt ttgccaatgt taagtttaag actctctaaa      1680
tcttggttgg ggctttaagg ttagtggact catstatata ttgtyatgc aaataattta      1740
tatcgcttaa gtaaatgatg tatatattgt tgatgcaaat aatttaaaag tatac
```

(2) INFORMATION FOR SEQ ID NO:1620:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 512 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..512
(D) OTHER INFORMATION: / Ceres Seq. ID 1500759

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1620:

```
Arg Asp Gln Glu Arg Asp Met Glu Arg Thr Leu Leu Gln Trp Arg Leu
1          5          10          15
Leu Pro Leu Leu Ala Leu Ile Val Ala Leu Phe Ser Phe Phe Phe Ala
20          25          30
Ser Pro Arg Ser Leu Gln Gly Asn Asn Lys Cys Ser Leu Leu Pro His
35          40          45
Asp His Tyr Trp Ile Ser Ser Lys Arg Ile Val Thr Pro Asn Gly Leu
50          55          60
Ile Ser Gly Ser Val Glu Val Lys Gly Gly Ile Ile Val Ser Val Val
```

65					70					75					80
Lys	Glu	Val	Asp	Trp	His	Lys	Ser	Gln	Arg	Ser	Arg	Val	Lys	Val	Ile
				85					90					95	
Asp	Tyr	Gly	Glu	Ala	Val	Leu	Met	Pro	Gly	Leu	Ile	Asp	Val	His	Val
			100					105					110		
His	Leu	Asp	Asp	Pro	Gly	Arg	Ser	Glu	Trp	Glu	Gly	Phe	Pro	Ser	Gly
		115					120					125			
Thr	Lys	Ala	Ala	Ala	Ala	Gly	Gly	Ile	Thr	Thr	Leu	Val	Asp	Met	Pro
		130				135					140				
Leu	Asn	Ser	Phe	Pro	Ser	Thr	Val	Ser	Pro	Glu	Thr	Leu	Lys	Leu	Lys
					150					155					160
Ile	Glu	Ala	Ala	Lys	Asn	Arg	Ile	His	Val	Asp	Val	Gly	Phe	Trp	Gly
				165					170					175	
Gly	Leu	Val	Pro	Asp	Asn	Ala	Leu	Asn	Ser	Ser	Ala	Leu	Glu	Ser	Leu
			180					185					190		
Leu	Asp	Ala	Gly	Val	Leu	Gly	Leu	Lys	Ser	Phe	Met	Cys	Pro	Ser	Gly
		195					200					205			
Ile	Asn	Asp	Phe	Pro	Met	Thr	Asn	Ile	Thr	His	Ile	Lys	Glu	Gly	Leu
		210				215					220				
Ser	Val	Leu	Ala	Lys	Tyr	Lys	Arg	Pro	Leu	Leu	Val	His	Ala	Glu	Ile
					230					235					240
Glu	Arg	Asp	Leu	Glu	Ile	Glu	Asp	Gly	Ser	Glu	Asn	Asp	Pro	Arg	Ser
				245				250						255	
Tyr	Leu	Thr	Tyr	Leu	Lys	Thr	Arg	Pro	Thr	Ser	Trp	Glu	Glu	Gly	Ala
			260					265					270		
Ile	Arg	Asn	Leu	Leu	Ser	Val	Thr	Glu	Asn	Thr	Arg	Ile	Gly	Gly	Ser
		275					280					285			
Ala	Glu	Gly	Ala	His	Leu	His	Ile	Val	His	Leu	Ser	Asp	Ala	Ser	Ser
		290				295					300				
Ser	Leu	Asp	Leu	Ile	Lys	Glu	Ala	Lys	Gly	Lys	Gly	Asp	Ser	Val	Thr
					310					315					320
Val	Glu	Thr	Cys	Pro	His	Tyr	Leu	Ala	Phe	Ser	Ala	Glu	Glu	Ile	Pro
				325					330					335	
Glu	Gly	Asp	Thr	Arg	Phe	Lys	Cys	Ser	Pro	Pro	Ile	Arg	Asp	Ala	Ala
			340					345				350			
Asn	Arg	Glu	Lys	Leu	Trp	Glu	Ala	Leu	Met	Glu	Gly	Asp	Ile	Asp	Met
		355					360					365			
Leu	Ser	Ser	Asp	His	Ser	Pro	Thr	Lys	Pro	Glu	Leu	Lys	Leu	Met	Ser
		370				375					380				
Asp	Gly	Asn	Phe	Leu	Lys	Ala	Trp	Gly	Gly	Ile	Ser	Ser	Leu	Gln	Phe
					390					395					400
Val	Leu	Pro	Ile	Thr	Trp	Ser	Tyr	Gly	Lys	Lys	Tyr	Gly	Val	Thr	Leu
				405					410					415	
Glu	Gln	Val	Thr	Ser	Trp	Trp	Ser	Asp	Arg	Pro	Ser	Lys	Leu	Ala	Arg
			420					425					430		
Leu	His	Ser	Lys	Gly	Ala	Val	Thr	Val	Gly	Lys	His	Ala	Asp	Leu	Val
			435				440					445			
Val	Trp	Glu	Pro	Glu	Ala	Glu	Phe	Asp	Val	Asp	Glu	Asp	His	Pro	Ile
		450				455					460				
His	Phe	Lys	His	Pro	Ser	Ile	Ser	Ala	Tyr	Leu	Gly	Arg	Arg	Leu	Ser
					470					475					480
Gly	Lys	Val	Val	Ser	Thr	Phe	Val	Arg	Gly	Asn	Leu	Val	Phe	Gly	Glu
				485					490					495	
Gly	Lys	His	Ala	Ser	Asp	Ala	Cys	Gly	Ser	Leu	Gln	Leu	Ala	Thr	Thr
			500					505					510		

(2) INFORMATION FOR SEQ ID NO:1621:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..506
(D) OTHER INFORMATION: / Ceres Seq. ID 1500760
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1621:

Met	Glu	Arg	Thr	Leu	Leu	Gln	Trp	Arg	Leu	Leu	Pro	Leu	Leu	Ala	Leu
1				5				10						15	
Ile	Val	Ala	Leu	Phe	Ser	Phe	Phe	Phe	Ala	Ser	Pro	Arg	Ser	Leu	Gln
			20					25					30		
Gly	Asn	Asn	Lys	Cys	Ser	Leu	Leu	Pro	His	Asp	His	Tyr	Trp	Ile	Ser
			35				40					45			
Ser	Lys	Arg	Ile	Val	Thr	Pro	Asn	Gly	Leu	Ile	Ser	Gly	Ser	Val	Glu
	50					55					60				
Val	Lys	Gly	Gly	Ile	Ile	Val	Ser	Val	Val	Lys	Glu	Val	Asp	Trp	His
65				70						75				80	
Lys	Ser	Gln	Arg	Ser	Arg	Val	Lys	Val	Ile	Asp	Tyr	Gly	Glu	Ala	Val
			85					90						95	
Leu	Met	Pro	Gly	Leu	Ile	Asp	Val	His	Val	His	Leu	Asp	Asp	Pro	Gly
			100					105					110		
Arg	Ser	Glu	Trp	Glu	Gly	Phe	Pro	Ser	Gly	Thr	Lys	Ala	Ala	Ala	Ala
			115					120					125		
Gly	Gly	Ile	Thr	Thr	Leu	Val	Asp	Met	Pro	Leu	Asn	Ser	Phe	Pro	Ser
	130					135						140			
Thr	Val	Ser	Pro	Glu	Thr	Leu	Lys	Leu	Lys	Ile	Glu	Ala	Ala	Lys	Asn
145					150					155				160	
Arg	Ile	His	Val	Asp	Val	Gly	Phe	Trp	Gly	Gly	Leu	Val	Pro	Asp	Asn
			165						170					175	
Ala	Leu	Asn	Ser	Ser	Ala	Leu	Glu	Ser	Leu	Leu	Asp	Ala	Gly	Val	Leu
			180					185					190		
Gly	Leu	Lys	Ser	Phe	Met	Cys	Pro	Ser	Gly	Ile	Asn	Asp	Phe	Pro	Met
	195						200					205			
Thr	Asn	Ile	Thr	His	Ile	Lys	Glu	Gly	Leu	Ser	Val	Leu	Ala	Lys	Tyr
	210					215					220				
Lys	Arg	Pro	Leu	Leu	Val	His	Ala	Glu	Ile	Glu	Arg	Asp	Leu	Glu	Ile
225					230					235				240	
Glu	Asp	Gly	Ser	Glu	Asn	Asp	Pro	Arg	Ser	Tyr	Leu	Thr	Tyr	Leu	Lys
			245						250					255	
Thr	Arg	Pro	Thr	Ser	Trp	Glu	Glu	Gly	Ala	Ile	Arg	Asn	Leu	Leu	Ser
			260					265					270		
Val	Thr	Glu	Asn	Thr	Arg	Ile	Gly	Ser	Ala	Glu	Gly	Ala	His	Leu	
	275						280					285			
His	Ile	Val	His	Leu	Ser	Asp	Ala	Ser	Ser	Ser	Leu	Asp	Leu	Ile	Lys
	290					295					300				
Glu	Ala	Lys	Gly	Lys	Gly	Asp	Ser	Val	Thr	Val	Glu	Thr	Cys	Pro	His
305					310					315				320	
Tyr	Leu	Ala	Phe	Ser	Ala	Glu	Glu	Ile	Pro	Glu	Gly	Asp	Thr	Arg	Phe
			325						330					335	
Lys	Cys	Ser	Pro	Pro	Ile	Arg	Asp	Ala	Ala	Asn	Arg	Glu	Lys	Leu	Trp
			340					345					350		
Glu	Ala	Leu	Met	Glu	Gly	Asp	Ile	Asp	Met	Leu	Ser	Ser	Asp	His	Ser
	355						360					365			
Pro	Thr	Lys	Pro	Glu	Leu	Lys	Leu	Met	Ser	Asp	Gly	Asn	Phe	Leu	Lys
	370					375					380				
Ala	Trp	Gly	Gly	Ile	Ser	Ser	Leu	Gln	Phe	Val	Leu	Pro	Ile	Thr	Trp
385					390					395				400	
Ser	Tyr	Gly	Lys	Lys	Tyr	Gly	Val	Thr	Leu	Glu	Gln	Val	Thr	Ser	Trp
			405						410					415	
Trp	Ser	Asp	Arg	Pro	Ser	Lys	Leu	Ala	Arg	Leu	His	Ser	Lys	Gly	Ala

		420					425					430			
Val	Thr	Val	Gly	Lys	His	Ala	Asp	Leu	Val	Val	Trp	Glu	Pro	Glu	Ala
		435					440					445			
Glu	Phe	Asp	Val	Asp	Glu	Asp	His	Pro	Ile	His	Phe	Lys	His	Pro	Ser
	450					455					460				
Ile	Ser	Ala	Tyr	Leu	Gly	Arg	Arg	Leu	Ser	Gly	Lys	Val	Val	Ser	Thr
465					470					475					480
Phe	Val	Arg	Gly	Asn	Leu	Val	Phe	Gly	Glu	Gly	Lys	His	Ala	Ser	Asp
				485				490						495	
Ala	Cys	Gly	Ser	Leu	Gln	Leu	Ala	Thr	Thr						
		500					505								

(2) INFORMATION FOR SEQ ID NO:1622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..409

(D) OTHER INFORMATION: / Ceres Seq. ID 1500761

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1622:

Met	Pro	Gly	Leu	Ile	Asp	Val	His	Val	His	Leu	Asp	Asp	Pro	Gly	Arg
1			5					10					15		
Ser	Glu	Trp	Glu	Gly	Phe	Pro	Ser	Gly	Thr	Lys	Ala	Ala	Ala	Ala	Gly
		20						25					30		
Gly	Ile	Thr	Thr	Leu	Val	Asp	Met	Pro	Leu	Asn	Ser	Phe	Pro	Ser	Thr
		35					40					45			
Val	Ser	Pro	Glu	Thr	Leu	Lys	Leu	Lys	Ile	Glu	Ala	Ala	Lys	Asn	Arg
		50				55				60					
Ile	His	Val	Asp	Val	Gly	Phe	Trp	Gly	Gly	Leu	Val	Pro	Asp	Asn	Ala
65				70					75					80	
Leu	Asn	Ser	Ser	Ala	Leu	Glu	Ser	Leu	Leu	Asp	Ala	Gly	Val	Leu	Gly
			85					90						95	
Leu	Lys	Ser	Phe	Met	Cys	Pro	Ser	Gly	Ile	Asn	Asp	Phe	Pro	Met	Thr
		100						105					110		
Asn	Ile	Thr	His	Ile	Lys	Glu	Gly	Leu	Ser	Val	Leu	Ala	Lys	Tyr	Lys
		115					120					125			
Arg	Pro	Leu	Leu	Val	His	Ala	Glu	Ile	Glu	Arg	Asp	Leu	Glu	Ile	Glu
		130				135					140				
Asp	Gly	Ser	Glu	Asn	Asp	Pro	Arg	Ser	Tyr	Leu	Thr	Tyr	Leu	Lys	Thr
145					150				155					160	
Arg	Pro	Thr	Ser	Trp	Glu	Gly	Ala	Ile	Arg	Asn	Leu	Leu	Ser	Val	
			165					170						175	
Thr	Glu	Asn	Thr	Arg	Ile	Gly	Gly	Ser	Ala	Glu	Gly	Ala	His	Leu	His
			180				185						190		
Ile	Val	His	Leu	Ser	Asp	Ala	Ser	Ser	Leu	Asp	Leu	Ile	Lys	Glu	
		195					200				205				
Ala	Lys	Gly	Lys	Gly	Asp	Ser	Val	Thr	Val	Glu	Thr	Cys	Pro	His	Tyr
		210				215					220				
Leu	Ala	Phe	Ser	Ala	Glu	Glu	Ile	Pro	Glu	Gly	Asp	Thr	Arg	Phe	Lys
225					230					235					240
Cys	Ser	Pro	Pro	Ile	Arg	Asp	Ala	Ala	Asn	Arg	Glu	Lys	Leu	Trp	Glu
			245						250					255	
Ala	Leu	Met	Glu	Gly	Asp	Ile	Asp	Met	Leu	Ser	Ser	Asp	His	Ser	Pro
		260						265					270		
Thr	Lys	Pro	Glu	Leu	Lys	Leu	Met	Ser	Asp	Gly	Asn	Phe	Leu	Lys	Ala
		275					280					285			
Trp	Gly	Gly	Ile	Ser	Ser	Leu	Gln	Phe	Val	Leu	Pro	Ile	Thr	Trp	Ser
		290				295					300				

Tyr Gly Lys Lys Tyr Gly Val Thr Leu Glu Gln Val Thr Ser Trp Trp
305 310 315 320
Ser Asp Arg Pro Ser Lys Leu Ala Arg Leu His Ser Lys Gly Ala Val
325 330 335
Thr Val Gly Lys His Ala Asp Leu Val Val Trp Glu Pro Glu Ala Glu
340 345 350
Phe Asp Val Asp Glu Asp His Pro Ile His Phe Lys His Pro Ser Ile
355 360 365
Ser Ala Tyr Leu Gly Arg Arg Leu Ser Gly Lys Val Val Ser Thr Phe
370 375 380
Val Arg Gly Asn Leu Val Phe Gly Glu Gly Lys His Ala Ser Asp Ala
385 390 395 400
Cys Gly Ser Leu Gln Leu Ala Thr Thr
405

(2) INFORMATION FOR SEQ ID NO:1623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1623:

atacaaatca taactcaaag aaaaacaacc cctcaacggt cgatgtgtga tcccattaga	60
gaagatggct ctaacaaaag aggcgcgctg agtaaggaaa aaaggccgta tattcataga	120
gaatggctgt gggccgatat aatacgagcg ttaaccgtta tcaatgtgca ctttttgtgt	180
ctcttggcac catttaacta caaatgggaa gcattacggt tcggtttcgt gctctacgcg	240
ttgacttcac tcagcatcac attctcatac cataggaact tgggctcacc ggagctttaa	300
gcttccgaaa tggcttgaat atccttttagc ttattttgtct gtttttgtct ttcagggtga	360
tccgttggat tgggtgagca tacatagggg tccatcacca gttcacagat tctgaccgtg	420
accacatag ccctatcgaa ggattttggt tcagtcattgt gtggtggata tgtgacactc	480
gttatatcaa atataagtgt ggaggacgta acaacgtgat ggacttgaag cagcaatggg	540
tctattgggt tctacgaatg acaattgggt tccacgtctt aatgttttgg actgtcctct	600
atctctatgg tggtttacct taccttacat gcggcggggg cgttggagggt gtgattgggt	660
accacgtgac atggctcgtg aactcggcat gccatatttg gggttcgaga tcatggaaga	720
ctaaagacac atctcgtaac gtttgggtgc taagcttatt tacaatggga gagagttggc	780
acaataatca ccacgccttt gagtcacgag cgaggcaagg attggagtgg tggcagatag	840
acataacttg gtatcttatt cgactatttg aggttctcgg gtagccact gacgtgaaat	900
tgccctcgga attccagaaa cagaaactgg ctctgactcg ttgatcatct gcatgagaga	960
tttatcagaa ttttatattt tttagaaaatt atcaaagtta ctataaaaaga ggataatata	1020
gatgagagtt tatgattggt atagtcttat tgatattttc cactataaat tgttgttttc	1080
tgtcttttga gtaggattta aatgcggcaa aaaaagggtat ctatttttttt ttttaataaa	1140
aggcttaagt tg	

(2) INFORMATION FOR SEQ ID NO:1624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500767

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1624:

Met Asp Leu Lys Gln Gln Trp Phe Tyr Trp Phe Leu Arg Met Thr Ile
1 5 10 15
Gly Phe His Val Leu Met Phe Trp Thr Val Leu Tyr Leu Tyr Gly Gly

20 25 30
Leu Pro Tyr Leu Thr Cys Gly Gly Gly Val Gly Gly Val Ile Gly Tyr
35 40 45
His Val Thr Trp Leu Val Asn Ser Ala Cys His Ile Trp Gly Ser Arg
50 55 60
Ser Trp Lys Thr Lys Asp Thr Ser Arg Asn Val Trp Trp Leu Ser Leu
65 70 75 80
Phe Thr Met Gly Glu Ser Trp His Asn Asn His His Ala Phe Glu Ser
85 90 95
Ser Ala Arg Gln Gly Leu Glu Trp Trp Gln Ile Asp Ile Thr Trp Tyr
100 105 110
Leu Ile Arg Leu Phe Glu Val Leu Gly Leu Ala Thr Asp Val Lys Leu
115 120 125
Pro Ser Glu Phe Gln Lys Gln Lys Leu Ala Leu Thr Arg
130 135 140

(2) INFORMATION FOR SEQ ID NO:1625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1500768

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1625:

Met Thr Ile Gly Phe His Val Leu Met Phe Trp Thr Val Leu Tyr Leu
1 5 10 15
Tyr Gly Gly Leu Pro Tyr Leu Thr Cys Gly Gly Gly Val Gly Gly Val
20 25 30
Ile Gly Tyr His Val Thr Trp Leu Val Asn Ser Ala Cys His Ile Trp
35 40 45
Gly Ser Arg Ser Trp Lys Thr Lys Asp Thr Ser Arg Asn Val Trp Trp
50 55 60
Leu Ser Leu Phe Thr Met Gly Glu Ser Trp His Asn Asn His His Ala
65 70 75 80
Phe Glu Ser Ser Ala Arg Gln Gly Leu Glu Trp Trp Gln Ile Asp Ile
85 90 95
Thr Trp Tyr Leu Ile Arg Leu Phe Glu Val Leu Gly Leu Ala Thr Asp
100 105 110
Val Lys Leu Pro Ser Glu Phe Gln Lys Gln Lys Leu Ala Leu Thr Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:1626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1500769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1626:

Met Phe Trp Thr Val Leu Tyr Leu Tyr Gly Leu Pro Tyr Leu Thr
1 5 10 15
Cys Gly Gly Gly Val Gly Gly Val Ile Gly Tyr His Val Thr Trp Leu
20 25 30

Val Asn Ser Ala Cys His Ile Trp Gly Ser Arg Ser Trp Lys Thr Lys
35 40 45
Asp Thr Ser Arg Asn Val Trp Trp Leu Ser Leu Phe Thr Met Gly Glu
50 55 60
Ser Trp His Asn Asn His His Ala Phe Glu Ser Ser Ala Arg Gln Gly
65 70 75 80
Leu Glu Trp Trp Gln Ile Asp Ile Thr Trp Tyr Leu Ile Arg Leu Phe
85 90 95
Glu Val Leu Gly Leu Ala Thr Asp Val Lys Leu Pro Ser Glu Phe Gln
100 105 110
Lys Gln Lys Lys Leu Ala Leu Thr Arg
115 120

(2) INFORMATION FOR SEQ ID NO:1627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1178

(D) OTHER INFORMATION: / Ceres Seq. ID 1500778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1627:

acaagtcaca	acccaccat	gcatgtcata	tctctttcgt	tatcctcaat	attctttttc	60
ctcttcctca	catcaaccat	tttgatttct	cgggtacaac	ccacaacctc	taagcctccg	120
gcaccacggc	cccacagaga	gctctccgcc	gattactact	ccaagaaatg	tcctcagctt	180
gaaactctcg	tcggttccgt	cactttctcag	cggttcaaag	aagtcccat	ctcagctcca	240
gccaccattc	gcctcttctt	tcacgactgc	ttcggttgagg	gttgatgatg	gtcgatattg	300
atagaaacaa	agaaaggaag	caagaaatta	gcagagagag	aagcatatga	gaataaggaa	360
ttgagagagg	aaggatttga	tagtatcatc	aaggcgaagg	ccttggttga	gtctcattgc	420
ccttctctcg	tctcttsctc	tgatattctc	gctattgccg	ctcgagattt	cattcatctg	480
gcaggtgggc	cttactatca	agtgaataaa	ggaagggtgg	acggaaaaag	atcaacggca	540
aagaacgtcc	ctccaaacat	acctcgatca	aactccaccg	ttgatcaact	catcaagctc	600
ttcgcgcca	aaggactaac	cgtagaggaa	ctcgctgctc	tttctgggtc	ccacaccatc	660
ggttcgcca	ttgtaaaaa	ttccttggtc	gtctctacga	ctacaaaggc	acaaaacgac	720
ccgacccgag	tcttgaccaa	agattactaa	aagagctccg	gatgtcttgt	cctttttccg	780
gcggaagctc	tgagtcgctc	cttccgctcg	acgctacaac	tccgtttgtg	tttgataatg	840
gatatttcac	aggctcagga	accaacatgg	gccttctcgg	gtcggaccaa	gctttgttcc	900
ttgacccgag	gacgaagccc	attgcacttg	agatggcaag	agataagcag	aagttttctc	960
aggcgtttgg	agacgctatg	gataaaatgg	gttccatttg	tgtaaagaga	gggaagagac	1020
atggggaaat	acgtacggat	tgctcagctc	ttttatagat	tttctttatt	gtcttgtctg	1080
atgggttttg	tcttgatctt	gatgtgttct	gtgtcatgtg	tcctttaatt	tattagcatt	1140
ttcgtgattg	ttttgttgat	agtataaggt	attttttt			

(2) INFORMATION FOR SEQ ID NO:1628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 1500779

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1628:

Thr Ser His Asn Pro Thr Met His Val Ile Ser Leu Ser Leu Ser Ser
1 5 10 15
Ile Phe Phe Phe Leu Phe Leu Thr Ser Thr Ile Leu Ile Ser Pro Val
20 25 30
Gln Pro Thr Thr Ser Lys Pro Pro Ala Pro Arg Pro His Arg Glu Leu

(2) INFORMATION FOR SEQ ID NO:1629:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1500780

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1629:

Met	His	Val	Ile	Ser	Leu	Ser	Leu	Ser	Ser	Ile	Phe	Phe	Leu	Phe	
1				5					10				15		
Leu	Thr	Ser	Thr	Ile	Leu	Ile	Ser	Pro	Val	Gln	Pro	Thr	Thr	Ser	Lys
			20					25					30		
Pro	Pro	Ala	Pro	Arg	Pro	His	Arg	Glu	Leu	Ser	Ala	Asp	Tyr	Tyr	Ser
		35					40					45			
Lys	Lys	Cys	Pro	Gln	Leu	Glu	Thr	Leu	Val	Gly	Ser	Val	Thr	Ser	Gln
		50				55					60				
Arg	Phe	Lys	Glu	Val	Pro	Ile	Ser	Ala	Pro	Ala	Thr	Ile	Arg	Leu	Phe
65				70					75					80	
Phe	His	Asp	Cys	Phe	Val	Glu	Gly	Cys	Asp	Gly	Ser	Ile	Leu	Ile	Glu
				85					90					95	
Thr	Lys	Lys	Gly	Ser	Lys	Lys	Leu	Ala	Glu	Arg	Glu	Ala	Tyr	Glu	Asn
			100					105					110		
Lys	Glu	Leu	Arg	Glu	Glu	Gly	Phe	Asp	Ser	Ile	Ile	Lys	Ala	Lys	Ala
		115					120					125			
Leu	Val	Glu	Ser	His	Cys	Pro	Ser	Leu	Val	Ser	Xaa	Ser	Asp	Ile	Leu
		130				135					140				
Ala	Ile	Ala	Ala	Arg	Asp	Phe	Ile	His	Leu	Ala	Gly	Gly	Pro	Tyr	Tyr
145				150						155				160	
Gln	Val	Lys	Lys	Gly	Arg	Trp	Asp	Gly	Lys	Arg	Ser	Thr	Ala	Lys	Asn
				165					170					175	

Val Pro Pro Asn Ile Pro Arg Ser Asn Ser Thr Val Asp Gln Leu Ile
180 185 190
Lys Leu Phe Ala Ser Lys Gly Leu Thr Val Glu Glu Leu Val Val Leu
195 200 205
Ser Gly Ser His Thr Ile Gly Ser Pro Ile Val Lys Ile Ser Leu Val
210 215 220
Val Ser Thr Thr Thr Lys Ala Gln Asn Asp Pro Thr Arg Val Leu Thr
225 230 235 240
Lys Asp Tyr

(2) INFORMATION FOR SEQ ID NO:1630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1123
(D) OTHER INFORMATION: / Ceres Seq. ID 1500785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1630:

aaaaacacaa acgtaacaag gattcgagct ctctctagac gatgcaagcc aaaatcaatt 60
ctttcttcaa gccctcctct tcttcttcta tcgctgcctc agtaacaaca gacacagacg 120
atrgsttttag ctgtctggga gaacaatcgg aacgccatcg tcaacaccta ccagcgtcga 180
tctgcgatta ccgaaagaag tgaagtgcct aaaggatgca tcgaaaagac gctgaagaaa 240
ggatcttctt ctgtacctaa aaatcacaaa aagaagcgta attatacaca attccacata 300
gagttgggcc aatctgattt tcttctcaga cattgcgcag aatgtggagc taagtatgct 360
cctggagatg aattagatga gaagaacct caaagttttc acaaggacta tatgtatgga 420
ctccctttta agggttggca gaacgagaaa gcgtttacat cacctttgtt catcaagaac 480
cgcatcggtt tggatcaga aaatgattcc cctgcacaca gaaacaaggt gcaagaggtt 540
gtgaaaatga tggaggttga gttgggtgag gattggattc ttcaccaaca ttgtaaggtt 600
tatctattca tatcctctca gaggatctct ggatgtctag ttgctgaacc aattaaggaa 660
gcatttaagc tcatagcttc tcctgatgat gaaagacagt tacaaaaaga gagctcatcc 720
tcgccttcaa cctccattca gtttggaaac attgtttctac aaagagaggt atcgaaaaga 780
tgtcgaacat cagatgatag attagataac ggagtcattg tatgtgaaga agaagctaaa 840
ccagctgttt gtgggattag agcgatttgg gtctcacctt ctaatagaag aaaaggcata 900
gccacatggt tactcgatac caccagggaa agcttttcga acaatgggtg catgctggag 960
aaatctcagt tagcattttt acaaccaacc tccataggaa gatcttttgg atctaaatat 1020
tttggaaact gttcattctt actttacaaa gctcagctaa ttgatactca cttttcttaa 1080
acggcatagg ttctatcaca tcacaacct catcttcaact gtc

(2) INFORMATION FOR SEQ ID NO:1631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..222
(D) OTHER INFORMATION: / Ceres Seq. ID 1500786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1631:

Met Tyr Gly Leu Pro Phe Lys Gly Trp Gln Asn Glu Lys Ala Phe Thr
1 5 10 15
Ser Pro Leu Phe Ile Lys Asn Arg Ile Val Met Val Ser Glu Asn Asp
20 25 30
Ser Pro Ala His Arg Asn Lys Val Gln Glu Val Val Lys Met Met Glu
35 40 45
Val Glu Leu Gly Glu Asp Trp Ile Leu His Gln His Cys Lys Val Tyr
50 55 60

Leu Phe Ile Ser Ser Gln Arg Ile Ser Gly Cys Leu Val Ala Glu Pro
65 70 75 80
Ile Lys Glu Ala Phe Lys Leu Ile Ala Ser Pro Asp Asp Glu Arg Gln
85 90 95
Leu Gln Lys Glu Ser Ser Ser Ser Pro Ser Thr Ser Ile Gln Phe Gly
100 105 110
Asn Ile Val Leu Gln Arg Glu Val Ser Lys Arg Cys Arg Thr Ser Asp
115 120 125
Asp Arg Leu Asp Asn Gly Val Ile Val Cys Glu Glu Glu Ala Lys Pro
130 135 140
Ala Val Cys Gly Ile Arg Ala Ile Trp Val Ser Pro Ser Asn Arg Arg
145 150 155 160
Lys Gly Ile Ala Thr Trp Leu Leu Asp Thr Thr Arg Glu Ser Phe Arg
165 170 175
Asn Asn Gly Cys Met Leu Glu Lys Ser Gln Leu Ala Phe Ser Gln Pro
180 185 190
Thr Ser Ile Gly Arg Ser Phe Gly Ser Lys Tyr Phe Gly Thr Cys Ser
195 200 205
Phe Leu Leu Tyr Lys Ala Gln Leu Ile Asp Thr His Phe Ser
210 215 220

(2) INFORMATION FOR SEQ ID NO:1632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 1500787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1632:

Met Val Ser Glu Asn Asp Ser Pro Ala His Arg Asn Lys Val Gln Glu
1 5 10 15
Val Val Lys Met Met Glu Val Glu Leu Gly Glu Asp Trp Ile Leu His
20 25 30
Gln His Cys Lys Val Tyr Leu Phe Ile Ser Ser Gln Arg Ile Ser Gly
35 40 45
Cys Leu Val Ala Glu Pro Ile Lys Glu Ala Phe Lys Leu Ile Ala Ser
50 55 60
Pro Asp Asp Glu Arg Gln Leu Gln Lys Glu Ser Ser Ser Pro Ser
65 70 75 80
Thr Ser Ile Gln Phe Gly Asn Ile Val Leu Gln Arg Glu Val Ser Lys
85 90 95
Arg Cys Arg Thr Ser Asp Asp Arg Leu Asp Asn Gly Val Ile Val Cys
100 105 110
Glu Glu Glu Ala Lys Pro Ala Val Cys Gly Ile Arg Ala Ile Trp Val
115 120 125
Ser Pro Ser Asn Arg Arg Lys Gly Ile Ala Thr Trp Leu Leu Asp Thr
130 135 140
Thr Arg Glu Ser Phe Arg Asn Asn Gly Cys Met Leu Glu Lys Ser Gln
145 150 155 160
Leu Ala Phe Ser Gln Pro Thr Ser Ile Gly Arg Ser Phe Gly Ser Lys
165 170 175
Tyr Phe Gly Thr Cys Ser Phe Leu Leu Tyr Lys Ala Gln Leu Ile Asp
180 185 190
Thr His Phe Ser
195

(2) INFORMATION FOR SEQ ID NO:1633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..177
(D) OTHER INFORMATION: / Ceres Seq. ID 1500788
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1633:

Met Met Glu Val Glu Leu Gly Glu Asp Trp Ile Leu His Gln His Cys
1 5 10 15
Lys Val Tyr Leu Phe Ile Ser Ser Gln Arg Ile Ser Gly Cys Leu Val
20 25 30
Ala Glu Pro Ile Lys Glu Ala Phe Lys Leu Ile Ala Ser Pro Asp Asp
35 40 45
Glu Arg Gln Leu Gln Lys Glu Ser Ser Ser Ser Pro Ser Thr Ser Ile
50 55 60
Gln Phe Gly Asn Ile Val Leu Gln Arg Glu Val Ser Lys Arg Cys Arg
65 70 75 80
Thr Ser Asp Asp Arg Leu Asp Asn Gly Val Ile Val Cys Glu Glu Glu
85 90 95
Ala Lys Pro Ala Val Cys Gly Ile Arg Ala Ile Trp Val Ser Pro Ser
100 105 110
Asn Arg Arg Lys Gly Ile Ala Thr Trp Leu Leu Asp Thr Thr Arg Glu
115 120 125
Ser Phe Arg Asn Asn Gly Cys Met Leu Glu Lys Ser Gln Leu Ala Phe
130 135 140
Ser Gln Pro Thr Ser Ile Gly Arg Ser Phe Gly Ser Lys Tyr Phe Gly
145 150 155 160
Thr Cys Ser Phe Leu Leu Tyr Lys Ala Gln Leu Ile Asp Thr His Phe
165 170 175
Ser

(2) INFORMATION FOR SEQ ID NO:1634:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1452 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..1452
(D) OTHER INFORMATION: / Ceres Seq. ID 1500793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1634:

aagcattttg cattcttggt tcttggtttt gtgttttagt tttgagagaa aatgggacag 60
attccgaggt ttctttcttg gaggaatatg ttggctcctc cgttggccat caacttcagc 120
ttgattctaa agattttgaa ggggtgataga gaacgaggag attcatggga cagaacagcg 180
tatgttagca tatggcccggt ggtatccacc acggcttcag aatcttcttc gttgtcttca 240
gcatcttgca actatagcaa gattgaagaa gacgatgata gaattatcaa tctcaaattt 300
gggtgatccaa cgggtgatga gagatattgg caggaaaatg gagaggtgac aacaatggtg 360
atacctggat ggcaatctct tagctatttt tcagatgaaa acaacctctg ttggtttctt 420
gagccagagc ttgccaaaga gattgtgagg gtgcataagg ttgttgggaa tgctgtaacg 480
caagaccgct tcattgttgt tggcactggc tcaacacaa tgatcaggc tgctctctat 540
gctctctccc cacatgatga ctccgggtccc attaatgtcg tgtcagccgc accctattat 600
agtacatacc cgttgattac agactgcctc aaatcaggtt tatatcgatg ggggtggagat 660
gcaaagacgt acaaagaaga tgggtccatac attgaacttg ttacatctcc aaacaaccct 720
gatgggttct tgagagaatc agtagtgaac agtactgaag gtatattgat ccatgatttg 780
gcttactatt ggccacagta tacaccgata acataaccag ctgatcacga tgttatgctc 840
ttcactgctt caaagagcac tggccatgca gggatacggg ttggvtgggc tttggtgaaa 900
gacagagaga cggctaggaa aatgatagag tacattgaac tcaacacgat tggggtttca 960

aaggactcac	agcttagagt	agccaagggt	cttaagggtg	tgtcagacag	ttgtgggaat	1020
gtaacgggca	aatcttttct	tgaccatagt	tatgatgcta	tgtatgagag	gtggaaacta	1080
ttgaaacaag	cagcaaagga	tactaaacgt	ttcagtgttc	ctgatttcgt	ctctcaacgt	1140
tgcaatttct	ttggcagggg	ctttgagcca	caaccagcat	ttgcatgggt	taagtgtgaa	1200
gaagggatag	tggattgtga	gaagtttctt	agagaggaga	agaagattct	aactaaaagt	1260
ggaaagtact	tgggagatga	gctaagtaat	gtgaggataa	gcatgttgga	tagagatact	1320
aactttaata	ttttccttca	caggattaca	tcttccttta	attcaacttt	gtaagtgcac	1380
atgcatgtga	ttatgatcga	ttgtcataac	ttgcaacaag	tgttttgctc	cataaatatt	1440
attggaaatt	tg					

(2) INFORMATION FOR SEQ ID NO:1635:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..254

(D) OTHER INFORMATION: / Ceres Seq. ID 1500794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1635:

Met	Gly	Gln	Ile	Pro	Arg	Phe	Leu	Ser	Trp	Arg	Asn	Met	Leu	Val	Leu	
1			5						10					15		
Ser	Leu	Ala	Ile	Asn	Phe	Ser	Leu	Ile	Leu	Lys	Ile	Leu	Lys	Gly	Asp	
		20						25					30			
Arg	Glu	Arg	Gly	Asp	Ser	Trp	Asp	Arg	Thr	Ala	Tyr	Val	Ser	Ile	Trp	
		35					40					45				
Pro	Val	Val	Ser	Thr	Thr	Ala	Ser	Glu	Ser	Ser	Ser	Leu	Ser	Ser	Ala	
		50				55					60					
Ser	Cys	Asn	Tyr	Ser	Lys	Ile	Glu	Glu	Asp	Asp	Asp	Arg	Ile	Ile	Asn	
65					70				75					80		
Leu	Lys	Phe	Gly	Asp	Pro	Thr	Val	Tyr	Glu	Arg	Tyr	Trp	Gln	Glu	Asn	
		85						90					95			
Gly	Glu	Val	Thr	Thr	Met	Val	Ile	Pro	Gly	Trp	Gln	Ser	Leu	Ser	Tyr	
		100						105				110				
Phe	Ser	Asp	Glu	Asn	Asn	Leu	Cys	Trp	Phe	Leu	Glu	Pro	Glu	Leu	Ala	
		115				120					125					
Lys	Glu	Ile	Val	Arg	Val	His	Lys	Val	Val	Gly	Asn	Ala	Val	Thr	Gln	
		130				135					140					
Asp	Arg	Phe	Ile	Val	Val	Gly	Thr	Gly	Ser	Thr	Gln	Leu	Tyr	Gln	Ala	
145					150				155					160		
Ala	Leu	Tyr	Ala	Leu	Ser	Pro	His	Asp	Asp	Ser	Gly	Pro	Ile	Asn	Val	
		165						170					175			
Val	Ser	Ala	Ala	Pro	Tyr	Tyr	Ser	Thr	Tyr	Pro	Leu	Ile	Thr	Asp	Cys	
		180						185				190				
Leu	Lys	Ser	Gly	Leu	Tyr	Arg	Trp	Gly	Gly	Asp	Ala	Lys	Thr	Tyr	Lys	
		195					200					205				
Glu	Asp	Gly	Pro	Tyr	Ile	Glu	Leu	Val	Thr	Ser	Pro	Asn	Asn	Pro	Asp	
		210				215					220					
Gly	Phe	Leu	Arg	Glu	Ser	Val	Val	Asn	Ser	Thr	Glu	Gly	Ile	Leu	Ile	
225					230					235				240		
His	Asp	Leu	Ala	Tyr	Trp	Pro	Gln	Tyr	Thr	Pro	Ile	Thr				
		245						250								

(2) INFORMATION FOR SEQ ID NO:1636:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..242

(D) OTHER INFORMATION: / Ceres Seq. ID 1500795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1636:

```
Met Leu Val Leu Ser Leu Ala Ile Asn Phe Ser Leu Ile Leu Lys Ile
1      5      10      15
Leu Lys Gly Asp Arg Glu Arg Gly Asp Ser Trp Asp Arg Thr Ala Tyr
20      25      30
Val Ser Ile Trp Pro Val Val Ser Thr Thr Ala Ser Glu Ser Ser Ser
35      40      45
Leu Ser Ser Ala Ser Cys Asn Tyr Ser Lys Ile Glu Glu Asp Asp Asp
50      55      60
Arg Ile Ile Asn Leu Lys Phe Gly Asp Pro Thr Val Tyr Glu Arg Tyr
65      70      75      80
Trp Gln Glu Asn Gly Glu Val Thr Thr Met Val Ile Pro Gly Trp Gln
85      90      95
Ser Leu Ser Tyr Phe Ser Asp Glu Asn Asn Leu Cys Trp Phe Leu Glu
100     105     110
Pro Glu Leu Ala Lys Glu Ile Val Arg Val His Lys Val Val Gly Asn
115     120     125
Ala Val Thr Gln Asp Arg Phe Ile Val Val Gly Thr Gly Ser Thr Gln
130     135     140
Leu Tyr Gln Ala Ala Leu Tyr Ala Leu Ser Pro His Asp Asp Ser Gly
145     150     155     160
Pro Ile Asn Val Val Ser Ala Ala Pro Tyr Tyr Ser Thr Tyr Pro Leu
165     170     175
Ile Thr Asp Cys Leu Lys Ser Gly Leu Tyr Arg Trp Gly Gly Asp Ala
180     185     190
Lys Thr Tyr Lys Glu Asp Gly Pro Tyr Ile Glu Leu Val Thr Ser Pro
195     200     205
Asn Asn Pro Asp Gly Phe Leu Arg Glu Ser Val Val Asn Ser Thr Glu
210     215     220
Gly Ile Leu Ile His Asp Leu Ala Tyr Tyr Trp Pro Gln Tyr Thr Pro
225     230     235     240
Ile Thr
```

(2) INFORMATION FOR SEQ ID NO:1637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1500796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1637:

```
Met Leu Phe Thr Ala Ser Lys Ser Thr Gly His Ala Gly Ile Arg Ile
1      5      10      15
Xaa Trp Ala Leu Val Lys Asp Arg Glu Thr Ala Arg Lys Met Ile Glu
20      25      30
Tyr Ile Glu Leu Asn Thr Ile Gly Val Ser Lys Asp Ser Gln Leu Arg
35      40      45
Val Ala Lys Val Leu Lys Val Val Ser Asp Ser Cys Gly Asn Val Thr
50      55      60
Gly Lys Ser Phe Phe Asp His Ser Tyr Asp Ala Met Tyr Glu Arg Trp
65      70      75      80
Lys Leu Leu Lys Gln Ala Ala Lys Asp Thr Lys Arg Phe Ser Val Pro
85      90      95
Asp Phe Val Ser Gln Arg Cys Asn Phe Phe Gly Arg Val Phe Glu Pro
```

100 105 110
Gln Pro Ala Phe Ala Trp Phe Lys Cys Glu Glu Gly Ile Val Asp Cys
115 120 125
Glu Lys Phe Leu Arg Glu Glu Lys Lys Ile Leu Thr Lys Ser Gly Lys
130 135 140
Tyr Phe Gly Asp Glu Leu Ser Asn Val Arg Ile Ser Met Leu Asp Arg
145 150 155 160
Asp Thr Asn Phe Asn Ile Phe Leu His Arg Ile Thr Ser Ser Phe Asn
165 170 175
Ser Thr Leu

(2) INFORMATION FOR SEQ ID NO:1638:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1235
(D) OTHER INFORMATION: / Ceres Seq. ID 1500797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1638:

aactaaatca gaagattact actaaacaga gtcttttttg acttgccaaa aacacatctg 60
tctctctctc tctttgcgga tctgaaatgg cgattcctgt tatcgatttc tccaaactca 120
atggtgaaga aagagagaag acactgtctg aaatcgctag agcttgcgaa gagtggggat 180
tttttcagct ggtgaacctt ggtattccat tggagcttct aaataagggt aagaagctga 240
gctcagattg ctacaaaaca gagagagaag aagcattcaa gacttctaata cccgtgaagt 300
tgctcaacga attggttcaa aagaactctg gcgagaagct agaaaacgtg gactgggaag 360
atgtcttcac tctcttgac cataaccaa acgaatggcc atccaaaatt aaagagacta 420
tgggagaata cagagaagaa gtgaggaagc tagcgagcaa gatgatggaa gtgatggatg 480
agaatttggg tttgcctaaa gggtacataa agaaagcttt caatgaagga atggaagatg 540
gagaagagac agctttcttt gggactaaag tcagccatta ccctccttgt cctcatcctg 600
agctagtcaa tggccttcga gctcactact atgcaggagg tgtcgttttg cttttccaag 660
acgatgaata tgatggcctt caggtcttga aagacggcga gtggatcgat gttcagcctc 720
tacctaattg cattgttatc aacactgggt atcagattga agttcttagc aacggaagggt 780
acaagagtgc gtggcacagg gtggtggcga gggaggaagg aaacagaagg tctatagctt 840
ccttctacaa tccgtcgtac aaggcggcga tagggccagc cacgggtggcg gaagaggaag 900
gaagtgaaga gaagtatcca aagtttgtgt ttggagatta catggatggt tatgcaaacc 960
agaagttcat gcctaaagag cctcgttttc tagctgtaaa gtctctctaa atgtactatt 1020
ttattttatt ttacagtact atcactgttt tatctacacc cattatgtat tttctcttaa 1080
gctataaatg ccaaattata tagttaaaaa tttggcatct gctctccagg ctttatattt 1140
ttttgttttt tttgtttttg ccatgtgatg tatgaatcct tcttgtgtga cctatgttct 1200
tagtttttga atataaatgt gtgtgccttt ttctt

(2) INFORMATION FOR SEQ ID NO:1639:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..307
(D) OTHER INFORMATION: / Ceres Seq. ID 1500798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639:

Met Ala Ile Pro Val Ile Asp Phe Ser Lys Leu Asn Gly Glu Glu Arg
1 5 10 15
Glu Lys Thr Leu Ser Glu Ile Ala Arg Ala Cys Glu Glu Trp Gly Phe
20 25 30
Phe Gln Leu Val Asn His Gly Ile Pro Leu Glu Leu Leu Asn Lys Val

35 40 45
Lys Lys Leu Ser Ser Asp Cys Tyr Lys Thr Glu Arg Glu Glu Ala Phe
50 55 60
Lys Thr Ser Asn Pro Val Lys Leu Leu Asn Glu Leu Val Gln Lys Asn
65 70 75 80
Ser Gly Glu Lys Leu Glu Asn Val Asp Trp Glu Asp Val Phe Thr Leu
85 90 95
Leu Asp His Asn Gln Asn Glu Trp Pro Ser Lys Ile Lys Glu Thr Met
100 105 110
Gly Glu Tyr Arg Glu Glu Val Arg Lys Leu Ala Ser Lys Met Met Glu
115 120 125
Val Met Asp Glu Asn Leu Gly Leu Pro Lys Gly Tyr Ile Lys Lys Ala
130 135 140
Phe Asn Glu Gly Met Glu Asp Gly Glu Glu Thr Ala Phe Phe Gly Thr
145 150 155 160
Lys Val Ser His Tyr Pro Pro Cys Pro His Pro Glu Leu Val Asn Gly
165 170 175
Leu Arg Ala His Thr Asp Ala Gly Gly Val Val Leu Leu Phe Gln Asp
180 185 190
Asp Glu Tyr Asp Gly Leu Gln Val Leu Lys Asp Gly Glu Trp Ile Asp
195 200 205
Val Gln Pro Leu Pro Asn Ala Ile Val Ile Asn Thr Gly Asp Gln Ile
210 215 220
Glu Val Leu Ser Asn Gly Arg Tyr Lys Ser Ala Trp His Arg Val Val
225 230 235 240
Ala Arg Glu Glu Gly Asn Arg Arg Ser Ile Ala Ser Phe Tyr Asn Pro
245 250 255
Ser Tyr Lys Ala Ala Ile Gly Pro Ala Thr Val Ala Glu Glu Glu Gly
260 265 270
Ser Glu Lys Lys Tyr Pro Lys Phe Val Phe Gly Asp Tyr Met Asp Val
275 280 285
Tyr Ala Asn Gln Lys Phe Met Pro Lys Glu Pro Arg Phe Leu Ala Val
290 295 300
Lys Ser Leu
305

(2) INFORMATION FOR SEQ ID NO:1640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..196
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640:

Met Gly Glu Tyr Arg Glu Glu Val Arg Lys Leu Ala Ser Lys Met Met
1 5 10 15
Glu Val Met Asp Glu Asn Leu Gly Leu Pro Lys Gly Tyr Ile Lys Lys
20 25 30
Ala Phe Asn Glu Gly Met Glu Asp Gly Glu Glu Thr Ala Phe Phe Gly
35 40 45
Thr Lys Val Ser His Tyr Pro Pro Cys Pro His Pro Glu Leu Val Asn
50 55 60
Gly Leu Arg Ala His Thr Asp Ala Gly Gly Val Val Leu Leu Phe Gln
65 70 75 80
Asp Asp Glu Tyr Asp Gly Leu Gln Val Leu Lys Asp Gly Glu Trp Ile
85 90 95
Asp Val Gln Pro Leu Pro Asn Ala Ile Val Ile Asn Thr Gly Asp Gln
100 105 110

Ile Glu Val Leu Ser Asn Gly Arg Tyr Lys Ser Ala Trp His Arg Val
115 120 125
Val Ala Arg Glu Glu Gly Asn Arg Arg Ser Ile Ala Ser Phe Tyr Asn
130 135 140
Pro Ser Tyr Lys Ala Ala Ile Gly Pro Ala Thr Val Ala Glu Glu Glu
145 150 155 160
Gly Ser Glu Lys Lys Tyr Pro Lys Phe Val Phe Gly Asp Tyr Met Asp
165 170 175
Val Tyr Ala Asn Gln Lys Phe Met Pro Lys Glu Pro Arg Phe Leu Ala
180 185 190
Val Lys Ser Leu
195

(2) INFORMATION FOR SEQ ID NO:1641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..182
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641:

Met Met Glu Val Met Asp Glu Asn Leu Gly Leu Pro Lys Gly Tyr Ile
1 5 10 15
Lys Lys Ala Phe Asn Glu Gly Met Glu Asp Gly Glu Glu Thr Ala Phe
20 25 30
Phe Gly Thr Lys Val Ser His Tyr Pro Pro Cys Pro His Pro Glu Leu
35 40 45
Val Asn Gly Leu Arg Ala His Thr Asp Ala Gly Gly Val Val Leu Leu
50 55 60
Phe Gln Asp Asp Glu Tyr Asp Gly Leu Gln Val Leu Lys Asp Gly Glu
65 70 75 80
Trp Ile Asp Val Gln Pro Leu Pro Asn Ala Ile Val Ile Asn Thr Gly
85 90 95
Asp Gln Ile Glu Val Leu Ser Asn Gly Arg Tyr Lys Ser Ala Thr Phe His
100 105 110
Arg Val Val Ala Arg Glu Glu Gly Asn Arg Arg Ser Ile Ala Ser Phe
115 120 125
Tyr Asn Pro Ser Tyr Lys Ala Ala Ile Gly Pro Ala Thr Val Ala Glu
130 135 140
Glu Glu Gly Ser Glu Lys Lys Tyr Pro Lys Phe Val Phe Gly Asp Tyr
145 150 155 160
Met Asp Val Tyr Ala Asn Gln Lys Phe Met Pro Lys Glu Pro Arg Phe
165 170 175
Leu Ala Val Lys Ser Leu
180

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..619
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642:

acaccggcgt ttggctgmsa tcatcgagat gatacacact gcaagcttga tacacgacga

tgtgttagac	gagagtgaca	tgccaagagg	aaaggaaaca	gttcatgagc	ttttcggcac	120
aagagtagcg	gtgctagctg	gagatttcat	gtttgctcaa	gcgtcatggt	acttagcaaa	180
tctcgagaat	cttgaagtta	ttaagctcat	cagtcaggtg	atcaaagact	ttgcaagcgg	240
agagataaag	caggcgtcca	gcttatttga	ctgcgacacc	aagctcgacg	agtacttact	300
caaaagtttc	tacaagacag	cctctttagt	ggctgcgagc	accaaaggag	ctgccatttt	360
cagcagagtt	gagcctgatg	tgacagaaca	aatgtacgag	tttgggaaga	atctcgggtct	420
ctctttccag	atagttgatg	atattttgga	tttctactcag	tcgacagagc	agctcgggaa	480
gccagcaggg	agtgatttgg	ctaaaggtaa	cttaacagca	cctgtgattt	tcgctctgga	540
gagggagcca	aggctaagag	agatcattga	gtcagagttt	tgtgaggcgg	gttctctgga	600
agaagcgatt	gaagcgggtg					

(2) INFORMATION FOR SEQ ID NO:1643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1500802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643:

His	Arg	Arg	Leu	Ala	Xaa	Ile	Ile	Glu	Met	Ile	His	Thr	Ala	Ser	Leu	
1				5					10					15		
Ile	His	Asp	Asp	Val	Leu	Asp	Glu	Ser	Asp	Met	Arg	Arg	Gly	Lys	Glu	
			20					25						30		
Thr	Val	His	Glu	Leu	Phe	Gly	Thr	Arg	Val	Ala	Val	Leu	Ala	Gly	Asp	
			35				40						45			
Phe	Met	Phe	Ala	Gln	Ala	Ser	Trp	Tyr	Leu	Ala	Asn	Leu	Glu	Asn	Leu	
			50				55				60					
Glu	Val	Ile	Lys	Leu	Ile	Ser	Gln	Val	Ile	Lys	Asp	Phe	Ala	Ser	Gly	
65				70					75					80		
Glu	Ile	Lys	Gln	Ala	Ser	Ser	Leu	Phe	Asp	Cys	Asp	Thr	Lys	Leu	Asp	
			85						90					95		
Glu	Tyr	Leu	Leu	Lys	Ser	Phe	Tyr	Lys	Thr	Ala	Ser	Leu	Val	Ala	Ala	
			100					105					110			
Ser	Thr	Lys	Gly	Ala	Ala	Ile	Phe	Ser	Arg	Val	Glu	Pro	Asp	Val	Thr	
			115				120						125			
Glu	Gln	Met	Tyr	Glu	Phe	Gly	Lys	Asn	Leu	Gly	Leu	Ser	Phe	Gln	Ile	
			130				135				140					
Val	Asp	Asp	Ile	Leu	Asp	Phe	Thr	Gln	Ser	Thr	Glu	Gln	Leu	Gly	Lys	
145				150					155						160	
Pro	Ala	Gly	Ser	Asp	Leu	Ala	Lys	Gly	Asn	Leu	Thr	Ala	Pro	Val	Ile	
			165						170					175		
Phe	Ala	Leu	Glu	Arg	Glu	Pro	Arg	Leu	Arg	Glu	Ile	Ile	Glu	Ser	Glu	
			180					185					190			
Phe	Cys	Glu	Ala	Gly	Ser	Leu	Glu	Ala	Ile	Glu	Ala	Val				
			195				200					205				

(2) INFORMATION FOR SEQ ID NO:1644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1500803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644:

Met Ile His Thr Ala Ser Leu Ile His Asp Asp Val Leu Asp Glu Ser

1	5	10	15
Asp Met Arg Arg Gly Lys Glu Thr Val His Glu Leu Phe Gly Thr Arg			
20	25	30	
Val Ala Val Leu Ala Gly Asp Phe Met Phe Ala Gln Ala Ser Trp Tyr			
35	40	45	
Leu Ala Asn Leu Glu Asn Leu Glu Val Ile Lys Leu Ile Ser Gln Val			
50	55	60	
Ile Lys Asp Phe Ala Ser Gly Glu Ile Lys Gln Ala Ser Ser Leu Phe			
65	70	75	80
Asp Cys Asp Thr Lys Leu Asp Glu Tyr Leu Leu Lys Ser Phe Tyr Lys			
85	90	95	
Thr Ala Ser Leu Val Ala Ala Ser Thr Lys Gly Ala Ala Ile Phe Ser			
100	105	110	
Arg Val Glu Pro Asp Val Thr Glu Gln Met Tyr Glu Phe Gly Lys Asn			
115	120	125	
Leu Gly Leu Ser Phe Gln Ile Val Asp Asp Ile Leu Asp Phe Thr Gln			
130	135	140	
Ser Thr Glu Gln Leu Gly Lys Pro Ala Gly Ser Asp Leu Ala Lys Gly			
145	150	155	160
Asn Leu Thr Ala Pro Val Ile Phe Ala Leu Glu Arg Glu Pro Arg Leu			
165	170	175	
Arg Glu Ile Ile Glu Ser Glu Phe Cys Glu Ala Gly Ser Leu Glu Glu			
180	185	190	
Ala Ile Glu Ala Val			
195			

(2) INFORMATION FOR SEQ ID NO:1645:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1500804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645:

Met Arg Arg Gly Lys Glu Thr Val His Glu Leu Phe Gly Thr Arg Val			
1	5	10	15
Ala Val Leu Ala Gly Asp Phe Met Phe Ala Gln Ala Ser Trp Tyr Leu			
20	25	30	
Ala Asn Leu Glu Asn Leu Glu Val Ile Lys Leu Ile Ser Gln Val Ile			
35	40	45	
Lys Asp Phe Ala Ser Gly Glu Ile Lys Gln Ala Ser Ser Leu Phe Asp			
50	55	60	
Cys Asp Thr Lys Leu Asp Glu Tyr Leu Leu Lys Ser Phe Tyr Lys Thr			
65	70	75	80
Ala Ser Leu Val Ala Ala Ser Thr Lys Gly Ala Ala Ile Phe Ser Arg			
85	90	95	
Val Glu Pro Asp Val Thr Glu Gln Met Tyr Glu Phe Gly Lys Asn Leu			
100	105	110	
Gly Leu Ser Phe Gln Ile Val Asp Asp Ile Leu Asp Phe Thr Gln Ser			
115	120	125	
Thr Glu Gln Leu Gly Lys Pro Ala Gly Ser Asp Leu Ala Lys Gly Asn			
130	135	140	
Leu Thr Ala Pro Val Ile Phe Ala Leu Glu Arg Glu Pro Arg Leu Arg			
145	150	155	160
Glu Ile Ile Glu Ser Glu Phe Cys Glu Ala Gly Ser Leu Glu Glu Ala			
165	170	175	
Ile Glu Ala Val			
180			

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(2) INFORMATION FOR SEQ ID NO:1646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1776 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1776
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646:

```
gtctcatcac ttcccacttt cctctctgca ttgttgtct ctctctcctg aaaacccttg      60
aattttgcta cacgatctct gaaacgtgtc tctttgactg acttcaatct tctttatcac      120
ttaccgtttc tgggttttat gaagcaactg agctaataaa aagcttcttc ttagactcgg      180
aagaagaaaa aaacagaaat ctttattgtt taaagcttcc aaattcgaga agagaatttg      240
aaacgaccaa gttcaggata ttctgttctt cgtctacttt ggtctcttcc tcttctcttt      300
cgaaaagggt ttattctgtc ttaaaagaaa cctttttgag agggtaaaaa aagcttcaat      360
tttcagagaa acacaaaagg cagaaacaga gaaaaacaaa tcatctaatt catgaaacag      420
ggttcaatga atagatcgtg tctctgtagt gtcttaatca ccactgctct gatttggtg      480
gcttacttca ttgcaatgc ttatcttgct aaagacttta aagagaagtt gctgaagtgg      540
gaaatcactg ataagatgca taacagtact gataagatgc agaatgcaac aacaaccagt      600
acatgcaaga atttcaataa cccagtgggt actgaagcac taccgcaagg aattatcgag      660
aaaacatcga acctggaaac acaacatcta tggaactacg atgacacaaa aaagagaagg      720
cctaaccatt cgatgagttt gttagccatg gcggtcggtg tcaagcaaaa ggagctagtt      780
aacaaagtta tccaaaagtt tcctcctcga gatttcgcgg tcatgttttt tcattatgat      840
gggtgtgtcg atgactggaa gcagtatcca tggaataatc atgctgattca tgtttccgtg      900
atgaatcaaa caaaatggtg gttcgccaag cgattcttgc atcccgatat agttgcagag      960
tacgagtata tatttctttg ggacgaagat cttggtgttg gtcatttcaa tcctcaacga     1020
tatctatcta ttgtcaaaga agaggggctt gagatatcgc aacctgctct tgacacttca     1080
aaatcagaag tgcatcatcc tataaccgct cgtcaaaaaa aatcaaaaagt tcatagaaga     1140
atgtataaat acaaaggtag cgggcgatgt gatgaccata gcaccaatcc tccttgcac     1200
gggtgggtgg aaatgatggc acctgttttc tctagagctg catggagatg ttcttggtat     1260
atgattcaga atgatttgat ccatgcttgg ggtctggata cgcagcttgg ttatttgtct     1320
caaggtgacc gaaagaaaaa tgtcgggtgt gttgatgcgg agtacataat tcattatggt     1380
cttccaacac tcggtgtggt tgaaaccgct tcaagcgctt tgcggaatga gacagactcg     1440
aaatcaacgg aatcattaga gtctcgtgaa gtggataata gaccagaagt gaggatgaaa     1500
tcattttgtg agatgaagag attcaaggaa cgttgaaga aagctgtgag ggatgataca     1560
tgttgggttg atccgtattg aaatccgagc ggtttaagta aaccgaatcg aaccgattc     1620
ttttccttgt tgagtgtgct ttgtggtcca ttgtatacca ttattttggt acatagattt     1680
tgttttactt cgagaaaaat tagtgtattt atgtgtttta tggaccacag tgtagattta     1740
acattttgga gcattatata aaagtgtttt tgtgcc
```

(2) INFORMATION FOR SEQ ID NO:1647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..389
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647:

```
Met Lys Gln Gly Ser Met Asn Arg Ser Cys Leu Cys Ser Val Leu Ile
1           5           10           15
Thr Thr Ala Leu Ile Cys Gly Ala Tyr Phe Ile Cys Asn Ala Tyr Leu
20           25           30
Ala Lys Asp Phe Lys Glu Lys Leu Lys Trp Glu Ile Thr Asp Lys
35           40           45
Met His Asn Ser Thr Asp Lys Met Gln Asn Ala Thr Thr Thr Ser Thr
```


50		55		60	
Cys Lys Asn Phe Asn Lys Pro Val Gly Thr Glu Ala Leu Pro Gln Gly					
65		70		75	80
Ile Ile Glu Lys Thr Ser Asn Leu Glu Thr Gln His Leu Trp Asn Tyr					
	85		90		95
Asp Asp Thr Lys Lys Arg Arg Pro Asn His Ser Met Ser Leu Leu Ala					
	100		105		110
Met Ala Val Gly Ile Lys Gln Lys Glu Leu Val Asn Lys Val Ile Gln					
	115		120		125
Lys Phe Pro Pro Arg Asp Phe Ala Val Met Leu Phe His Tyr Asp Gly					
	130		135		140
Val Val Asp Asp Trp Lys Gln Tyr Pro Trp Asn Asn His Ala Ile His					
145		150		155	160
Val Ser Val Met Asn Gln Thr Lys Trp Trp Phe Ala Lys Arg Phe Leu					
	165		170		175
His Pro Asp Ile Val Ala Glu Tyr Glu Tyr Ile Phe Leu Trp Asp Glu					
	180		185		190
Asp Leu Gly Val Gly His Phe Asn Pro Gln Arg Tyr Leu Ser Ile Val					
	195		200		205
Lys Glu Glu Gly Leu Glu Ile Ser Gln Pro Ala Leu Asp Thr Ser Lys					
	210		215		220
Ser Glu Val His His Pro Ile Thr Ala Arg Gln Lys Lys Ser Lys Val					
225		230		235	240
His Arg Arg Met Tyr Lys Tyr Lys Gly Ser Gly Arg Cys Asp Asp His					
	245		250		255
Ser Thr Asn Pro Pro Cys Ile Gly Trp Val Glu Met Met Ala Pro Val					
	260		265		270
Phe Ser Arg Ala Ala Trp Arg Cys Ser Trp Tyr Met Ile Gln Asn Asp					
	275		280		285
Leu Ile His Ala Trp Gly Leu Asp Thr Gln Leu Gly Tyr Cys Ala Gln					
	290		295		300
Gly Asp Arg Lys Lys Asn Val Gly Val Val Asp Ala Glu Tyr Ile Ile					
305		310		315	320
His Tyr Gly Leu Pro Thr Leu Gly Val Val Glu Thr Ala Ser Ser Ala					
	325		330		335
Leu Arg Asn Glu Thr Asp Ser Lys Ser Thr Glu Ser Leu Glu Ser Arg					
	340		345		350
Glu Val Asp Asn Arg Pro Glu Val Arg Met Lys Ser Phe Val Glu Met					
	355		360		365
Lys Arg Phe Lys Glu Arg Trp Lys Lys Ala Val Arg Asp Asp Thr Cys					
	370		375		380
Trp Val Asp Pro Tyr					
385					

(2) INFORMATION FOR SEQ ID NO:1648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..384

(D) OTHER INFORMATION: / Ceres Seq. ID 1500807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648:

Met Asn Arg Ser Cys Leu Cys Ser Val Leu Ile Thr Thr Ala Leu Ile		
1	5	10
Cys Gly Ala Tyr Phe Ile Cys Asn Ala Tyr Leu Ala Lys Asp Phe Lys		
	20	25
Glu Lys Leu Leu Lys Trp Glu Ile Thr Asp Lys Met His Asn Ser Thr		
	35	40
		45

Asp	Lys	Met	Gln	Asn	Ala	Thr	Thr	Thr	Ser	Thr	Cys	Lys	Asn	Phe	Asn	
50						55					60					
Lys	Pro	Val	Gly	Thr	Glu	Ala	Leu	Pro	Gln	Gly	Ile	Ile	Glu	Lys	Thr	
65					70					75					80	
Ser	Asn	Leu	Glu	Thr	Gln	His	Leu	Trp	Asn	Tyr	Asp	Asp	Thr	Lys	Lys	
				85					90					95		
Arg	Arg	Pro	Asn	His	Ser	Met	Ser	Leu	Leu	Ala	Met	Ala	Val	Gly	Ile	
			100					105					110			
Lys	Gln	Lys	Glu	Leu	Val	Asn	Lys	Val	Ile	Gln	Lys	Phe	Pro	Pro	Arg	
		115					120					125				
Asp	Phe	Ala	Val	Met	Leu	Phe	His	Tyr	Asp	Gly	Val	Val	Asp	Asp	Trp	
130						135					140					
Lys	Gln	Tyr	Pro	Trp	Asn	Asn	His	Ala	Ile	His	Val	Ser	Val	Met	Asn	
145					150					155					160	
Gln	Thr	Lys	Trp	Trp	Phe	Ala	Lys	Arg	Phe	Leu	His	Pro	Asp	Ile	Val	
				165					170					175		
Ala	Glu	Tyr	Glu	Tyr	Ile	Phe	Leu	Trp	Asp	Glu	Asp	Leu	Gly	Val	Gly	
			180					185					190			
His	Phe	Asn	Pro	Gln	Arg	Tyr	Leu	Ser	Ile	Val	Lys	Glu	Glu	Gly	Leu	
		195					200					205				
Glu	Ile	Ser	Gln	Pro	Ala	Leu	Asp	Thr	Ser	Lys	Ser	Glu	Val	His	His	
210						215					220					
Pro	Ile	Thr	Ala	Arg	Gln	Lys	Lys	Ser	Lys	Val	His	Arg	Arg	Met	Tyr	
225					230					235					240	
Lys	Tyr	Lys	Gly	Ser	Gly	Arg	Cys	Asp	Asp	His	Ser	Thr	Asn	Pro	Pro	
				245					250					255		
Cys	Ile	Gly	Trp	Val	Glu	Met	Met	Ala	Pro	Val	Phe	Ser	Arg	Ala	Ala	
			260					265					270			
Trp	Arg	Cys	Ser	Trp	Tyr	Met	Ile	Gln	Asn	Asp	Leu	Ile	His	Ala	Trp	
			275				280						285			
Gly	Leu	Asp	Thr	Gln	Leu	Gly	Tyr	Cys	Ala	Gln	Gly	Asp	Arg	Lys	Lys	
290						295					300					
Asn	Val	Gly	Val	Val	Asp	Ala	Glu	Tyr	Ile	Ile	His	Tyr	Gly	Leu	Pro	
305					310					315					320	
Thr	Leu	Gly	Val	Val	Glu	Thr	Ala	Ser	Ser	Ala	Leu	Arg	Asn	Glu	Thr	
				325					330					335		
Asp	Ser	Lys	Ser	Thr	Glu	Ser	Leu	Glu	Ser	Arg	Glu	Val	Asp	Asn	Arg	
			340					345					350			
Pro	Glu	Val	Arg	Met	Lys	Ser	Phe	Val	Glu	Met	Lys	Arg	Phe	Lys	Glu	
			355				360					365				
Arg	Trp	Lys	Lys	Ala	Val	Arg	Asp	Asp	Thr	Cys	Trp	Val	Asp	Pro	Tyr	
370						375						380				

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1500808

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649:

Met	His	Asn	Ser	Thr	Asp	Lys	Met	Gln	Asn	Ala	Thr	Thr	Thr	Ser	Thr	
1				5				10						15		
Cys	Lys	Asn	Phe	Asn	Lys	Pro	Val	Gly	Thr	Glu	Ala	Leu	Pro	Gln	Gly	
		20						25					30			
Ile	Ile	Glu	Lys	Thr	Ser	Asn	Leu	Glu	Thr	Gln	His	Leu	Trp	Asn	Tyr	

35	40	45
Asp Asp Thr Lys Lys Arg Arg Pro Asn His Ser Met Ser Leu Leu Ala		
50	55	60
Met Ala Val Gly Ile Lys Gln Lys Glu Leu Val Asn Lys Val Ile Gln		
65	70	75
Lys Phe Pro Pro Arg Asp Phe Ala Val Met Leu Phe His Tyr Asp Gly		
85	90	95
Val Val Asp Asp Trp Lys Gln Tyr Pro Trp Asn Asn His Ala Ile His		
100	105	110
Val Ser Val Met Asn Gln Thr Lys Trp Trp Phe Ala Lys Arg Phe Leu		
115	120	125
His Pro Asp Ile Val Ala Glu Tyr Glu Tyr Ile Phe Leu Trp Asp Glu		
130	135	140
Asp Leu Gly Val Gly His Phe Asn Pro Gln Arg Tyr Leu Ser Ile Val		
145	150	155
Lys Glu Glu Gly Leu Glu Ile Ser Gln Pro Ala Leu Asp Thr Ser Lys		
165	170	175
Ser Glu Val His His Pro Ile Thr Ala Arg Gln Lys Lys Ser Lys Val		
180	185	190
His Arg Arg Met Tyr Lys Tyr Lys Gly Ser Gly Arg Cys Asp Asp His		
195	200	205
Ser Thr Asn Pro Pro Cys Ile Gly Trp Val Glu Met Met Ala Pro Val		
210	215	220
Phe Ser Arg Ala Ala Trp Arg Cys Ser Trp Tyr Met Ile Gln Asn Asp		
225	230	235
Leu Ile His Ala Trp Gly Leu Asp Thr Gln Leu Gly Tyr Cys Ala Gln		
245	250	255
Gly Asp Arg Lys Lys Asn Val Gly Val Val Asp Ala Glu Tyr Ile Ile		
260	265	270
His Tyr Gly Leu Pro Thr Leu Gly Val Val Glu Thr Ala Ser Ser Ala		
275	280	285
Leu Arg Asn Glu Thr Asp Ser Lys Ser Thr Glu Ser Leu Glu Ser Arg		
290	295	300
Glu Val Asp Asn Arg Pro Glu Val Arg Met Lys Ser Phe Val Glu Met		
305	310	315
Lys Arg Phe Lys Glu Arg Trp Lys Lys Ala Val Arg Asp Asp Thr Cys		
325	330	335
Trp Val Asp Pro Tyr		
340		

(2) INFORMATION FOR SEQ ID NO:1650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..543
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650:

aacctccact	ggttaataaac	tcaaacctct	gcaattgtct	tcttctcttc	aactccatca	60
tctccaccac	cggcattctc	gccggaatcc	aatggagctt	accagcttcc	atcgctcttc	120
tctctttatc	ctcatctcac	taacattgat	cattctcccg	acgacaacaa	cttcaatcgg	180
agtaaaactac	ggtcaaatacg	gagacaacct	cccctcccca	accgacgtaa	tcccactaat	240
aaaatcaatc	ggagcaacaa	aagtaaaact	ctacgacgca	aatccacaaa	tcctcaaagc	300
tttctccaac	accggaatcg	aattcatcat	cggactcggc	aacgaatacc	tctccaaaat	360
gaaagatcct	tcaaaaagcct	taacatggat	caaacaaaac	gttactccat	ttttacctgc	420
gactaacatc	acatgcataa	ctatcggtaa	cgaaatcctc	gctctcaacg	actcttcact	480
cactaccaat	ctcctcccag	cgatgcaagg	agttcactct	gctttaatca	ccgccggtct	540
ctc						

(2) INFORMATION FOR SEQ ID NO:1651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..180
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651:

Thr Ser Thr Val Asn Lys Leu Lys Pro Leu Gln Leu Ser Ser Ser Leu
1 5 10 15
Gln Leu His His Leu His His Arg His Ser Arg Arg Asn Pro Met Glu
20 25 30
Leu Thr Ser Phe His Arg Ser Ser Ser Leu Phe Leu Ile Ser Leu Thr
35 40 45
Leu Ile Ile Leu Pro Thr Thr Thr Thr Ser Ile Gly Val Asn Tyr Gly
50 55 60
Gln Ile Gly Asp Asn Leu Pro Ser Pro Thr Asp Val Ile Pro Leu Ile
65 70 75 80
Lys Ser Ile Gly Ala Thr Lys Val Lys Leu Tyr Asp Ala Asn Pro Gln
85 90 95
Ile Leu Lys Ala Phe Ser Asn Thr Gly Ile Glu Phe Ile Ile Gly Leu
100 105 110
Gly Asn Glu Tyr Leu Ser Lys Met Lys Asp Pro Ser Lys Ala Leu Thr
115 120 125
Trp Ile Lys Gln Asn Val Thr Pro Phe Leu Pro Ala Thr Asn Ile Thr
130 135 140
Cys Ile Thr Ile Gly Asn Glu Ile Leu Ala Leu Asn Asp Ser Ser Leu
145 150 155 160
Thr Thr Asn Leu Leu Pro Ala Met Gln Gly Val His Ser Ala Leu Ile
165 170 175
Thr Ala Gly Leu
180

(2) INFORMATION FOR SEQ ID NO:1652:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652:

Met Glu Leu Thr Ser Phe His Arg Ser Ser Leu Leu Phe Leu Ile Ser
1 5 10 15
Leu Thr Leu Ile Ile Leu Pro Thr Thr Thr Ser Ile Gly Val Asn
20 25 30
Tyr Gly Gln Ile Gly Asp Asn Leu Pro Ser Pro Thr Asp Val Ile Pro
35 40 45
Leu Ile Lys Ser Ile Gly Ala Thr Lys Val Lys Leu Tyr Asp Ala Asn
50 55 60
Pro Gln Ile Leu Lys Ala Phe Ser Asn Thr Gly Ile Glu Phe Ile Ile
65 70 75 80
Gly Leu Gly Asn Glu Tyr Leu Ser Lys Met Lys Asp Pro Ser Lys Ala
85 90 95
Leu Thr Trp Ile Lys Gln Asn Val Thr Pro Phe Leu Pro Ala Thr Asn

100 105 110
Ile Thr Cys Ile Thr Ile Gly Asn Glu Ile Leu Ala Leu Asn Asp Ser
115 120 125
Ser Leu Thr Thr Asn Leu Leu Pro Ala Met Gln Gly Val His Ser Ala
130 135 140
Leu Ile Thr Ala Gly Leu
145 150

(2) INFORMATION FOR SEQ ID NO:1653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..667
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653:

caagtgatca	aacaaaaaav	gaccaagtct	ttttgggtwtt	tcagatcgag	aaaaaatgtg	60
gttgcaaggt	ttgaagtaat	cttgcaatgg	attctttgac	tggatttaga	atggaaccca	120
aatggcaaat	tgatcctcag	cttctctttg	ttgggtccaaa	gattgggtgaa	ggagctcatg	180
ctaaagtcta	tgagggaaaa	tacaagaatc	agacagttgc	tataaagata	gttcacagag	240
gagaaacacc	agaagagatt	gctaaaagag	attcaagatt	ccttagagaa	gtagaaatgc	300
tctcacgtgt	tcaacacaag	aatttgggtca	agttcattgg	tgcttgcaag	gagcctgtaa	360
tggtgatagt	tacagaactt	cttcaaggcg	gtacattgcg	taaataatcta	ttaaacttga	420
gacccgcatg	tttggagact	cgtgtggcta	tcggttttgc	gcttgatatt	gctcgtggta	480
tggaatgctt	gcattcccat	gggatcattc	accgtgatct	caaaccgag	aacttgcttt	540
taactgcaga	ccataaaaaca	gtaaaactag	cagatttttg	attagcaaga	gaagagtcac	600
tgactgagat	gatgacggct	gagacaggaa	cataccgatg	gatggcacct	gagttgtaca	660
gcacggt						

(2) INFORMATION FOR SEQ ID NO:1654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..193
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654:

Met	Asp	Ser	Leu	Thr	Gly	Phe	Arg	Met	Glu	Pro	Lys	Trp	Gln	Ile	Asp
1			5					10					15		
Pro	Gln	Leu	Leu	Phe	Val	Gly	Pro	Lys	Ile	Gly	Glu	Gly	Ala	His	Ala
		20					25				30				
Lys	Val	Tyr	Glu	Gly	Lys	Tyr	Lys	Asn	Gln	Thr	Val	Ala	Ile	Lys	Ile
		35				40				45					
Val	His	Arg	Gly	Glu	Thr	Pro	Glu	Glu	Ile	Ala	Lys	Arg	Asp	Ser	Arg
	50			55				60							
Phe	Leu	Arg	Glu	Val	Glu	Met	Leu	Ser	Arg	Val	Gln	His	Lys	Asn	Leu
65			70					75					80		
Val	Lys	Phe	Ile	Gly	Ala	Cys	Lys	Glu	Pro	Val	Met	Val	Ile	Val	Thr
		85					90						95		
Glu	Leu	Leu	Gln	Gly	Gly	Thr	Leu	Arg	Lys	Tyr	Leu	Leu	Asn	Leu	Arg
		100					105						110		
Pro	Ala	Cys	Leu	Glu	Thr	Arg	Val	Ala	Ile	Gly	Phe	Ala	Leu	Asp	Ile
	115					120						125			
Ala	Arg	Gly	Met	Glu	Cys	Leu	His	Ser	His	Gly	Ile	Ile	His	Arg	Asp
	130					135					140				

Leu Lys Pro Glu Asn Leu Leu Leu Thr Ala Asp His Lys Thr Val Lys
145 150 155 160
Leu Ala Asp Phe Gly Leu Ala Arg Glu Glu Ser Leu Thr Glu Met Met
165 170 175
Thr Ala Glu Thr Gly Thr Tyr Arg Trp Met Ala Pro Glu Leu Tyr Ser
180 185 190
Thr

(2) INFORMATION FOR SEQ ID NO:1655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655:

Met Glu Pro Lys Trp Gln Ile Asp Pro Gln Leu Leu Phe Val Gly Pro
1 5 10 15
Lys Ile Gly Glu Gly Ala His Ala Lys Val Tyr Glu Gly Lys Tyr Lys
20 25 30
Asn Gln Thr Val Ala Ile Lys Ile Val His Arg Gly Glu Thr Pro Glu
35 40 45
Glu Ile Ala Lys Arg Asp Ser Arg Phe Leu Arg Glu Val Glu Met Leu
50 55 60
Ser Arg Val Gln His Lys Asn Leu Val Lys Phe Ile Gly Ala Cys Lys
65 70 75 80
Glu Pro Val Met Val Ile Val Thr Glu Leu Leu Gln Gly Gly Thr Leu
85 90 95
Arg Lys Tyr Leu Leu Asn Leu Arg Pro Ala Cys Leu Glu Thr Arg Val
100 105 110
Ala Ile Gly Phe Ala Leu Asp Ile Ala Arg Gly Met Glu Cys Leu His
115 120 125
Ser His Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu
130 135 140
Thr Ala Asp His Lys Thr Val Lys Leu Ala Asp Phe Gly Leu Ala Arg
145 150 155 160
Glu Glu Ser Leu Thr Glu Met Met Thr Ala Glu Thr Gly Thr Tyr Arg
165 170 175
Trp Met Ala Pro Glu Leu Tyr Ser Thr
180 185

(2) INFORMATION FOR SEQ ID NO:1656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500823

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656:

Met Leu Ser Arg Val Gln His Lys Asn Leu Val Lys Phe Ile Gly Ala
1 5 10 15
Cys Lys Glu Pro Val Met Val Ile Val Thr Glu Leu Leu Gln Gly Gly
20 25 30
Thr Leu Arg Lys Tyr Leu Leu Asn Leu Arg Pro Ala Cys Leu Glu Thr

35 40 45
Arg Val Ala Ile Gly Phe Ala Leu Asp Ile Ala Arg Gly Met Glu Cys
50 55 60
Leu His Ser His Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Leu
65 70 75 80
Leu Leu Thr Ala Asp His Lys Thr Val Lys Leu Ala Asp Phe Gly Leu
85 90 95
Ala Arg Glu Glu Ser Leu Thr Glu Met Met Thr Ala Glu Thr Gly Thr
100 105 110
Tyr Arg Trp Met Ala Pro Glu Leu Tyr Ser Thr
115 120

(2) INFORMATION FOR SEQ ID NO:1657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1887 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1887
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657:

cacacattct	tgcagaaggt	tttagaatca	caaagcataa	ctcacctacc	cctaaaccaa	60
ctccaatttc	tctcctcctc	tattaaatct	ttctcaatca	tctttctttg	agtcttttgc	120
cttggaatcc	tgatcatggc	gtcttctctc	acttccaaat	ccattcctcg	gatgcaccaa	180
acccgcttct	tcttcttttc	tatccgctcg	agctccgctg	tctctcttct	cccgccgttc	240
agatatctct	ccattcacaa	accaggaaga	acttccggca	gtcgtgggga	ttgaagaaga	300
gtgatctgat	gctaaatggg	tctgagattc	gtcctgtgaa	ggttagggct	tctgtttcca	360
cggcggagaa	agcttcggag	attgtgcttc	aaccatttag	agaaatctcg	ggtctcatta	420
agcttccttg	ctccaagtct	ctctctaata	gaattctgct	tctcgtgctg	ctatctgagg	480
gaactactgt	agtggacaac	ttgttgaaca	gtgatgacat	caattacatg	cttgatgcgt	540
tgaagatatt	gggacttaat	gtggaaactc	acagtgaaaa	caatcgtgct	gtagttgaag	600
gatgtggcgg	ggtatttcca	gcttccattg	attccaagag	tgatatcgaa	ctttacctcg	660
gcaatgcagg	aacagcaatg	cgtccactta	ccgccgcagt	tactgctgca	ggtggcaacg	720
caagttatgt	ccttgatggg	gtgcctcaga	tgagagagag	acctataggg	gatttggttg	780
ttggtcttaa	gcagcttggt	gctgatgttg	aatgtactct	tggcactaac	tgccctcctg	840
ttcgtgtcaa	cgctaattgt	ggccttctct	gtggaaaggt	gaagctttct	ggatctatta	900
gtagtcagta	ccttgaccgt	ctgctcatgg	cagctccctt	agctcttgga	gacgtcgaaa	960
ttgaaattgt	cgataaattg	atctctgttc	cgatatgttg	aatgacattg	aagttgatgg	1020
aacgttttgg	ggtaagtgtg	gagcatagtg	aaagctggga	tcgtttcttt	gttaagggtg	1080
ggcaaaaata	caagtcgccg	ggtaatgctt	acgtagaagg	tgatgcttct	agtgcagttt	1140
atttccttgg	tggtgctgcc	attaccgggt	aaactgtcac	tggtgaaggt	tgtggaacga	1200
ccagtttgca	gggagatgtg	aaatttgccg	agggtcttga	gaaaatggga	tgtaaagtgt	1260
cctggacaga	gaacagtgtg	actgtgacag	ggcgtcttag	agatgctttt	ggaatgagac	1320
acttgccggc	tattgatgtc	aacatgaaca	aaatgcctga	tgtagcaatg	actcttgccg	1380
tcgttgctct	ctttgccgat	gggtccaacca	ccattagaga	tgtggctagc	tggagagtaa	1440
aggagacgga	aaggatgatt	gccatttgca	cagagcttag	aaaactggga	gctacagtgg	1500
aagaagggtc	agattattgt	gtgattactc	cgcgaaaaaa	gggtgaaaccg	gcagagattg	1560
atacatatga	tgatcataga	atggcaatgg	cattctctct	tcagcgttgt	gctgatgttc	1620
caatcaccat	caatgacccc	ggttgcacca	ggaaaacctt	ccccgactac	ttccaagtcc	1680
ttgaaagaat	cacaaagcat	taaacaaaaa	aactctaaaa	tctccactgt	tttttcttct	1740
gatccaagct	tatctgtttc	catttttctt	gtctctgtaa	cattattaga	aagcaagagt	1800
agtgtttgtt	tgtgtgtacc	tgaactgagt	gagatttgag	atgcaatcat	tgaatcggct	1860
ttggtatata	attttactct	gttttcc				

(2) INFORMATION FOR SEQ ID NO:1658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..464

(D) OTHER INFORMATION: / Ceres Seq. ID 1500829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658:

Met	Leu	Asn	Gly	Ser	Glu	Ile	Arg	Pro	Val	Lys	Val	Arg	Ala	Ser	Val
1				5					10					15	
Ser	Thr	Ala	Glu	Lys	Ala	Ser	Glu	Ile	Val	Leu	Gln	Pro	Ile	Arg	Glu
			20					25					30		
Ile	Ser	Gly	Leu	Ile	Lys	Leu	Pro	Gly	Ser	Lys	Ser	Leu	Ser	Asn	Arg
		35					40					45			
Ile	Leu	Leu	Leu	Ala	Ala	Leu	Ser	Glu	Gly	Thr	Thr	Val	Val	Asp	Asn
	50					55					60				
Leu	Leu	Asn	Ser	Asp	Asp	Ile	Asn	Tyr	Met	Leu	Asp	Ala	Leu	Lys	Ile
65					70				75					80	
Leu	Gly	Leu	Asn	Val	Glu	Thr	His	Ser	Glu	Asn	Asn	Arg	Ala	Val	Val
				85					90					95	
Glu	Gly	Cys	Gly	Gly	Val	Phe	Pro	Ala	Ser	Ile	Asp	Ser	Lys	Ser	Asp
			100					105					110		
Ile	Glu	Leu	Tyr	Leu	Gly	Asn	Ala	Gly	Thr	Ala	Met	Arg	Pro	Leu	Thr
		115					120					125			
Ala	Ala	Val	Thr	Ala	Ala	Gly	Gly	Asn	Ala	Ser	Tyr	Val	Leu	Asp	Gly
		130				135					140				
Val	Pro	Gln	Met	Arg	Glu	Arg	Pro	Ile	Gly	Asp	Leu	Val	Val	Gly	Leu
145					150					155				160	
Lys	Gln	Leu	Gly	Ala	Asp	Val	Glu	Cys	Thr	Leu	Gly	Thr	Asn	Cys	Pro
			165						170					175	
Pro	Val	Arg	Val	Asn	Ala	Asn	Gly	Gly	Leu	Pro	Gly	Gly	Lys	Val	Lys
			180				185						190		
Leu	Ser	Gly	Ser	Ile	Ser	Ser	Gln	Tyr	Leu	Thr	Ala	Leu	Leu	Met	Ala
		195					200					205			
Ala	Pro	Leu	Ala	Leu	Gly	Asp	Val	Glu	Ile	Glu	Ile	Val	Asp	Lys	Leu
	210					215					220				
Ile	Ser	Val	Pro	Tyr	Val	Glu	Met	Thr	Leu	Lys	Leu	Met	Glu	Arg	Phe
225					230					235				240	
Gly	Val	Ser	Ala	Glu	His	Ser	Glu	Ser	Trp	Asp	Arg	Phe	Phe	Val	Lys
			245						250					255	
Gly	Gly	Gln	Lys	Tyr	Lys	Ser	Pro	Gly	Asn	Ala	Tyr	Val	Glu	Gly	Asp
		260						265					270		
Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala	Gly	Ala	Ala	Ile	Thr	Gly	Glu
		275					280					285			
Thr	Val	Thr	Val	Glu	Gly	Cys	Gly	Thr	Thr	Ser	Leu	Gln	Gly	Asp	Val
	290					295					300				
Lys	Phe	Ala	Glu	Val	Leu	Glu	Lys	Met	Gly	Cys	Lys	Val	Ser	Trp	Thr
305					310					315				320	
Glu	Asn	Ser	Val	Thr	Val	Thr	Gly	Pro	Ser	Arg	Asp	Ala	Phe	Gly	Met
			325					330						335	
Arg	His	Leu	Arg	Ala	Ile	Asp	Val	Asn	Met	Asn	Lys	Met	Pro	Asp	Val
		340						345					350		
Ala	Met	Thr	Leu	Ala	Val	Val	Ala	Leu	Phe	Ala	Asp	Gly	Pro	Thr	Thr
		355					360					365			
Ile	Arg	Asp	Val	Ala	Ser	Trp	Arg	Val	Lys	Glu	Thr	Glu	Arg	Met	Ile
	370					375						380			
Ala	Ile	Cys	Thr	Glu	Leu	Arg	Lys	Leu	Gly	Ala	Thr	Val	Glu	Glu	Gly
385					390					395				400	
Ser	Asp	Tyr	Cys	Val	Ile	Thr	Pro	Pro	Lys	Lys	Val	Lys	Pro	Ala	Glu
			405						410					415	
Ile	Asp	Thr	Tyr	Asp	Asp	His	Arg	Met	Ala	Met	Ala	Phe	Ser	Leu	Ala
		420						425					430		
Ala	Cys	Ala	Asp	Val	Pro	Ile	Thr	Ile	Asn	Asp	Pro	Gly	Cys	Thr	Arg

	435		440		445										
Lys	Thr	Phe	Pro	Asp	Tyr	Phe	Gln	Val	Leu	Glu	Arg	Ile	Thr	Lys	His
450						455					460				

(2) INFORMATION FOR SEQ ID NO:1659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..391

(D) OTHER INFORMATION: / Ceres Seq. ID 1500830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659:

Met	Leu	Asp	Ala	Leu	Lys	Ile	Leu	Gly	Leu	Asn	Val	Glu	Thr	His	Ser
1				5					10					15	
Glu	Asn	Asn	Arg	Ala	Val	Val	Glu	Gly	Cys	Gly	Gly	Val	Phe	Pro	Ala
			20					25					30		
Ser	Ile	Asp	Ser	Lys	Ser	Asp	Ile	Glu	Leu	Tyr	Leu	Gly	Asn	Ala	Gly
		35					40					45			
Thr	Ala	Met	Arg	Pro	Leu	Thr	Ala	Ala	Val	Thr	Ala	Ala	Gly	Gly	Asn
	50					55					60				
Ala	Ser	Tyr	Val	Leu	Asp	Gly	Val	Pro	Gln	Met	Arg	Glu	Arg	Pro	Ile
65				70					75					80	
Gly	Asp	Leu	Val	Val	Gly	Leu	Lys	Gln	Leu	Gly	Ala	Asp	Val	Glu	Cys
			85					90						95	
Thr	Leu	Gly	Thr	Asn	Cys	Pro	Pro	Val	Arg	Val	Asn	Ala	Asn	Gly	Gly
			100					105					110		
Leu	Pro	Gly	Gly	Lys	Val	Lys	Leu	Ser	Gly	Ser	Ile	Ser	Ser	Gln	Tyr
		115					120					125			
Leu	Thr	Ala	Leu	Leu	Met	Ala	Ala	Pro	Leu	Ala	Leu	Gly	Asp	Val	Glu
	130					135						140			
Ile	Glu	Ile	Val	Asp	Lys	Leu	Ile	Ser	Val	Pro	Tyr	Val	Glu	Met	Thr
145				150					155					160	
Leu	Lys	Leu	Met	Glu	Arg	Phe	Gly	Val	Ser	Ala	Glu	His	Ser	Glu	Ser
			165						170					175	
Trp	Asp	Arg	Phe	Phe	Val	Lys	Gly	Gly	Gln	Lys	Tyr	Lys	Ser	Pro	Gly
			180					185					190		
Asn	Ala	Tyr	Val	Glu	Gly	Asp	Ala	Ser	Ser	Ala	Ser	Tyr	Phe	Leu	Ala
		195				200						205			
Gly	Ala	Ala	Ile	Thr	Gly	Glu	Thr	Val	Thr	Val	Glu	Gly	Cys	Gly	Thr
	210					215					220				
Thr	Ser	Leu	Gln	Gly	Asp	Val	Lys	Phe	Ala	Glu	Val	Leu	Glu	Lys	Met
225				230					235					240	
Gly	Cys	Lys	Val	Ser	Trp	Thr	Glu	Asn	Ser	Val	Thr	Val	Thr	Gly	Pro
			245						250					255	
Ser	Arg	Asp	Ala	Phe	Gly	Met	Arg	His	Leu	Arg	Ala	Ile	Asp	Val	Asn
		260						265					270		
Met	Asn	Lys	Met	Pro	Asp	Val	Ala	Met	Thr	Leu	Ala	Val	Val	Ala	Leu
		275					280						285		
Phe	Ala	Asp	Gly	Pro	Thr	Thr	Ile	Arg	Asp	Val	Ala	Ser	Trp	Arg	Val
	290					295						300			
Lys	Glu	Thr	Glu	Arg	Met	Ile	Ala	Ile	Cys	Thr	Glu	Leu	Arg	Lys	Leu
305				310					315					320	
Gly	Ala	Thr	Val	Glu	Glu	Gly	Ser	Asp	Tyr	Cys	Val	Ile	Thr	Pro	Pro
			325						330					335	
Lys	Lys	Val	Lys	Pro	Ala	Glu	Ile	Asp	Thr	Tyr	Asp	Asp	His	Arg	Met
			340					345					350		

Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Ile Thr Ile
355 360 365
Asn Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Gln Val
370 375 380
Leu Glu Arg Ile Thr Lys His
385 390

(2) INFORMATION FOR SEQ ID NO:1660:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 341 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..341

(D) OTHER INFORMATION: / Ceres Seq. ID 1500831

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660:

Met Arg Pro Leu Thr Ala Ala Val Thr Ala Ala Gly Gly Asn Ala Ser
1 5 10 15
Tyr Val Leu Asp Gly Val Pro Gln Met Arg Glu Arg Pro Ile Gly Asp
20 25 30
Leu Val Val Gly Leu Lys Gln Leu Gly Ala Asp Val Glu Cys Thr Leu
35 40 45
Gly Thr Asn Cys Pro Pro Val Arg Val Asn Ala Asn Gly Gly Leu Pro
50 55 60
Gly Gly Lys Val Lys Leu Ser Gly Ser Ile Ser Ser Gln Tyr Leu Thr
65 70 75 80
Ala Leu Leu Met Ala Ala Pro Leu Ala Leu Gly Asp Val Glu Ile Glu
85 90 95
Ile Val Asp Lys Leu Ile Ser Val Pro Tyr Val Glu Met Thr Leu Lys
100 105 110
Leu Met Glu Arg Phe Gly Val Ser Ala Glu His Ser Glu Ser Trp Asp
115 120 125
Arg Phe Phe Val Lys Gly Gly Gln Lys Tyr Lys Ser Pro Gly Asn Ala
130 135 140
Tyr Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Gly Ala
145 150 155 160
Ala Ile Thr Gly Glu Thr Val Thr Val Glu Gly Cys Gly Thr Thr Ser
165 170 175
Leu Gln Gly Asp Val Lys Phe Ala Glu Val Leu Glu Lys Met Gly Cys
180 185 190
Lys Val Ser Trp Thr Glu Asn Ser Val Thr Val Thr Gly Pro Ser Arg
195 200 205
Asp Ala Phe Gly Met Arg His Leu Arg Ala Ile Asp Val Asn Met Asn
210 215 220
Lys Met Pro Asp Val Ala Met Thr Leu Ala Val Val Ala Leu Phe Ala
225 230 235 240
Asp Gly Pro Thr Thr Ile Arg Asp Val Ala Ser Trp Arg Val Lys Glu
245 250 255
Thr Glu Arg Met Ile Ala Ile Cys Thr Glu Leu Arg Lys Leu Gly Ala
260 265 270
Thr Val Glu Gly Ser Asp Tyr Cys Val Ile Thr Pro Pro Lys Lys
275 280 285
Val Lys Pro Ala Glu Ile Asp Thr Tyr Asp Asp His Arg Met Ala Met
290 295 300
Ala Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Ile Thr Ile Asn Asp
305 310 315 320
Pro Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Gln Val Leu Glu
325 330 335
Arg Ile Thr Lys His

340

(2) INFORMATION FOR SEQ ID NO:1661:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..1673
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661:

```
aacgaggctg tggagaaaag aaccaaaggt gactgttggt agagatgagg aatgcagagc 60
tcatcttcat cccaacacca actgttggtc atcttggtcc gtttcttgaa tttgctaggc 120
gtctcattga gcaggatgat aaaatccgta tcaccttcct ctgatgaag caacaagggtc 180
agtctcatct ggattcctat gttaagacaa ttccctcgtc tctgccgttt gtttagattta 240
ttgatgtccc tgagtttagag gagaaaccaa cacttggtac acagtctgtg gaagcctatg 300
gtgtacgatt ttattgaaac aaatgtccct cttgtgcaaa atataatcat ggggtatccta 360
tcttctcctg catttgatgg agttacggtc aagggtatcg ttgctgattt tttctgtctc 420
ccgatgattg atgttgcaaa agatgcaagt ctcccttttt atgtgttctt gacttcaaatt 480
tccggattcc tagctatgat gcagtatctg gcatatggac ataagaaaga tacctcagtt 540
tttgcaagaa actctgaaga aatgttgtca attcctggat ttgtaaacc tgtcccagcc 600
aaagtactgc cgtcagctct gtttattgag gatggttatg atgctgacgt taaactggct 660
atattgttta caaaggctaa tggaaatccta gtgaatacct ctttgatat tgagcctacc 720
tctctgaatc attttcttga agaagagaat tacccttctg tttatgctgt tggccccata 780
tttaaccgga aggccccatc tcatccagat caagacctcg cctgttgtga cgagtcgatg 840
aaatggcttg atgctcaacc cgaggcatca gttgtattcc tttgttttgg gagtatgggt 900
agcttaagag gtcctctagt gaaggaaata gcacatggac ttgagctatg tcagtataga 960
ttcctctggt cactccgcac agaagaagtg acaaatgatg atcttttgcc agadggattc 1020
atggaccgtg tcagtggacg gggaaatgata tgcggttggt ctccctcagg ggaaatactg 1080
gcccataaag cagtgggagg ttttgtttct cattgtggat ggaactcaat agtagagagt 1140
ttatggtttg gtgtgccaat tgtgacatgg cccaatgat gcagagcaac agctcaatgc 1200
gtttctgatg gtgaaggaaac tgaagctcgc agtgagctg aaactcgatt atagtgtaca 1260
tagtggtgag attgtaagtg caaacgagat agagacagcg atttcttgtg taatgaacaa 1320
ggataataat gttgtgagga aacgagtgat ggatatctcg cagatgatcc agagagctac 1380
gaagaatggt ggatcttcgt ttgccgcaat tgagaaattc atacatgacg tgataggaac 1440
caggacttag cttttcttat cggattctcc ataaactgta acctgattat gcaacagtcc 1500
tttgaatctg ctttgtttct aatatttttt tctattcttt tgtcatcagc tttgctttta 1560
actttgtctg tgttgattcc tttatctacc aagctgtgag tttctttgtt agccaatgct 1620
gcatttcttc tgttatggat tttgttcaaa attgggtaca tctcttattc ttt
```

(2) INFORMATION FOR SEQ ID NO:1662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662:

```
Met Val Tyr Asp Phe Ile Glu Thr Asn Val Pro Leu Val Gln Asn Ile
1           5           10           15
Ile Met Gly Ile Leu Ser Ser Pro Ala Phe Asp Gly Val Thr Val Lys
20           25           30
Gly Phe Val Ala Asp Phe Phe Cys Leu Pro Met Ile Asp Val Ala Lys
35           40           45
Asp Ala Ser Leu Pro Phe Tyr Val Phe Leu Thr Ser Asn Ser Gly Phe
50           55           60
```

Leu Ala Met Met Gln Tyr Leu Ala Tyr Gly His Lys Lys Asp Thr Ser
65 70 75 80
Val Phe Ala Arg Asn Ser Glu Glu Met Leu Ser Ile Pro Gly Phe Val
85 90 95
Asn Pro Val Pro Ala Lys Val Leu Pro Ser Ala Leu Phe Ile Glu Asp
100 105 110
Gly Tyr Asp Ala Asp Val Lys Leu Ala Ile Leu Phe Thr Lys Ala Asn
115 120 125
Gly Ile Leu Val Asn Thr Ser Phe Asp Ile Glu Pro Thr Ser Leu Asn
130 135 140
His Phe Leu Glu Glu Glu Asn Tyr Pro Ser Val Tyr Ala Val Gly Pro
145 150 155 160
Ile Phe Asn Pro Lys Ala His Pro His Pro Asp Gln Asp Leu Ala Cys
165 170 175
Cys Asp Glu Ser Met Lys Trp Leu Asp Ala Gln Pro Glu Ala Ser Val
180 185 190
Val Phe Leu Cys Phe Gly Ser Met Gly Ser Leu Arg Gly Pro Leu Val
195 200 205
Lys Glu Ile Ala His Gly Leu Glu Leu Cys Gln Tyr Arg Phe Leu Trp
210 215 220
Ser Leu Arg Thr Glu Glu Val Thr Asn Asp Asp Leu Leu Pro Xaa Gly
225 230 235 240
Phe Met Asp Arg Val Ser Gly Arg Gly Met Ile Cys Gly Trp Ser Pro
245 250 255
Gln Val Glu Ile Leu Ala His Lys Ala Val Gly Gly Phe Val Ser His
260 265 270
Cys Gly Trp Asn Ser Ile Val Glu Ser Leu Trp Phe Gly Val Pro Ile
275 280 285
Val Thr Trp Pro Asn Val Cys Arg Ala Thr Ala Gln Cys Val Ser Asp
290 295 300
Gly Glu Gly Thr Glu Ala Arg Ser Gly Ala Glu Thr Arg Leu
305 310 315

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..301

(D) OTHER INFORMATION: / Ceres Seq. ID 1500834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663:

Met Gly Ile Leu Ser Ser Pro Ala Phe Asp Gly Val Thr Val Lys Gly
1 5 10 15
Phe Val Ala Asp Phe Phe Cys Leu Pro Met Ile Asp Val Ala Lys Asp
20 25 30
Ala Ser Leu Pro Phe Tyr Val Phe Leu Thr Ser Asn Ser Gly Phe Leu
35 40 45
Ala Met Met Gln Tyr Leu Ala Tyr Gly His Lys Lys Asp Thr Ser Val
50 55 60
Phe Ala Arg Asn Ser Glu Met Leu Ser Ile Pro Gly Phe Val Asn
65 70 75 80
Pro Val Pro Ala Lys Val Leu Pro Ser Ala Leu Phe Ile Glu Asp Gly
85 90 95
Tyr Asp Ala Asp Val Lys Leu Ala Ile Leu Phe Thr Lys Ala Asn Gly
100 105 110
Ile Leu Val Asn Thr Ser Phe Asp Ile Glu Pro Thr Ser Leu Asn His
115 120 125
Phe Leu Glu Glu Glu Asn Tyr Pro Ser Val Tyr Ala Val Gly Pro Ile

130	135	140
Phe Asn Pro Lys Ala His	Pro His Pro Asp Gln	Asp Leu Ala Cys Cys
145	150	155
Asp Glu Ser Met Lys Trp	Leu Asp Ala Gln Pro	Glu Ala Ser Val Val
165	170	175
Phe Leu Cys Phe Gly Ser	Met Gly Ser Leu Arg	Gly Pro Leu Val Lys
180	185	190
Glu Ile Ala His Gly Leu	Glu Leu Cys Gln Tyr	Arg Phe Leu Trp Ser
195	200	205
Leu Arg Thr Glu Glu Val	Thr Asn Asp Asp Leu	Leu Pro Xaa Gly Phe
210	215	220
Met Asp Arg Val Ser Gly	Arg Gly Met Ile Cys	Gly Trp Ser Pro Gln
225	230	235
Val Glu Ile Leu Ala His	Lys Ala Val Gly Gly	Phe Val Ser His Cys
245	250	255
Gly Trp Asn Ser Ile Val	Glu Ser Leu Trp Phe	Gly Val Pro Ile Val
260	265	270
Thr Trp Pro Asn Val Cys	Arg Ala Thr Ala Gln	Cys Val Ser Asp Gly
275	280	285
Glu Gly Thr Glu Ala Arg	Ser Gly Ala Glu Thr	Arg Leu
290	295	300

(2) INFORMATION FOR SEQ ID NO:1664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1500835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664:

Met Ile Asp Val Ala Lys	Asp Ala Ser Leu Pro Phe	Tyr Val Phe Leu
1	5	10
Thr Ser Asn Ser Gly Phe	Leu Ala Met Met Gln Tyr	Leu Ala Tyr Gly
20	25	30
His Lys Lys Asp Thr Ser	Val Phe Ala Arg Asn Ser	Glu Glu Met Leu
35	40	45
Ser Ile Pro Gly Phe Val	Asn Pro Val Pro Ala Lys	Val Leu Pro Ser
50	55	60
Ala Leu Phe Ile Glu Asp	Gly Tyr Asp Ala Asp	Val Lys Leu Ala Ile
65	70	75
Leu Phe Thr Lys Ala Asn	Gly Ile Leu Val Asn Thr	Ser Phe Asp Ile
85	90	95
Glu Pro Thr Ser Leu Asn	His Phe Leu Glu Glu Glu	Asn Tyr Pro Ser
100	105	110
Val Tyr Ala Val Gly Pro	Ile Phe Asn Pro Lys Ala	His Pro His Pro
115	120	125
Asp Gln Asp Leu Ala Cys	Cys Asp Glu Ser Met Lys	Trp Leu Asp Ala
130	135	140
Gln Pro Glu Ala Ser Val	Val Phe Leu Cys Phe Gly	Ser Met Gly Ser
145	150	155
Leu Arg Gly Pro Leu Val	Lys Glu Ile Ala His Gly	Leu Glu Leu Cys
165	170	175
Gln Tyr Arg Phe Leu Trp	Ser Leu Arg Thr Glu Glu	Val Thr Asn Asp
180	185	190
Asp Leu Leu Pro Xaa Gly	Phe Met Asp Arg Val Ser	Gly Arg Gly Met
195	200	205
Ile Cys Gly Trp Ser Pro	Gln Val Glu Ile Leu Ala	His Lys Ala Val
210	215	220

Gly Gly Phe Val Ser His Cys Gly Trp Asn Ser Ile Val Glu Ser Leu
225 230 235 240
Trp Phe Gly Val Pro Ile Val Thr Trp Pro Asn Val Cys Arg Ala Thr
245 250 255
Ala Gln Cys Val Ser Asp Gly Glu Gly Thr Glu Ala Arg Ser Gly Ala
260 265 270
Glu Thr Arg Leu
275

(2) INFORMATION FOR SEQ ID NO:1665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..566
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665:

actacgaatt tagcacatag cggagctcc gatcatgtca tcttgctccg acgaagcgat	60
tcccggccaa ccaatcgctc tcggttggtg tcaactttgt ctgattact tagtcacagt	120
ggcgtctttt ccaattccc atcaaaagat ccgaggcaca agcttcaagg tccaaggagt	180
tggtaacact gggaatgctt taacatgtgt tgctcgtttg ggtttgcctt gtcgaatctt	240
ggctaagggt gctgatgatt ctcacgggcg atatatggta gaagaactcg aatctagcgg	300
tgtggatact tcgttttgta tgagtgttaa agatggagct tcacatttta attacgtcat	360
tgtagataac caaacgaata ctctacttgg tatttacact ccaggataatc ctcctttgct	420
accagatgac cttactgaat ctctacttct agatgttctt gatggagtaa gagttctata	480
tgtaaatgga aggtcccgtg aagccgaatt gcttcttgctg caaaaggcac atagcaagaa	540
atataccaat cttaattaat gcagag	

(2) INFORMATION FOR SEQ ID NO:1666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666:

Met Ser Ser Cys Ser Asp Glu Ala Ile Pro Gly Gln Pro Ile Val Leu	
1 5 10 15	
Gly Cys Gly Gln Leu Cys Leu Asp Tyr Leu Val Thr Val Ala Ser Phe	
20 25 30	
Pro Ile Pro Asp Gln Lys Ile Arg Gly Thr Ser Phe Lys Val Gln Gly	
35 40 45	
Val Gly Asn Thr Gly Asn Ala Leu Thr Cys Val Ala Arg Leu Gly Leu	
50 55 60	
Pro Cys Arg Ile Leu Ala Lys Val Ala Asp Asp Ser His Gly Arg Tyr	
65 70 75 80	
Met Val Glu Glu Leu Glu Ser Ser Gly Val Asp Thr Ser Phe Cys Met	
85 90 95	
Ser Ala Lys Asp Gly Ala Ser His Phe Asn Tyr Val Ile Val Asp Asn	
100 105 110	
Gln Thr Asn Thr Arg Thr Cys Ile Tyr Thr Pro Gly Tyr Pro Pro Leu	
115 120 125	
Leu Pro Asp Asp Leu Thr Glu Ser Leu Leu Leu Asp Val Leu Asp Gly	
130 135 140	
Val Arg Val Leu Tyr Val Asn Gly Arg Ser Arg Glu Ala Glu Leu Leu	

145 150 155 160
Leu Ala Gln Lys Ala His Ser Lys Lys Tyr Thr Asn Leu Asn
 165 170

(2) INFORMATION FOR SEQ ID NO:1667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500838

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667:

Met Val Glu Glu Leu Glu Ser Ser Gly Val Asp Thr Ser Phe Cys Met
1 5 10 15
Ser Ala Lys Asp Gly Ala Ser His Phe Asn Tyr Val Ile Val Asp Asn
 20 25 30
Gln Thr Asn Thr Arg Thr Cys Ile Tyr Thr Pro Gly Tyr Pro Pro Leu
 35 40 45
Leu Pro Asp Asp Leu Thr Glu Ser Leu Leu Leu Asp Val Leu Asp Gly
 50 55 60
Val Arg Val Leu Tyr Val Asn Gly Arg Ser Arg Glu Ala Glu Leu Leu
65 70 75 80
Leu Ala Gln Lys Ala His Ser Lys Lys Tyr Thr Asn Leu Asn
 85 90

(2) INFORMATION FOR SEQ ID NO:1668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..581
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500847

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668:

aataaaca aaa aaattaatac aacaagatcc tgctatgtcg tccacggcga gaaatatttc 60
tggcagcggg aaccgaaagt cgagtaggct gcagcggcgg gctccaccgc ctcttaagat 120
aaacccttgc gaacgaantt ggaaagtggc tattcctctt ctatcaccta cggagtcgcc 180
gccacagaaa ccaccggcgg taatgaagag ggaggagcaa cgggtggggt aagaggcgga 240
gaagccgccg rtttttaaga agtggcagca cccggcagct ccgttttact accagccagc 300
accgtcatcg aatcagccgt ttgcatggcc aaattaacgg tctcttaata ttaggtctat 360
cacacaaata cataaatatt tgaatctttt taattgtatg ccgatcatat tgacaaatag 420
catattttat ttttatttaa cattaccatc tttatgcagt atgtatgttg ggtttgatgt 480
tgttatgtcc ttgtaaccat gaatttaatc actaatatat atagtgtatt gtttcgtata 540
ctgtgtaatg ttgaagacac tagctaagat cgccgtgtaa t

(2) INFORMATION FOR SEQ ID NO:1669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669:

Ile Asn Lys Lys Leu Ile Gln Gln Asp Pro Ala Met Ser Ser Thr Ala
1 5 10 15
Arg Asn Ile Ser Gly Ser Gly Asn Arg Lys Ser Ser Arg Leu Gln Arg
20 25 30
Arg Ala Pro Pro Leu Lys Ile Asn Pro Cys Glu Arg Xaa Trp Lys
35 40 45
Val Ala Ile Pro Leu Leu Ser Pro Thr Glu Ser Pro Pro Gln Lys Pro
50 55 60
Pro Ala Val Met Lys Arg Glu Glu Gln Arg Trp Gly Lys Glu Ala Glu
65 70 75 80
Lys Pro Pro Xaa Phe Lys Lys Trp Gln His Pro Ala Ala Pro Phe Tyr
85 90 95
Tyr Gln Pro Ala Pro Ser Ser Asn Gln Pro Phe Ala Trp Pro Asn
100 105 110

(2) INFORMATION FOR SEQ ID NO:1670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670:

Met Ser Ser Thr Ala Arg Asn Ile Ser Gly Ser Gly Asn Arg Lys Ser
1 5 10 15
Ser Arg Leu Gln Arg Arg Ala Pro Pro Pro Leu Lys Ile Asn Pro Cys
20 25 30
Glu Arg Xaa Trp Lys Val Ala Ile Pro Leu Leu Ser Pro Thr Glu Ser
35 40 45
Pro Pro Gln Lys Pro Pro Ala Val Met Lys Arg Glu Glu Gln Arg Trp
50 55 60
Gly Lys Glu Ala Glu Lys Pro Pro Xaa Phe Lys Lys Trp Gln His Pro
65 70 75 80
Ala Ala Pro Phe Tyr Gln Pro Ala Pro Ser Ser Asn Gln Pro Phe
85 90 95
Ala Trp Pro Asn
100

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..517
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671:

gcataatcag	ctgtcaggtc	agattccccg	agatcttggg	gagctctcct	ttctgtcaac	60
catgaacttc	gcccacaaca	atctcgaagg	tccaatgcca	cgcggaacac	aatttcaaag	120
ccaaaactgt	tcttcattca	tggacaaccc	caagctttac	ggtcttgatg	atatctgcag	180
aaaaactcat	gtcccaaata	ctagaccaca	agaattagag	aaagtatcag	agccggaaga	240
agagcaagtg	attaactgga	catcagcagc	aatagcgtat	ggacctgggtg	tgttttgctg	300
attagtgtat	ggacatatct	tcatttcgca	taagcaggag	tggttaattg	aaaagtttcg	360
tagaaacaag	cccagagttg	tcacagaag	cgctcgttga	acacgtgcat	atgtatgtgt	420
ttgtgaaaaa	ctctttcgtg	tgcgttgtaa	tgttctaata	tatggttttg	taataaacgt	480
ctttgggtggc	ggtacgtatt	tgatacatat	tggttttg			

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672:

His	Asn	Gln	Leu	Ser	Gly	Gln	Ile	Pro	Arg	Asp	Leu	Gly	Glu	Leu	Ser
1				5					10					15	
Phe	Leu	Ser	Thr	Met	Asn	Phe	Ala	His	Asn	Asn	Leu	Glu	Gly	Pro	Met
			20					25					30		
Pro	Arg	Gly	Thr	Gln	Phe	Gln	Ser	Gln	Asn	Cys	Ser	Ser	Phe	Met	Asp
		35					40					45			
Asn	Pro	Lys	Leu	Tyr	Gly	Leu	Asp	Asp	Ile	Cys	Arg	Lys	Thr	His	Val
	50					55					60				
Pro	Asn	Pro	Arg	Pro	Gln	Glu	Leu	Glu	Lys	Val	Ser	Glu	Pro	Glu	Glu
65					70					75				80	
Glu	Gln	Val	Ile	Asn	Trp	Thr	Ser	Ala	Ala	Ile	Ala	Tyr	Gly	Pro	Gly
			85						90					95	
Val	Phe	Cys	Gly	Leu	Val	Ile	Gly	His	Ile	Phe	Ile	Ser	His	Lys	Gln
			100					105					110		
Glu	Trp	Leu	Met	Glu	Lys	Phe	Arg	Asn	Lys	Pro	Arg	Val	Val	Ile	
		115					120					125			
Arg	Ser	Ala	Arg												
															130

(2) INFORMATION FOR SEQ ID NO:1673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500856

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673:

Met	Asn	Phe	Ala	His	Asn	Asn	Leu	Glu	Gly	Pro	Met	Pro	Arg	Gly	Thr
1				5					10					15	
Gln	Phe	Gln	Ser	Gln	Asn	Cys	Ser	Ser	Phe	Met	Asp	Asn	Pro	Lys	Leu
			20					25					30		
Tyr	Gly	Leu	Asp	Asp	Ile	Cys	Arg	Lys	Thr	His	Val	Pro	Asn	Pro	Arg
		35					40					45			
Pro	Gln	Glu	Leu	Glu	Lys	Val	Ser	Glu	Pro	Glu	Glu	Glu	Gln	Val	Ile
	50					55					60				
Asn	Trp	Thr	Ser	Ala	Ala	Ile	Ala	Tyr	Gly	Pro	Gly	Val	Phe	Cys	Gly
65					70					75				80	
Leu	Val	Ile	Gly	His	Ile	Phe	Ile	Ser	His	Lys	Gln	Glu	Trp	Leu	Met
			85						90					95	
Glu	Lys	Phe	Arg	Arg	Asn	Lys	Pro	Arg	Val	Val	Ile	Arg	Ser	Ala	Arg
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:1674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..101
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500857
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674:

Met Pro Arg Gly Thr Gln Phe Gln Ser Gln Asn Cys Ser Ser Phe Met
1 5 10 15
Asp Asn Pro Lys Leu Tyr Gly Leu Asp Asp Ile Cys Arg Lys Thr His
20 25 30
Val Pro Asn Pro Arg Pro Gln Glu Leu Glu Lys Val Ser Glu Pro Glu
35 40 45
Glu Glu Gln Val Ile Asn Trp Thr Ser Ala Ala Ile Ala Tyr Gly Pro
50 55 60
Gly Val Phe Cys Gly Leu Val Ile Gly His Ile Phe Ile Ser His Lys
65 70 75 80
Gln Glu Trp Leu Met Glu Lys Phe Arg Arg Asn Lys Pro Arg Val Val
85 90 95
Ile Arg Ser Ala Arg
100

(2) INFORMATION FOR SEQ ID NO:1675:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..615
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500862
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675:

gataatatttt cattttcrtc gtttctttct ttctaagttt cgatgtcagt tcctaatactc	60
tatggcggttc atgatagcca aatggtaact ttggtggcct aatgtatgtc acgtaaatta	120
tccacgtggc actcactttt ttgcatcttt ctcaaaatat atcaaaggag acttcataaa	180
gaaagaatct ttagtgtgga gagactaaaa ggacaccaca agcttatttc ataagaaact	240
tcaaattaga atcagaaaca agagcatcct tcttcattta cacaggtaaa ttaggtgtaa	300
aaatggtgat gagaagtgtg gatctacgat cagataccgt tactagaccg acagatgcga	360
tgcgagaagc aatgtgtaac gcagaggtgg atgatgacgt cctcgatat gacccaacgg	420
ctagacgtct tgaagaggag atggctaaga tgatggggaa agaggctgct ctgttcgtgc	480
catccgggac aatgggggaat ctgatcagcg tgatggttca ctgcgacgtg agaggcagcg	540
aggtgattct tggcgacaat tgtcacatcc atgtttacga gaatggaggg atatcgacta	600
tcgggggagtg gcatc	

(2) INFORMATION FOR SEQ ID NO:1676:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..104
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500863
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676:

Met Val Met Arg Ser Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro
1 5 10 15
Thr Asp Ala Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Asp

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```

                20                25                30
Val Leu Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Glu Met Ala
      35                40                45
Lys Met Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met
      50                55                60
Gly Asn Leu Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu
65      70                75                80
Val Ile Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly
      85                90                95
Ile Ser Thr Ile Gly Gly Val His
                100

```

(2) INFORMATION FOR SEQ ID NO:1677:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1500864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677:

```

Met Arg Ser Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro Thr Asp
1      5                10                15
Ala Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Asp Val Leu
      20                25                30
Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Glu Met Ala Lys Met
      35                40                45
Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met Gly Asn
      50                55                60
Leu Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu Val Ile
65      70                75                80
Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly Ile Ser
      85                90                95
Thr Ile Gly Gly Val His
                100

```

(2) INFORMATION FOR SEQ ID NO:1678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1500865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678:

```

Met Arg Glu Ala Met Cys Asn Ala Glu Val Asp Asp Asp Val Leu Gly
1      5                10                15
Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Met Ala Lys Met Met
      20                25                30
Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met Gly Asn Leu
      35                40                45
Ile Ser Val Met Val His Cys Asp Val Arg Gly Ser Glu Val Ile Leu
      50                55                60
Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly Ile Ser Thr
65      70                75                80
Ile Gly Gly Val His
                85

```

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(2) INFORMATION FOR SEQ ID NO:1679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 643 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..643
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679:

atttttttagg	ttgtttcagc	tgttttacgg	agtcgctttt	gagatatcga	tcttacgaag	60
aagcaaaaat	ggcgggtccc	ttgcttacca	agaagggtgt	gaagaagagg	tctactaagt	120
tcatcagacc	ccagagtgac	cgtagaatca	ccgtcaagga	aagctggagg	aggccaaagg	180
gtattgattc	aaggatgaga	agaaagttca	aagggtgtgac	tttgatgccc	aatggttggt	240
acggatctga	caagaagact	cgtcactatc	ttcccaatgg	attcaagaaa	ttcgttggtc	300
acaacacaag	tgagctcgag	ttgttgatga	tgacacaacag	gacttactgt	gctgagattg	360
ctcacacagt	ctccactaag	aagagaaagg	caattggtga	gagagcttct	cagctagacg	420
ttgttggttac	caacaggctt	gctaggctcc	gtagccaaga	agacgagtga	agaagaatct	480
tgccgactac	ttagtgtgtt	cttctgtttt	gttgcatttc	ctttttgtta	taagacgatt	540
tttgattact	gctgtgtttg	tgtttgagg	gaacaaacat	gagttttggt	tttagtatga	600
aacagatcaa	gttaagacct	ttgttaaag	ctatttcgga	ttc		

(2) INFORMATION FOR SEQ ID NO:1680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680:

Phe	Leu	Gly	Leu	Phe	Ser	Cys	Phe	Thr	Glu	Ser	Leu	Leu	Arg	Tyr	Arg	
1			5						10					15		
Ser	Tyr	Glu	Glu	Ala	Lys	Met	Ala	Val	Pro	Leu	Leu	Thr	Lys	Lys	Val	
			20					25					30			
Val	Lys	Lys	Arg	Ser	Thr	Lys	Phe	Ile	Arg	Pro	Gln	Ser	Asp	Arg	Arg	
			35				40					45				
Ile	Thr	Val	Lys	Glu	Ser	Trp	Arg	Arg	Pro	Lys	Gly	Ile	Asp	Ser	Arg	
			50			55					60					
Met	Arg	Arg	Lys	Phe	Lys	Gly	Val	Thr	Leu	Met	Pro	Asn	Val	Gly	Tyr	
65					70				75					80		
Gly	Ser	Asp	Lys	Lys	Thr	Arg	His	Tyr	Leu	Pro	Asn	Gly	Phe	Lys	Lys	
			85					90					95			
Phe	Val	Val	His	Asn	Thr	Ser	Glu	Leu	Glu	Leu	Leu	Met	Met	His	Asn	
			100				105					110				
Arg	Thr	Tyr	Cys	Ala	Glu	Ile	Ala	His	Asn	Val	Ser	Thr	Lys	Lys	Arg	
			115				120					125				
Lys	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gln	Leu	Asp	Val	Val	Val	Thr	Asn	
			130				135					140				
Arg	Leu	Ala	Arg	Leu	Arg	Ser	Gln	Glu	Asp	Glu						
145				150						155						

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..133
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500868
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681:

Met Ala Val Pro Leu Leu Thr Lys Lys Val Val Lys Lys Arg Ser Thr
1 5 10 15
Lys Phe Ile Arg Pro Gln Ser Asp Arg Arg Ile Thr Val Lys Glu Ser
 20 25 30
Trp Arg Arg Pro Lys Gly Ile Asp Ser Arg Met Arg Arg Lys Phe Lys
 35 40 45
Gly Val Thr Leu Met Pro Asn Val Gly Tyr Gly Ser Asp Lys Lys Thr
50 55 60
Arg His Tyr Leu Pro Asn Gly Phe Lys Lys Phe Val Val His Asn Thr
65 70 75 80
Ser Glu Leu Glu Leu Leu Met Met His Asn Arg Thr Tyr Cys Ala Glu
 85 90 95
Ile Ala His Asn Val Ser Thr Lys Lys Arg Lys Ala Ile Val Glu Arg
 100 105 110
Ala Ser Gln Leu Asp Val Val Val Thr Asn Arg Leu Ala Arg Leu Arg
115 120 125
Ser Gln Glu Asp Glu
130

- (2) INFORMATION FOR SEQ ID NO:1682:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..91
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500869
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682:

Met Arg Arg Lys Phe Lys Gly Val Thr Leu Met Pro Asn Val Gly Tyr
1 5 10 15
Gly Ser Asp Lys Lys Thr Arg His Tyr Leu Pro Asn Gly Phe Lys Lys
 20 25 30
Phe Val Val His Asn Thr Ser Glu Leu Glu Leu Leu Met Met His Asn
35 40 45
Arg Thr Tyr Cys Ala Glu Ile Ala His Asn Val Ser Thr Lys Lys Arg
50 55 60
Lys Ala Ile Val Glu Arg Ala Ser Gln Leu Asp Val Val Val Thr Asn
65 70 75 80
Arg Leu Ala Arg Leu Arg Ser Gln Glu Asp Glu
 85 90

- (2) INFORMATION FOR SEQ ID NO:1683:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..493
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500877
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683:

tacctacccc ctgcgcttgc acaaaatcct tcttgatccg cacaggaagg tggaagggtcc

```
cggcagaaga acttggcggg cgaaaggcga aaccgacgtg ctcccrggcg ggcggcgaca 120
cggcatggag cgagagcgnc aggcagtggc gaggaacagg aaggtggtgc tgcgcgggta 180
catcgaccgc gcgcccaggg aggaagacat ggagctcgtc gacggcrgcg ccgtggagct 240
gcgcgtcccc gadggcggcg gcggccccgc ggtgctggtg aagaacctct acctatcctg 300
cgaccottac atgcgcggca ggatgcggga cttccgcaac tcctacatcc cgcccttcaa 360
acctggatca cctattgang ggtttggcgt ggggarggcg gtcgactcca ctcatccagg 420
attcagtgcc ggtgacgttg tttccgggat gactggatgg gaggactaca gtctgatcac 480
caatcctgaa cag
```

(2) INFORMATION FOR SEQ ID NO:1684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500878

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684:

```
Thr Tyr Pro Leu Arg Leu His Lys Ile Leu Leu Asp Pro His Arg Lys
1      5      10      15
Val Glu Gly Pro Gly Arg Arg Thr Trp Arg Ala Lys Gly Glu Thr Asp
20     25     30
Val Leu Xaa Gly Gly Arg Arg His Gly Met Glu Arg Glu Xaa Gln Ala
35     40     45
Val Ala Arg Asn Arg Lys Val Val Leu Arg Gly Tyr Ile Asp Arg Ala
50     55     60
Pro Arg Glu Glu Asp Met Glu Leu Val Asp Gly Xaa Ala Val Glu Leu
65     70     75     80
Arg Val Pro Xaa Gly Gly Gly Pro Ala Val Leu Val Lys Asn Leu
85     90     95
Tyr Leu Ser Cys Asp Pro Tyr Met Arg Gly Arg Met Arg Asp Phe Arg
100    105    110
Asn Ser Tyr Ile Pro Pro Phe Lys Pro Gly Ser Pro Ile Xaa Gly Phe
115    120    125
Gly Val Gly Xaa Val Val Asp Ser Thr His Pro Gly Phe Ser Ala Gly
130    135    140
Asp Val Val Ser Gly Met Thr Gly Trp Glu Asp Tyr Ser Leu Ile Thr
145    150    155    160
Asn Pro Glu Gln
```

(2) INFORMATION FOR SEQ ID NO:1685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685:

```
Met Glu Arg Glu Xaa Gln Ala Val Ala Arg Asn Arg Lys Val Val Leu
1      5      10      15
Arg Gly Tyr Ile Asp Arg Ala Pro Arg Glu Glu Asp Met Glu Leu Val
20     25     30
Asp Gly Xaa Ala Val Glu Leu Arg Val Pro Xaa Gly Gly Gly Pro
35     40     45
Ala Val Leu Val Lys Asn Leu Tyr Leu Ser Cys Asp Pro Tyr Met Arg
```

50 55 60
Gly Arg Met Arg Asp Phe Arg Asn Ser Tyr Ile Pro Pro Phe Lys Pro
65 70 75 80
Gly Ser Pro Ile Xaa Gly Phe Gly Val Gly Xaa Val Val Asp Ser Thr
85 90 95
His Pro Gly Phe Ser Ala Gly Asp Val Val Ser Gly Met Thr Gly Trp
100 105 110
Glu Asp Tyr Ser Leu Ile Thr Asn Pro Glu Gln
115 120

(2) INFORMATION FOR SEQ ID NO:1686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686:

Met Glu Leu Val Asp Gly Xaa Ala Val Glu Leu Arg Val Pro Xaa Gly
1 5 10 15
Gly Gly Gly Pro Ala Val Leu Val Lys Asn Leu Tyr Leu Ser Cys Asp
20 25 30
Pro Tyr Met Arg Gly Arg Met Arg Asp Phe Arg Asn Ser Tyr Ile Pro
35 40 45
Pro Phe Lys Pro Gly Ser Pro Ile Xaa Gly Phe Gly Val Gly Xaa Val
50 55 60
Val Asp Ser Thr His Pro Gly Phe Ser Ala Gly Asp Val Val Ser Gly
65 70 75 80
Met Thr Gly Trp Glu Asp Tyr Ser Leu Ile Thr Asn Pro Glu Gln
85 90 95

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..535
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687:

aagtcagagg gacattgcat tggggaacta cagaaaaggg tccgaatcga atccgtggtg 60
cactgccccct tcctccccca caagccgccc cgcccgccgt gaggactccg gcgaatggcg 120
tcccgcgtcg cctcgggccc cctccgccc cgcccgccgt ccacactagg cctcctaagg 180
agttatgcac atgtcagaag ctacaacagt caactttcag ctttggtttc tgctacatct 240
gaatgctcaa atctgccgag aagatgctat tacttaccta atccctctcc ataccaagtt 300
tgagtaggt catttgcttc agacaacgga gacaagtttg aggctgttgt gcccttcagt 360
ggtgaatctg taactgatgg aactcttgct aacttcttaa agaaacctgg agacagagtc 420
gaggctgatg aacctatagc gcagattgaa actgataagg tcactataga tgtcgcaagt 480
cctgargctg gtgttattga aaagctcatt gctagtgaag gcgacacagt tactc

(2) INFORMATION FOR SEQ ID NO:1688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1500882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688:

```
Val Arg Gly Thr Leu His Trp Gly Thr Glu Lys Gly Pro Asn Arg
1          5          10          15
Ile Arg Gly Ala Leu Pro Leu Pro Pro Pro Gln Ala Ala Ala Ala Ala
20          25          30
Val Arg Thr Pro Ala Asn Gly Val Pro Arg Arg Leu Gly Pro Pro Pro
35          40          45
Pro Pro Arg Arg Arg His Thr Arg Pro Pro Lys Glu Leu Cys Thr Cys
50          55          60
Gln Lys Leu Gln Gln Ser Thr Phe Ser Phe Gly Phe Cys Tyr Ile
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:1689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1500883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689:

```
Met Ala Ser Arg Val Ala Ser Gly Leu Leu Arg Arg Arg Ala Gly Ala
1          5          10          15
Thr Leu Gly Leu Leu Arg Ser Tyr Ala His Val Arg Ser Tyr Asn Ser
20          25          30
Gln Leu Ser Ala Leu Val Ser Ala Thr Ser Glu Cys Ser Asn Leu Pro
35          40          45
Arg Arg Cys Tyr Tyr Leu Pro Asn Pro Ser Pro Tyr Gln Val Trp Ser
50          55          60
Arg Ser Phe Ala Ser Asp Asn Gly Asp Lys Phe Glu Ala Val Val Pro
65          70          75          80
Phe Met Gly Glu Ser Val Thr Asp Gly Thr Leu Ala Asn Phe Leu Lys
85          90          95
Lys Pro Gly Asp Arg Val Glu Ala Asp Glu Pro Ile Ala Gln Ile Glu
100          105          110
Thr Asp Lys Val Thr Ile Asp Val Ala Ser Pro Xaa Ala Gly Val Ile
115          120          125
Glu Lys Leu Ile Ala Ser Glu Gly Asp Thr Val Thr
130          135          140
```

(2) INFORMATION FOR SEQ ID NO:1690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1500884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690:

```
ataccgcaac cagctattga gctactgcct ctgaccaagt cccaagctgc gctgcgcctg      60
ctatgtcgtc gtcctcgccc gtatcgcgcg tctcatcagc cactgcgcgc cactgcgtgg      120
acgactgcct cggcatcgtg cagcttctta tgcgatggcac cgtgacgcgc tccgsgacta      180
ctccgacatc cctctcctgg gcgaggtgcc gtccaacctg cccgtccagt ggaaggacgt      240
```


cgtctacgac cccgcgcacg cgctccgcct ccgcatgtac aggccccaccg acaccgacgg 300
cggcaggacg accaacaaca agctgccggg gctagtctac ttccacggcg gcggcttctg 360
catctgcagc ttcgagatgc cccacttcca cgccggcggg ctccgcctcg ccgccgagct 420
cccggcgctc gtgctctmcg ccgactacmg cctggggccc gagcaccgcc t

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54

(D) OTHER INFORMATION: / Ceres Seq. ID 1500885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691:

Ile Pro Gln Pro Ala Ile Glu Leu Leu Pro Leu Thr Lys Ser Gln Ala
1 5 10 15
Ala Leu Arg Leu Leu Cys Arg Arg Pro Arg Pro Tyr Arg Arg Ser His
20 25 30
Gln Pro Leu Arg Arg Thr Ser Trp Thr Thr Ala Ser Ala Ser Cys Ser
35 40 45
Phe Leu Ala Met Ala Pro
50

(2) INFORMATION FOR SEQ ID NO:1692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1500886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692:

Met Ser Ser Ser Pro Val Ser Ala Val Ser Ser Ala Thr Ala Pro
1 5 10 15
His Val Val Asp Asp Cys Leu Gly Ile Val Gln Leu Leu Ser Asp Gly
20 25 30
Thr Val Thr Arg Ser Xaa Thr Thr Pro Thr Ser Leu Ser Trp Ala Arg
35 40 45
Cys Arg Pro Thr Cys Pro Ser Ser Gly Arg Thr Ser Ser Thr Thr Pro
50 55 60
Arg Thr Arg Ser Ala Ser Ala Cys Thr Gly Pro Pro Thr Pro Thr Ala
65 70 75 80
Ala Gly Arg Pro Thr Thr Ser Cys Arg Cys
85 90

(2) INFORMATION FOR SEQ ID NO:1693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1500887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693:

Met Tyr Arg Pro Thr Asp Thr Asp Gly Gly Arg Thr Thr Asn Asn Lys

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1 5 10 15
Leu Pro Val Leu Val Tyr Phe His Gly Gly Gly Phe Cys Ile Cys Ser
20 25 30
Phe Glu Met Pro His Phe His Ala Gly Gly Leu Arg Leu Ala Ala Glu
35 40 45
Leu Pro Ala Leu Val Leu Xaa Ala Asp Tyr Xaa Leu Gly Pro Glu His
50 55 60

Arg
65

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..591
(D) OTHER INFORMATION: / Ceres Seq. ID 1500888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694:

cttcgctgc	ttttcctttc	tctctcttcc	cctttcctct	ccccaagcag	gcggggcgag	60
cgagcccagc	aggcgctctt	cctctcgctcc	atccgtttcc	tcctccccct	gcttcccggc	120
tgcctccct	cccctccctg	tgcgcctctt	tcatgcgcg	aggagggacc	gtggggacca	180
ccaccaccag	caccaccacc	tccatccgtg	cgcctctcgc	tctcgctggt	ggtgctcctc	240
ctctctctcc	tgtctccggg	gcggggcgcc	tccttttcca	cctcctgctg	gtgcmagggc	300
cgggagggcg	tmgcggaggt	ggcgcgcgatg	gggctcgcmg	gggamgggtc	ggcggacacm	360
gcmcacctca	gtaataatga	aaatrggcgg	ttmatattatg	gagttgcgag	ttctcctggt	420
aaaagagcat	cgatggagga	cttctatgag	gcaagaatag	acgamgttga	tggagagaaa	480
attggaatgt	tcggtgtata	tgatgggtcat	ggaggagtcc	gagcagctga	gtatgttaag	540
cagcaccttt	tcagcaattt	aatcaaacac	ccaaagtcca	tcactgatac	c	

(2) INFORMATION FOR SEQ ID NO:1695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..197
(D) OTHER INFORMATION: / Ceres Seq. ID 1500889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695:

Leu	Pro	Leu	Leu	Phe	Leu	Ser	Pro	Leu	Ser	Pro	Phe	Leu	Ser	Pro	Ser	
1				5				10				15				
Arg	Arg	Gly	Glu	Arg	Ala	Gln	Gln	Ala	Ser	Leu	Leu	Ser	Ser	Ile	Arg	
			20					25				30				
Phe	Leu	Leu	Pro	Leu	Leu	Pro	Gly	Ser	Pro	Pro	Ser	Pro	Pro	Cys	Ala	
		35					40				45					
Pro	Leu	Phe	Met	Arg	Glu	Glu	Gly	Pro	Trp	Gly	Pro	Pro	Pro	Pro	Ala	
	50				55			60								
Pro	Pro	Pro	Pro	Ser	Val	Arg	Leu	Ser	Leu	Ser	Leu	Val	Val	Leu	Leu	
65				70				75						80		
Leu	Leu	Leu	Leu	Leu	Pro	Gly	Arg	Ala	Ala	Ser	Phe	Ser	Thr	Ser	Cys	
				85				90					95			
Trp	Cys	Xaa	Gly	Arg	Glu	Gly	Xaa	Ala	Glu	Val	Ala	Arg	Met	Gly	Leu	
		100					105					110				
Xaa	Gly	Xaa	Gly	Ser	Ala	Asp	Xaa	Xaa	His	Leu	Ser	Asn	Asn	Glu	Asn	
	115					120					125					
Xaa	Arg	Xaa	Ile	Tyr	Gly	Val	Ala	Ser	Ser	Pro	Gly	Lys	Arg	Ala	Ser	
	130					135					140					

Met Glu Asp Phe Tyr Glu Ala Arg Ile Asp Xaa Val Asp Gly Glu Lys
145 150 155 160
Ile Gly Met Phe Gly Val Tyr Asp Gly His Gly Gly Val Arg Ala Ala
165 170 175
Glu Tyr Val Lys Gln His Leu Phe Ser Asn Leu Ile Lys His Pro Lys
180 185 190
Phe Ile Thr Asp Thr
195

(2) INFORMATION FOR SEQ ID NO:1696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696:

Phe Arg Cys Phe Ser Phe Leu Leu Ser Pro Leu Ser Ser Pro Gln Ala
1 5 10 15
Gly Gly Ala Ser Glu Pro Ser Arg Arg Leu Ser Ser Arg Pro Ser Val
20 25 30
Ser Ser Ser Pro Cys Phe Pro Ala Arg Leu Pro Pro Leu Pro Val Arg
35 40 45
Leu Phe Ser Cys Ala Arg Arg Asp Arg Gly Asp His His Gln His
50 55 60
His His Leu His Pro Cys Ala Ser Arg Ser Arg Trp Trp Cys Ser Ser
65 70 75 80
Ser Ser Ser Cys Ser Arg Gly Gly Arg Pro Pro Phe Pro Pro Ala
85 90 95
Gly Xaa Arg Ala Gly Arg Ala Xaa Arg Trp Arg Ala Trp Gly Ser
100 105 110
Xaa Gly Xaa Gly Arg Arg Thr Xaa Xaa Thr Ser Val Ile Met Lys Xaa
115 120 125
Gly Gly Xaa Phe Met Glu Leu Arg Val Leu Leu Val Lys Glu His Arg
130 135 140
Trp Arg Thr Ser Met Arg Gln Glu
145 150

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697:

Met Arg Glu Glu Gly Pro Trp Gly Pro Pro Pro Pro Ala Pro Pro Pro
1 5 10 15
Pro Ser Val Arg Leu Ser Leu Ser Leu Val Val Leu Leu Leu Leu Leu
20 25 30
Leu Leu Pro Gly Arg Ala Ala Ser Phe Ser Thr Ser Cys Trp Cys Xaa
35 40 45
Gly Arg Glu Gly Xaa Ala Glu Val Ala Arg Met Gly Leu Xaa Gly Xaa
50 55 60
Gly Ser Ala Asp Xaa Xaa His Leu Ser Asn Asn Glu Asn Xaa Arg Xaa

65 70 75 80
Ile Tyr Gly Val Ala Ser Ser Pro Gly Lys Arg Ala Ser Met Glu Asp
85 90 95
Phe Tyr Glu Ala Arg Ile Asp Xaa Val Asp Gly Glu Lys Ile Gly Met
100 105 110
Phe Gly Val Tyr Asp Gly His Gly Val Arg Ala Ala Glu Tyr Val
115 120 125
Lys Gln His Leu Phe Ser Asn Leu Ile Lys His Pro Lys Phe Ile Thr
130 135 140
Asp Thr
145

(2) INFORMATION FOR SEQ ID NO:1698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..654
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698:

```
ctccgccgtc gctgtccac tttccccgtg cttctccgcc gtcgaggccg cgtcccagtg      60
cgaagagacc acgactcaga tggccagccg ctgggtcccg cccgaggtgt acccgctgtt      120
cgcggaacg ggcgtggccg tcggcatctg cggatttcag ctcttccgga acatcaccgg      180
caaccggaa gtcagggtaa acaaggcagg gagggcagct ggtgtgcttg agaaccatga      240
ggaggggagg cgttacgcca tgcattggcct aacgcctacc ctcttatggg ttctttcagc      300
agcactggcc tcaactatttc ttctaaatta ccaagattct cggacatgta cactctcaca      360
atagcaagtg cggatccaca gtctatctct gcaaacaagc cagttcattt cactaagagc      420
gtaacaaagt ggtttacaaa ggaaggagtt cttgtggagg gcctgttctg gaaggatgtc      480
gagaagctga ttgatgacta caacagttag cgcaagagta aatgaattgg tagctcgtgt      540
ctctggccat ctggggagac atcgctgtct agagaaatcc gtcaaagttt agcttaattc      600
gaacaggcat ttttgctata ctgtaccggt tgaccagtga atgaatgatg ttct
```

(2) INFORMATION FOR SEQ ID NO:1699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699:

Ser Ala Val Ala Cys Pro Leu Ser Pro Cys Phe Ser Ala Val Glu Ala
1 5 10 15
Ala Ser Gln Cys Glu Glu Thr Thr Thr Gln Met Ala Ser Arg Trp Val
20 25 30
Arg Pro Glu Val Tyr Pro Leu Phe Ala Ala Thr Gly Val Ala Val Gly
35 40 45
Ile Cys Gly Phe Gln Leu Phe Arg Asn Ile Thr Gly Asn Pro Glu Val
50 55 60
Arg Val Asn Lys Ala Gly Arg Ala Ala Gly Val Leu Glu Asn His Glu
65 70 75 80
Glu Gly Arg Arg Tyr Ala Met His Gly Leu Thr Pro Thr Leu Leu Trp
85 90 95
Val Leu Ser Ala Ala Leu Ala Ser Leu Phe Leu Leu Asn Tyr Gln Asp
100 105 110
Ser Arg Thr Cys Thr Leu Ser Gln

115 120
(2) INFORMATION FOR SEQ ID NO:1700:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..94
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500902
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700:
Met Ala Ser Arg Trp Val Arg Pro Glu Val Tyr Pro Leu Phe Ala Ala
1 5 10 15
Thr Gly Val Ala Val Gly Ile Cys Gly Phe Gln Leu Phe Arg Asn Ile
20 25 30
Thr Gly Asn Pro Glu Val Arg Val Asn Lys Ala Gly Arg Ala Ala Gly
35 40 45
Val Leu Glu Asn His Glu Glu Gly Arg Arg Tyr Ala Met His Gly Leu
50 55 60
Thr Pro Thr Leu Leu Trp Val Leu Ser Ala Ala Leu Ala Ser Leu Phe
65 70 75 80
Leu Leu Asn Tyr Gln Asp Ser Arg Thr Cys Thr Leu Ser Gln
85 90
(2) INFORMATION FOR SEQ ID NO:1701:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 79 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..79
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500903
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701:
Met Gly Ser Phe Ser Ser Thr Gly Leu Thr Ile Ser Ser Lys Leu Pro
1 5 10 15
Arg Phe Ser Asp Met Tyr Thr Leu Thr Ile Ala Ser Ala Asp Pro Gln
20 25 30
Ser Ile Ser Ala Asn Lys Pro Val His Phe Thr Lys Ser Val Thr Lys
35 40 45
Trp Phe Thr Lys Glu Gly Val Leu Val Glu Gly Leu Phe Trp Lys Asp
50 55 60
Val Glu Lys Leu Ile Asp Tyr Asn Ser Glu Arg Lys Ser Lys
65 70 75
(2) INFORMATION FOR SEQ ID NO:1702:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 465 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..465
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500907
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702:
acacaacacc agtaagcaag caccgccagc acgcacaagc aggcaaagct ctcgaccatc 60
gctctgaggg attaattggcg gcgggaggag gaggcggcgg catcgcgacg agaaggcccc 120

tgctgctgag gcgttcggcg ggcacctgga ggcggcggag atgacggagg cggaggagga 180
acacagcggc gtcaagtccc ggctgtcggg tctgctgtgg cacggcgggt cggcgtacga 240
cgctgtggtc agctgcgcgt cgaaccaggt ggcgcaggtg ctgctgacgc tgccctactc 300
gttcgcgcac tggggatgct garcggcgtg ctgttcacgc tcttctacgg cctgctgggc 360
agctggacgg cgtacctgat cagcatcctg tacctggagt accgcaccgc tcgggagcgc 420
gagaaggccg cggacttccg gaaccacgtg atccagtggg tcgag

(2) INFORMATION FOR SEQ ID NO:1703:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1500908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703:

Thr Thr Pro Val Ser Lys His Arg Gln His Ala Gln Ala Gly Lys Ala
1 5 10 15
Leu Asp His Arg Ser Glu Gly Leu Met Ala Ala Gly Gly Gly Gly
20 25 30
Gly Ile Ala Thr Arg Arg Pro Leu Leu Arg Arg Ser Ala Gly Thr
35 40 45
Trp Arg Arg Arg Arg
50

(2) INFORMATION FOR SEQ ID NO:1704:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1500909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704:

Met Thr Glu Ala Glu Glu Glu His Ser Gly Val Lys Ser Arg Leu Ser
1 5 10 15
Gly Leu Leu Trp His Gly Gly Ser Ala Tyr Asp Ala Trp Phe Ser Cys
20 25 30
Ala Ser Asn Gln Val Ala Gln Val Leu Leu Thr Leu Pro Tyr Ser Phe
35 40 45
Ala His Trp Gly Cys
50

(2) INFORMATION FOR SEQ ID NO:1705:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1500910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705:

Met Leu Xaa Gly Val Leu Phe Gln Leu Phe Tyr Gly Leu Leu Gly Ser
1 5 10 15
Trp Thr Ala Tyr Leu Ile Ser Ile Leu Tyr Leu Glu Tyr Arg Thr Arg

20 25 30
Arg Glu Xaa Glu Lys Ala Ala Asp Phe Arg Asn His Val Ile Gln Trp
35 40 45
Phe Glu
50

(2) INFORMATION FOR SEQ ID NO:1706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..548

(D) OTHER INFORMATION: / Ceres Seq. ID 1500915

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706:

gttacatccc accatgtgct gttcaccttc cctcccgttt gcctcctctc gctgtctcgt	60
agcttctttc ctccggcgac ggctgggcga gcggccgcca gtcgggccct tcgtcggcga	120
cgagcatcca cctgcgcggc gcccacatctt ccgctccttc ccttactcgc gctcggcaca	180
caggcgacgg cggcggcggc gctcaggatc gggctatcac cgacggggtc cggcttctcc	240
gcccgcctct cgccactcgc ctgcgcgcct cgccctccggc cctccgcaca ccggccggcg	300
atcctgcaag ggttgatga tgggcgagat ctgaaggatg ctgatttcta taagcagcaa	360
gctaaacttc ttttcaagaa cttgtcaaaa gggcatcatg aagcttcacg gatgtmaatt	420
gagacagggc cctactatctt ccactacatt attgarggca gagtatgtta tctgactatg	480
tgtgamcgct cttatccgaa gaaacttgca ttccagtacc tagaagatct gaaaaatgaa	540
tttgagag	

(2) INFORMATION FOR SEQ ID NO:1707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 1500916

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707:

Val Thr Ser His His Leu Leu Phe Thr Phe Pro Pro Val Cys Leu Leu	
1 5 10 15	
Ser Leu Ser Arg Ser Phe Phe Pro Pro Ala Thr Ala Gly Arg Ala Ala	
20 25 30	
Ala Ser Arg Ala Leu Arg Arg Arg Ala Ser Thr Cys Ala Ala Pro	
35 40 45	
His Leu Pro Leu Leu Pro Leu Leu Ala Leu Gly Thr Gln Ala Thr Ala	
50 55 60	
Ala Ala Ala Leu Arg Ile Gly Leu Ser Pro Thr Gly Ser Gly Phe Ser	
65 70 75 80	
Ala Arg Leu Ser Pro Leu Ala Ser Arg Pro Arg Leu Arg Ser Ser Ala	
85 90 95	
His Arg Pro Ala Ile Leu Gln Gly Leu Asp Asp Gly Arg Asp Leu Lys	
100 105 110	
Asp Ala Asp Phe Tyr Lys Gln Gln Ala Lys Leu Leu Phe Lys Asn Leu	
115 120 125	
Ser Lys Gly His His Glu Ala Ser Arg Met Xaa Ile Glu Thr Gly Pro	
130 135 140	
Tyr Tyr Phe His Tyr Ile Ile Xaa Gly Arg Val Cys Tyr Leu Thr Met	
145 150 155 160	
Cys Xaa Arg Ser Tyr Pro Lys Lys Leu Ala Phe Gln Tyr Leu Glu Asp	
165 170 175	

Leu Lys Asn Glu Phe Glu
180

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500917

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708:

Leu	His	Pro	Thr	Ile	Cys	Cys	Ser	Pro	Ser	Leu	Pro	Phe	Ala	Ser	Ser
1				5				10						15	
Arg	Cys	Leu	Val	Ala	Ser	Phe	Leu	Arg	Arg	Leu	Gly	Glu	Arg	Pro	
			20					25				30			
Pro	Val	Gly	Pro	Phe	Val	Gly	Asp	Glu	His	Pro	Pro	Ala	Arg	Arg	Pro
		35					40					45			
Ile	Phe	Arg	Ser	Phe	Pro	Tyr	Ser	Arg	Ser	Ala	His	Arg	Arg	Arg	Arg
	50					55				60					
Arg	Arg	Arg	Ser	Gly	Ser	Gly	Tyr	His	Arg	Arg	Gly	Pro	Ala	Ser	Pro
65					70				75					80	
Pro	Ala	Ser	Arg	His	Ser	Pro	Arg	Ala	Leu	Ala	Ser	Gly	Pro	Pro	His
				85				90						95	
Thr	Gly	Arg	Arg	Ser	Cys	Lys	Gly	Trp	Met	Met	Gly	Glu	Ile		
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..790
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709:

atgctctacc	ggagtagcgc	aactccgcaa	gcaaatacctc	ctatctccaa	gcctccaatc	60
tgtgaacggt	gaaccccaat	cgaatgacgc	cgacggsagc	ctcctcctcc	cggctcccc	120
attcgtctct	atctccgatg	tgcgccgcct	ccagctcccc	ccgcgcggcg	gccaccggcc	180
tcgcccctgc	tgggaaggct	tggagtgcyg	ctccgtacag	acgcggatgg	tctcttcttt	240
cgttgggagc	agaacacgcc	gcagaaacgt	tatatgtgct	tccctgttcg	gagttggagc	300
tcccgaagca	ctggtcattg	gagtagtcgc	cttggttggtg	ttcggcccca	agggcttagc	360
agaggtagcc	aggaatttgg	ggaagacttt	gcgtgctttc	caaccaacca	ttagagagat	420
acaggatgta	tcaagggagt	tcaggagcac	tcttgaacga	gaaatcggaa	ttgatgaggt	480
ttcccagtcg	acgaattata	caccacgcac	catgaataac	aaccaacaac	ctgctgccga	540
ctcaaatatc	aagcctgcac	ctgcacctta	caccagcgat	gaacttgtga	aagtaactga	600
agaacaaatt	gctgcacag	ctgctgcaga	gagttatcgt	cagttggtgc	ggtgtgtccg	660
cttaaaacttt	atttgtggtt	ggttggtact	tttgtggtgg	ttattttttt	ggacctcggt	720
atagtcggtc	ggttcaatgt	tatcgcggct	actggcaaac	cttaagtgat	acggtattct	780
tcttttcggt						

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..239

(D) OTHER INFORMATION: / Ceres Seq. ID 1500927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710:

Cys	Ser	Thr	Gly	Val	Ala	Gln	Leu	Arg	Lys	Gln	Ile	Leu	Leu	Ser	Pro
1				5					10					15	
Ser	Leu	Gln	Ser	Val	Asn	Gly	Glu	Pro	Gln	Ser	Asn	Asp	Ala	Asp	Xaa
				20				25					30		
Ser	Leu	Leu	Leu	Pro	Ala	Pro	Pro	Phe	Val	Ser	Ile	Ser	Asp	Val	Arg
				35				40					45		
Arg	Leu	Gln	Leu	Pro	Pro	Arg	Gly	Gly	His	Arg	Pro	Arg	Pro	Cys	Trp
				50			55				60				
Lys	Gly	Leu	Glu	Cys	Gly	Ser	Val	Gln	Thr	Arg	Met	Val	Ser	Ser	Phe
65					70					75					80
Val	Gly	Ser	Arg	Thr	Arg	Arg	Arg	Asn	Val	Ile	Cys	Ala	Ser	Leu	Phe
				85					90					95	
Gly	Val	Gly	Ala	Pro	Glu	Ala	Leu	Val	Ile	Gly	Val	Val	Ala	Leu	Leu
				100				105					110		
Val	Phe	Gly	Pro	Lys	Gly	Leu	Ala	Glu	Val	Ala	Arg	Asn	Leu	Gly	Lys
				115				120				125			
Thr	Leu	Arg	Ala	Phe	Gln	Pro	Thr	Ile	Arg	Glu	Ile	Gln	Asp	Val	Ser
						135					140				
Arg	Glu	Phe	Arg	Ser	Thr	Leu	Glu	Arg	Glu	Ile	Gly	Ile	Asp	Glu	Val
145					150					155					160
Ser	Gln	Ser	Thr	Asn	Tyr	Thr	Pro	Thr	Thr	Met	Asn	Asn	Asn	Gln	Gln
				165					170					175	
Pro	Ala	Ala	Asp	Ser	Asn	Ile	Lys	Pro	Ala	Pro	Ala	Pro	Tyr	Thr	Ser
				180				185					190		
Asp	Glu	Leu	Val	Lys	Val	Thr	Glu	Gln	Ile	Ala	Ala	Ser	Ala	Ala	
				195				200				205			
Ala	Glu	Ser	Tyr	Arg	Gln	Leu	Val	Arg	Cys	Val	Arg	Leu	Asn	Phe	Ile
						215					220				
Cys	Gly	Trp	Leu	Val	Leu	Leu	Trp	Trp	Leu	Phe	Phe	Trp	Thr	Ser	
225					230					235					

(2) INFORMATION FOR SEQ ID NO:1711:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1500928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711:

Met	Val	Ser	Ser	Phe	Val	Gly	Ser	Arg	Thr	Arg	Arg	Arg	Asn	Val	Ile
1				5					10					15	
Cys	Ala	Ser	Leu	Phe	Gly	Val	Gly	Ala	Pro	Glu	Ala	Leu	Val	Ile	Gly
				20				25					30		
Val	Val	Ala	Leu	Leu	Val	Phe	Gly	Pro	Lys	Gly	Leu	Ala	Glu	Val	Ala
				35				40					45		
Arg	Asn	Leu	Gly	Lys	Thr	Leu	Arg	Ala	Phe	Gln	Pro	Thr	Ile	Arg	Glu
				50			55				60				
Ile	Gln	Asp	Val	Ser	Arg	Glu	Phe	Arg	Ser	Thr	Leu	Glu	Arg	Glu	Ile
65					70					75					80
Gly	Ile	Asp	Glu	Val	Ser	Gln	Ser	Thr	Asn	Tyr	Thr	Pro	Thr	Thr	Met
				85					90					95	
Asn	Asn	Asn	Gln	Gln	Pro	Ala	Ala	Asp	Ser	Asn	Ile	Lys	Pro	Ala	Pro
				100				105					110		

Ala Pro Tyr Thr Ser Asp Glu Leu Val Lys Val Thr Glu Glu Gln Ile
115 120 125
Ala Ala Ser Ala Ala Ala Glu Ser Tyr Arg Gln Leu Val Arg Cys Val
130 135 140
Arg Leu Asn Phe Ile Cys Gly Trp Leu Val Leu Trp Trp Leu Phe
145 150 155 160
Phe Trp Thr Ser

(2) INFORMATION FOR SEQ ID NO:1712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712:

aaggattttt	gcaccgtgcc	tctgcctcca	ggattgtcgt	gccgcgcctc	caccattttc	60
gccgcgcgcg	ccccgacacc	acctccaagg	atccttgccc	ccgcccctgt	actcctcgcg	120
tccgcatctc	ccgctccatt	tccgtgccc	gcgatgcgt	cgcacgtgtc	gccgcctcg	180
gccgcggggc	cgcgattacm	ccccctccca	tcaccacctc	gctgtggtgt	acccccgtcc	240
ttggcgccgc	caccccgcac	cccgtccgag	attggctctt	ccaccgctcc	ccctggagat	300
gagcgctcgc	ttagggttag	gcgtccaacg	gttggtacct	ccaccacaag	cgagaggaga	360
tcgctggaag	aggggggctg	ggagacgaac	aggaacacgg	tccacatctg	ggtgcmctcg	420
cmtcccactc	tctcgaatcc	tgamgcccac	acagcgccctc	cgcmtcgtgt	agaccgcgac	480
gc						

(2) INFORMATION FOR SEQ ID NO:1713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713:

Lys	Asp	Phe	Cys	Thr	Val	Pro	Leu	Pro	Pro	Gly	Leu	Ser	Cys	Arg	Ala
1			5					10					15		
Ser	Thr	Ile	Phe	Ala	Ala	Ala	Pro	Pro	Thr	Pro	Pro	Pro	Arg	Ile	Leu
		20					25					30			
Ala	Pro	Ala	Pro	Val	Leu	Leu	Ala	Ser	Ala	Ser	Pro	Ala	Pro	Phe	Pro
		35					40				45				
Leu	Pro	Ala	Met	Arg	Ser	His	Val	Ser	Pro	Pro	Ser	Ala	Arg	Gly	Pro
	50					55					60				
Arg	Leu	Xaa	Pro	Ser	Pro	Ser	Pro	Pro	Arg	Cys	Gly	Val	Pro	Pro	Ser
65					70				75				80		
Leu	Ala	Pro	Pro	Pro	Arg	Thr	Pro	Ser	Glu	Ile	Gly	Ser	Ser	Thr	Ala
			85					90					95		
Pro	Pro	Gly	Asp	Glu	Arg	Ser	Leu	Arg	Val	Arg	Arg	Pro	Thr	Val	Val
		100					105					110			
Pro	Ser	Thr	Thr	Ser	Glu	Arg	Arg	Ser	Leu	Glu	Glu	Gly	Gly	Trp	Glu
		115					120					125			
Thr	Asn	Arg	Asn	Thr	Val	His	Ile	Trp	Val	Xaa	Ser	Xaa	Pro	Thr	Leu
	130					135				140					
Ser	Asn	Pro	Xaa	Ala	His	Thr	Ala	Pro	Pro	Xaa	Ser				
145					150					155					

(2) INFORMATION FOR SEQ ID NO:1714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..160
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714:

Arg	Ile	Phe	Ala	Pro	Cys	Leu	Cys	Leu	Gln	Asp	Cys	Arg	Ala	Ala	Pro	
1				5					10					15		
Pro	Pro	Phe	Ser	Pro	Pro	Arg	Pro	Arg	His	His	Leu	Gln	Gly	Ser	Leu	
			20					25					30			
Pro	Pro	Pro	Leu	Tyr	Ser	Ser	Arg	Pro	His	Leu	Pro	Leu	His	Phe	Arg	
		35					40					45				
Cys	Pro	Arg	Cys	Ala	Arg	Thr	Cys	Arg	Arg	Pro	Arg	Pro	Ala	Gly	Arg	
	50					55				60						
Asp	Tyr	Xaa	Pro	Pro	His	His	Leu	Ala	Val	Val	Tyr	Pro	Arg	Pro		
65					70				75					80		
Trp	Arg	Arg	His	Pro	Ala	Pro	Arg	Pro	Arg	Leu	Ala	Leu	Pro	Pro	Leu	
			85					90					95			
Pro	Leu	Glu	Met	Ser	Ala	Arg	Leu	Gly	Leu	Gly	Val	Gln	Arg	Leu	Tyr	
		100						105				110				
Pro	Pro	Pro	Gln	Ala	Arg	Gly	Asp	Arg	Trp	Lys	Arg	Gly	Ala	Gly	Arg	
		115				120					125					
Arg	Thr	Gly	Thr	Arg	Ser	Thr	Ser	Gly	Cys	Xaa	Arg	Xaa	Pro	Leu	Ser	
	130					135					140					
Arg	Ile	Leu	Xaa	Pro	Thr	Gln	Arg	Leu	Arg	Xaa	Arg	Glu	Thr	Ala	Thr	
145					150				155						160	

(2) INFORMATION FOR SEQ ID NO:1715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715:

Met	Arg	Ser	His	Val	Ser	Pro	Pro	Ser	Ala	Arg	Gly	Pro	Arg	Leu	Xaa	
1				5					10					15		
Pro	Ser	Pro	Ser	Pro	Pro	Arg	Cys	Gly	Val	Pro	Pro	Ser	Leu	Ala	Pro	
		20						25					30			
Pro	Pro	Arg	Thr	Pro	Ser	Glu	Ile	Gly	Ser	Ser	Thr	Ala	Pro	Pro	Gly	
		35				40					45					
Asp	Glu	Arg	Ser	Leu	Arg	Val	Arg	Arg	Pro	Thr	Val	Pro	Ser	Thr		
	50					55				60						
Thr	Ser	Glu	Arg	Arg	Ser	Leu	Glu	Glu	Gly	Gly	Trp	Glu	Thr	Asn	Arg	
65					70					75				80		
Asn	Thr	Val	His	Ile	Trp	Val	Xaa	Ser	Xaa	Pro	Thr	Leu	Ser	Asn	Pro	
			85					90						95		
Xaa	Ala	His	Thr	Ala	Pro	Pro	Xaa	Ser								
		100						105								

(2) INFORMATION FOR SEQ ID NO:1716:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..463
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500945
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716:

aatcaacaca	ccaccaccac	cagcagcaca	tcaatttagc	tagttccagg	aacacgcgag	60
gaaaccgcag	catggccaac	aaccgcatct	tcgacgagta	caaccccgcc	gtcgaatgga	120
gccgctccga	cgaggcggac	gccgtccgga	tctcgctccc	agggttcaag	agggaggaca	180
tacgcgtgct	ggtggacagc	cacggccacc	tgcgagcgcg	cggcgagcgg	cacatcgccg	240
gcaacaggtg	gagccgcttc	cagacggacg	tcgacctccc	cgccaactgc	aacgccgacg	300
gcatccgcgc	caagttcgag	aacgacaggg	tcaccatcac	gctccccaag	agcacctcct	360
cggcgcccat	tccggcgccg	ccgcagaggg	cgcacgtgaa	ggcgccgctg	acgtcgctcg	420
cgaggcttcc	gccggtgact	gctaggccag	tggcgaggcc	tgc		

(2) INFORMATION FOR SEQ ID NO:1717:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..153
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500946
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717:

Ser	Thr	His	His	His	Gln	Gln	His	Ile	Asn	Leu	Ala	Ser	Ser	Arg
1				5				10				15		
Asn	Thr	Arg	Gly	Asn	Arg	Ser	Met	Ala	Asn	Asn	Arg	Ile	Phe	Asp
				20				25				30		
Tyr	Asn	Pro	Ala	Val	Glu	Trp	Ser	Arg	Ser	Asp	Glu	Ala	Asp	Ala
				35				40				45		
Arg	Ile	Ser	Leu	Pro	Gly	Phe	Lys	Arg	Glu	Asp	Ile	Arg	Val	Leu
				50				55				60		
Asp	Ser	His	Gly	His	Leu	Arg	Thr	Arg	Gly	Glu	Arg	His	Ile	Ala
				65				70				75		
Asn	Arg	Trp	Ser	Arg	Phe	Gln	Thr	Asp	Val	Asp	Leu	Pro	Ala	Asn
				85				90				95		
Asn	Ala	Asp	Gly	Ile	Arg	Ala	Lys	Phe	Glu	Asn	Asp	Arg	Leu	Thr
				100				105				110		
Thr	Leu	Pro	Lys	Ser	Thr	Ser	Ser	Ala	Pro	Ile	Pro	Ala	Pro	Pro
				115				120				125		
Arg	Pro	His	Val	Lys	Ala	Pro	Ser	Thr	Ser	Ser	Ala	Arg	Leu	Pro
				130				135				140		
Val	Thr	Ala	Arg	Pro	Val	Ala	Arg	Pro						
				145				150						

(2) INFORMATION FOR SEQ ID NO:1718:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1500947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718:

```
Met Ala Asn Asn Arg Ile Phe Asp Glu Tyr Asn Pro Ala Val Glu Trp
1          5          10          15
Ser Arg Ser Asp Glu Ala Asp Ala Val Arg Ile Ser Leu Pro Gly Phe
          20          25          30
Lys Arg Glu Asp Ile Arg Val Leu Val Asp Ser His Gly His Leu Arg
          35          40          45
Thr Arg Gly Glu Arg His Ile Ala Gly Asn Arg Trp Ser Arg Phe Gln
          50          55          60
Thr Asp Val Asp Leu Pro Ala Asn Cys Asn Ala Asp Gly Ile Arg Ala
65          70          75          80
Lys Phe Glu Asn Asp Arg Leu Thr Ile Thr Leu Pro Lys Ser Thr Ser
          85          90          95
Ser Ala Pro Ile Pro Ala Pro Pro Gln Arg Pro His Val Lys Ala Pro
          100          105          110
Ser Thr Ser Ser Ala Arg Leu Pro Pro Val Thr Ala Arg Pro Val Ala
          115          120          125
Arg Pro
130
```

(2) INFORMATION FOR SEQ ID NO:1719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1500948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719:

```
Met Glu Pro Leu Arg Arg Gly Gly Arg Pro Asp Leu Ala Pro Arg
1          5          10          15
Val Gln Glu Gly Gly His Thr Arg Ala Gly Gly Gln Pro Arg Pro Pro
          20          25          30
Ala Asp Ala Arg Arg Ala Ala His Arg Arg Gln Gln Val Glu Pro Leu
          35          40          45
Pro Asp Gly Arg Arg Pro Pro Arg Gln Leu Gln Arg Arg Arg His Pro
          50          55          60
Arg Gln Val Arg Glu Arg Gln Ala His His His Ala Pro Gln Glu His
65          70          75          80
Leu Leu Gly Ala His Ser Gly Ala Ala Ala Glu Ala Ala Arg Glu Gly
          85          90          95
Ala Val Asp Val Val Gly Glu Ala Ser Ala Gly Asp Cys
          100          105
```

(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..520

(D) OTHER INFORMATION: / Ceres Seq. ID 1500953

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720:

```
ctcgcagcca gcaggacacc actcatcttc ttctcccccgc cctcgtttcc atcgccacca      60
ccctcttctc ctgcggtcct ccccggtccc actcccaccc ccctcgcctc cgcctccact      120
gcagctgccg ccatgcagag cctcctcctg cccaccgctg ccgtggcccc ggtggcgctt      180
```

ccgtgcggaa ggcggaatct cccggggacgc ctctccgtcc gcgcctccgc gacgggtggtta 240
gcgggcaccgc ggcgggagac ggatcccaag aagcgggtgg tgatcacggg gatggggctg 300
gtctccgttt tcgggaacga tgtagacgct tactacgacc gcctgctagt cggggagagc 360
ggcatcgggc ccatcgaccg ctctgacgct tctaagttcc ccaccgctt tgccggtcag 420
atccggggct tctcctccga gggatacatc gacggaaaga acgaccgcmg ccttgatgat 480
tgcctccgat actgcatcgt cagtggcaag aaggctctcg

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..173

(D) OTHER INFORMATION: / Ceres Seq. ID 1500954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721:

Leu Ala Ala Ser Arg Thr Pro Leu Ile Phe Phe Ser Pro Ala Ser Phe
1 5 10 15
Pro Ser Pro Pro Ser Ser Pro Ala Val Leu Pro Arg Pro Thr Pro
20 25 30
Thr Pro Leu Ala Ser Ala Ser Thr Ala Ala Ala Met Gln Ser Leu
35 40 45
Leu Leu Pro Thr Ala Ala Val Ala Pro Val Ala Pro Pro Cys Gly Arg
50 55 60
Arg Asn Leu Pro Gly Arg Leu Ser Val Arg Ala Ser Ala Thr Val Val
65 70 75 80
Ala Ala Pro Arg Arg Glu Thr Asp Pro Lys Lys Arg Val Val Ile Thr
85 90 95
Gly Met Gly Leu Val Ser Val Phe Gly Asn Asp Val Asp Ala Tyr Tyr
100 105 110
Asp Arg Leu Leu Val Gly Glu Ser Gly Ile Gly Pro Ile Asp Arg Phe
115 120 125
Asp Ala Ser Lys Phe Pro Thr Arg Phe Ala Gly Gln Ile Arg Gly Phe
130 135 140
Ser Ser Glu Gly Tyr Ile Asp Gly Lys Asn Asp Arg Xaa Leu Asp Asp
145 150 155 160
Cys Leu Arg Tyr Cys Ile Val Ser Gly Lys Lys Ala Leu
165 170

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1500955

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722:

Arg Ser Gln Gln Asp Thr Thr His Leu Leu Leu Pro Arg Leu Val Ser
1 5 10 15
Ile Ala Thr Thr Leu Phe Ser Cys Gly Pro Pro Pro Ser His Ser His
20 25 30
Pro Pro Arg Leu Arg Leu His Cys Ser Cys Arg His Ala Glu Pro Pro
35 40 45
Pro Ala His Arg Cys Arg Gly Pro Gly Gly Ala Ser Val Arg Lys Ala
50 55 60
Glu Ser Pro Gly Thr Pro Leu Arg Pro Arg Leu Arg Asp Gly Gly Ser

(2) INFORMATION FOR SEQ ID NO:1723:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1500956

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723:

(2) INFORMATION FOR SEQ ID NO:1724:

(A) LENGTH: 485 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..485

(D) OTHER INFORMATION: / Ceres Seq. ID 1500963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724:

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..94
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500964
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725:
Met Lys Leu Leu Gly Trp Met His Arg Lys Leu Arg Gln Asn Ser Asn
1 5 10 15
Asp Val Phe Lys Glu Phe Asn Asn Ala Gly Gly Gly Thr Cys Asn Cys
 20 25 30
Ile Thr Gly Leu Ala Ala Ser Asp Pro Ala Thr Phe Leu Ala Thr Ala
 35 40 45
Asn Glu Tyr Phe Ala Ala Asp Asn Asp Phe Thr Asn Asn His Pro Ser
50 55 60
Ser Pro Ala Ala Asp Leu Phe Thr Phe Gly Gly Ser Gly Leu Leu Thr
65 70 75 80
Ile Gly Thr Leu Gly Ile Ala Pro Ser Arg Val Cys Arg Cys
 85 90

(2) INFORMATION FOR SEQ ID NO:1726:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..88
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500965
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726:
Met His Arg Lys Leu Arg Gln Asn Ser Asn Asp Val Phe Lys Glu Phe
1 5 10 15
Asn Asn Ala Gly Gly Gly Thr Cys Asn Cys Ile Thr Gly Leu Ala Ala
 20 25 30
Ser Asp Pro Ala Thr Phe Leu Ala Thr Ala Asn Glu Tyr Phe Ala Ala
35 40 45
Asp Asn Asp Phe Thr Asn Asn His Pro Ser Ser Pro Ala Ala Asp Leu
50 55 60
Phe Thr Phe Gly Gly Ser Gly Leu Leu Thr Ile Gly Thr Leu Gly Ile
65 70 75 80
Ala Pro Ser Arg Val Cys Arg Cys
 85

(2) INFORMATION FOR SEQ ID NO:1727:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..68
 (D) OTHER INFORMATION: / Ceres Seq. ID 1500966
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727:
Met Met Cys Ser Lys Ser Ser Thr Thr Leu Glu Val Gly Arg Ala Thr
1 5 10 15

Ala Ser Pro Gly Trp Pro Arg Arg Thr Arg Pro Leu Ser Ser Pro Pro
20 25 30
Pro Thr Asn Thr Ser Pro Pro Thr Thr Thr Ser Pro Thr Ile Ile His
35 40 45
Arg Arg Arg Pro Pro Thr Ser Ser Pro Leu Val Ala Ala Ala Ser Ser
50 55 60
Pro Leu Ala Arg
65

(2) INFORMATION FOR SEQ ID NO:1728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..410
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500974

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728:

tccgttccgy	tccttcctcc	ccctatctag	ctagccttcc	cgttcctgca	tcgcggcgga	60
gatgggccc	tcaccacgc	cgctcgcgc	ggcggcggcg	ctgcttctgc	tgctgctcgc	120
gccgctcgcc	gcggcgccg	acagcatgtc	gatcgtctcc	tacggcgagc	ggasmdgmsn	180
aggaggcgcg	gcggatgtac	gccgagtggg	tggcggcgca	cggccggacc	tacaacgccg	240
tcggsaggag	gagcgcaggt	tcgaggtggt	cagggacaac	ctccgctacg	tcgacgccc	300
caacgccgcc	gccgamcg	gcgtccactc	cttccgcctc	gggctcaacc	gcttcgccga	360
cctcaccaac	gacgagtacc	gcrccamcta	cctcggcgc	aggagcaggc		

(2) INFORMATION FOR SEQ ID NO:1729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1500975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729:

Arg Ser Xaa Pro Ser Ser Pro Tyr Leu Ala Ser Leu Pro Val Pro Ala
1 5 10 15
Ser Arg Arg Arg Trp Ala Pro Pro Pro Arg Arg Ser Arg Arg Arg Arg
20 25 30
Arg Cys Phe Cys Cys Cys Ser Arg Arg Ser Pro Arg Arg Arg Thr Ala
35 40 45
Cys Arg Ser Ser Pro Thr Ala Ser Gly Xaa Xaa Xaa Glu Ala Arg Arg
50 55 60
Met Tyr Ala Glu Trp Met Ala Ala His Gly Arg Thr Tyr Asn Ala Val
65 70 75 80
Xaa Arg Arg Ser Ala Gly Ser Arg Cys Ser Gly Thr Thr Ser Ala Thr
85 90 95
Ser Thr Pro Thr Thr Pro Pro Pro Xaa Arg Ala Ser Thr Pro Ser Ala
100 105 110
Ser Gly Ser Thr Ala Ser Pro Thr Ser Pro Thr Thr Ser Thr Xaa Pro
115 120 125
Xaa Thr Ser Ala Ser Gly Ala Gly
130 135

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..116
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500976
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730:

Met Gly Ala Ser Thr Thr Pro Leu Ala Ser Ala Ala Ala Leu Leu Leu
1 5 10 15
Leu Leu Leu Ala Pro Leu Ala Ala Ala Asp Ser Met Ser Ile Val
20 25 30
Ser Tyr Gly Glu Arg Xaa Xaa Xaa Gly Gly Ala Ala Asp Val Arg Arg
35 40 45
Val Asp Gly Gly Ala Arg Pro Asp Leu Gln Arg Arg Arg Xaa Glu Glu
50 55 60
Arg Arg Phe Glu Val Phe Arg Asp Asn Leu Arg Tyr Val Asp Ala His
65 70 75 80
Asn Ala Ala Ala Xaa Ala Gly Val His Ser Phe Arg Leu Gly Leu Asn
85 90 95
Arg Phe Ala Asp Leu Thr Asn Asp Glu Tyr Arg Xaa Xaa Tyr Leu Gly
100 105 110
Val Arg Ser Arg
115

(2) INFORMATION FOR SEQ ID NO:1731:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..88
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500977
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731:

Met Ser Ile Val Ser Tyr Gly Glu Arg Xaa Xaa Gly Gly Ala Ala
1 5 10 15
Asp Val Arg Arg Val Asp Gly Gly Ala Arg Pro Asp Leu Gln Arg Arg
20 25 30
Arg Xaa Glu Glu Arg Arg Phe Glu Val Phe Arg Asp Asn Leu Arg Tyr
35 40 45
Val Asp Ala His Asn Ala Ala Ala Xaa Ala Gly Val His Ser Phe Arg
50 55 60
Leu Gly Leu Asn Arg Phe Ala Asp Leu Thr Asn Asp Glu Tyr Arg Xaa
65 70 75 80
Xaa Tyr Leu Gly Val Arg Ser Arg
85

(2) INFORMATION FOR SEQ ID NO:1732:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 485 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..485
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1500985
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732:

agcacatcga tcagtcgcgt gtctaggttt cctctctcac catagcgccc gctctgtcgc

(2) INFORMATION FOR SEQ ID NO:1733:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1.52

(D) OTHER INFORMATION: / Ceres Seq. ID 1500986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1734:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1500987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734:

Met	Glu	Lys	Lys	Pro	Thr	Ile	Leu	Met	Asn	Arg	Tyr	Glu	Leu	Gly	Arg
1				5					10					15	
Thr	Leu	Gly	Gln	Gly	Thr	Phe	Ala	Lys	Val	Tyr	His	Gly	Arg	Asn	Leu
			20					25					30		
Ala	Ser	Gly	Glu	Ser	Val	Ala	Ile	Lys	Val	Ile	Asp	Lys	Glu	Lys	Val
			35				40					45			
Met	Arg	Val	Gly	Met	Ile	Asp	Gln	Ile	Lys	Arg	Glu	Ile	Ser	Val	Met
	50					55					60				
Arg	Leu	Val	Arg	His	Pro	Asn	Val	Val	Gln	Leu	His	Glu	Gly	Asp	Gly
65					70					75					80
Gln	Gln	Glu	Gln	Asp	Ile	Leu	Arg	His	Gly	Val	Arg				
				85					90						

(2) INFORMATION FOR SEQ ID NO:1735:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1500988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735:

Met	Asn	Arg	Tyr	Glu	Leu	Gly	Arg	Thr	Leu	Gly	Gln	Gly	Thr	Phe	Ala
1				5					10					15	
Lys	Val	Tyr	His	Gly	Arg	Asn	Leu	Ala	Ser	Gly	Glu	Ser	Val	Ala	Ile
			20					25					30		
Lys	Val	Ile	Asp	Lys	Glu	Lys	Val	Met	Arg	Val	Gly	Met	Ile	Asp	Gln
		35					40					45			
Ile	Lys	Arg	Glu	Ile	Ser	Val	Met	Arg	Leu	Val	Arg	His	Pro	Asn	Val
	50					55					60				
Val	Gln	Leu	His	Glu	Gly	Asp	Gly	Gln	Gln	Glu	Gln	Asp	Ile	Leu	Arg
65				70						75				80	
His	Gly	Val	Arg												

(2) INFORMATION FOR SEQ ID NO:1736:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 462 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..462

(D) OTHER INFORMATION: / Ceres Seq. ID 1500992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736:

aacatctcct	cacttcacac	cactcccgcc	attgtcctgc	gcctttctgc	accgccacac	60
acaccccgct	ccaatccaat	ggcgccctgc	caagccgtcc	tcgcggtcgt	ggtcctcgcc	120
gcgctgctcc	cgctcgccct	ctctcgcggg	ctgcggcttg	gccaccaccg	cccagccgca	180
cccgaggccg	cacggtcacg	caccgctcgg	aggtggcgcg	tggtcctcgg	cccacgccac	240
cttctacggc	ggcgggcgacg	cgcccgccac	catgggcgga	cgtgtgggta	cggcaacctt	300
tacagccagg	ggtacggcac	caacacggcg	gcgctgagca	cggcgctctt	caacaacggc	360
ctcagctgcg	gcgcctgctt	cgaggtgcgg	tgcgmgcg	cggggggcgg	cggccgctcg	420
trcmtgcmgg	gctccgctgt	ggtgacggcc	accaacttct	gc		

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1500993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737:

Asn	Ile	Ser	Leu	His	Thr	Thr	Pro	Ala	Ile	Val	Leu	Arg	Leu	Ser
1			5					10					15	
Ala	Pro	Pro	His	Thr	Pro	Arg	Ser	Asn	Pro	Met	Ala	Pro	Arg	Gln
			20					25					30	
Val	Leu	Ala	Val	Val	Val	Leu	Ala	Ala	Leu	Leu	Pro	Leu	Ala	Leu
		35					40					45		
Arg	Gly	Leu	Arg	Leu	Gly	His	His	Arg	Pro	Ala	Ala	Pro	Glu	Ala
	50					55					60			
Arg	Ser	Arg	Thr	Ala	Arg	Arg	Trp	Arg	Val	Val	Leu	Gly	Pro	Arg
65				70					75					80
Leu	Leu	Arg	Arg	Arg	Arg	Arg	Val	Arg	His	His	Gly	Arg	Thr	Cys
			85						90				95	
Tyr	Gly	Asn	Leu	Tyr	Ser	Gln	Gly	Tyr	Gly	Thr	Asn	Thr	Ala	Ala
			100					105					110	

Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser Cys Gly Ala Cys Phe Glu
115 120 125
Val Arg Cys Xaa Ala Ala Gly Gly Gly Arg Ser Xaa Xaa Xaa Gly
130 135 140
Ser Val Val Val Thr Ala Thr Asn Phe Cys
145 150

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1500994

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738:

His Leu Leu Thr Ser His His Ser Arg His Cys Pro Ala Pro Phe Cys
1 5 10 15
Thr Ala Thr His Thr Pro Leu Gln Ser Asn Gly Ala Ser Pro Ser Arg
20 25 30
Pro Arg Gly Arg Gly Pro Arg Arg Ala Ala Pro Ala Arg Pro Leu Ser
35 40 45
Arg Ala Ala Ala Trp Pro Pro Pro Pro Ser Arg Thr Arg Gly Arg Thr
50 55 60
Val Thr His Arg Ser Glu Val Ala Arg Gly Pro Arg Pro Thr Pro Pro
65 70 75 80
Ser Thr Ala Ala Ala Thr Arg Pro Ala Pro Trp Ala Asp Val Trp Val
85 90 95
Arg Gln Pro Leu Gln Pro Gly Val Arg His Gln His Gly Gly Ala Glu
100 105 110
His Gly Ala Leu Gln Gln Arg Pro Gln Leu Arg Arg Leu Leu Arg Gly
115 120 125
Ala Val Arg Xaa Gly Gly Gly Arg Arg Pro Leu Xaa Xaa Xaa Gly Leu
130 135 140
Arg Arg Gly Asp Gly His Gln Leu Leu
145 150

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1500995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739:

Met Ala Pro Arg Gln Ala Val Leu Ala Val Val Val Leu Ala Ala Leu
1 5 10 15
Leu Pro Leu Ala Leu Ser Arg Gly Leu Arg Leu Gly His His Arg Pro
20 25 30
Ala Ala Pro Glu Ala Ala Arg Ser Arg Thr Ala Arg Arg Trp Arg Val
35 40 45
Val Leu Gly Pro Arg His Leu Leu Arg Arg Arg Arg Arg Val Arg His
50 55 60
His Gly Arg Thr Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly
65 70 75 80
Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Ser

(2) INFORMATION FOR SEQ ID NO:1740:

(A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(A) NAME/KEY: -
(B) LOCATION: 1..436
(D) OTHER INFORMATION: / Ceres Seq. ID 1501005

ggctatccag	gctccagtcg	tccccggatt	agttgtactg	tacattgttc	ctgcgaagac	60
actgggtcgt	ccgggtcaat	cggcagcttg	aacaagccat	ggcggcgcac	cggccgaac:g	120
ccgcggcgcc	gctgctcgcc	aagctcgacg	ccaccgccac	gccgcggcg	aasgcana:a	180
agtagccctt	cttctgcgcc	gtgctcgcat	ccatgacctc	cgtgctcat	ggctacaac:g	240
tcgcggtgac	gagcggcgcg	cagatcttca	tggcggagga	cctcgggatg	agcgacgcgc	300
agatcgaggt	gctctcgggg	gtcatcaaca	tatactcgct	cgtcggcgcg	ctgctggcag	360
gctggacctc	cgaccgtctc	ggccggcgcc	tcaccatcgt	cctcgccaac	gccttcttc:c	420
tcgtcgggcc	gctcgc					

(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(A) NAME/KEY: peptide
(B) LOCATION: 1..71
(D) OTHER INFORMATION: / Ceres Seq. ID 1501006

Gly 1	Tyr	Pro	Gly	Ser 5	Ser	Arg	Pro	Arg	Ile 10	Ser	Cys	Thr	Val	His 15	Cys
Ser	Cys	Glu	Asp 20	Thr	Gly	Ser	Ser	Gly 25	Ser	Ile	Gly	Ser	Leu 30	Asn	Lys
Pro	Trp	Arg 35	Arg	Thr	Gly	Arg	Thr 40	Pro	Arg	Arg	Arg	Cys 45	Ser	Pro	Ser
Ser	Thr 50	Pro	Pro	Pro	Arg	Arg 55	Arg	Arg	Xaa	Xaa	Thr 60	Ser	Thr	Pro	Ser
Ser 65	Ala	Pro	Cys	Ser	His 70	Pro									

(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(A) NAME/KEY: peptide
(B) LOCATION: 1..112
(D) OTHER INFORMATION: / Ceres Seq. ID 1501007

(xi) SEQUENCE DESCRIPTION: SEO ID NO:1742:

Met Ala Ala His Arg Pro Asn Ala Ala Ala Pro Leu Leu Ala Lys Leu
1 5 10 15
Asp Ala Thr Ala Thr Pro Pro Ala Xaa Ala Xaa Lys Tyr Pro Phe Phe
20 25 30
Cys Ala Val Leu Ala Ser Met Thr Ser Val Leu Met Gly Tyr Asn Val
35 40 45
Ala Val Thr Ser Gly Ala Gln Ile Phe Met Ala Glu Asp Leu Gly Met
50 55 60
Ser Asp Ala Gln Ile Glu Val Leu Ser Gly Val Ile Asn Ile Tyr Ser
65 70 75 80
Leu Val Gly Ala Leu Leu Ala Gly Trp Thr Ser Asp Arg Leu Gly Arg
85 90 95
Arg Leu Thr Ile Val Leu Ala Asn Ala Phe Phe Leu Val Gly Pro Leu
100 105 110

(2) INFORMATION FOR SEQ ID NO:1743:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1501008

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743:

Met Thr Ser Val Leu Met Gly Tyr Asn Val Ala Val Thr Ser Gly Ala
1 5 10 15
Gln Ile Phe Met Ala Glu Asp Leu Gly Met Ser Asp Ala Gln Ile Glu
20 25 30
Val Leu Ser Gly Val Ile Asn Ile Tyr Ser Leu Val Gly Ala Leu Leu
35 40 45
Ala Gly Trp Thr Ser Asp Arg Leu Gly Arg Arg Leu Thr Ile Val Leu
50 55 60
Ala Asn Ala Phe Phe Leu Val Gly Pro Leu
65 70

(2) INFORMATION FOR SEQ ID NO:1744:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 528 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..528

(D) OTHER INFORMATION: / Ceres Seq. ID 1501016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744:

aagacttcgt cgtcaccaaa aaaataaagc agaaaaaaac agagagtagt agactacgac 60
agcgtccgtc gaaccggagg gtcggaggcg gagcgaga tgaggaagaa gtcggcacc 120
cggttccccg cggctcgaat caaaaagata atgcaagcag atgaggatgt tggaaagatt 180
gcattagcag tgcctgtttt agtctcgagg gctcttgaat tgtttttaca agatttaatt 240
gaccggactt atgaaattac tcttcaaagt ggagcaaaga cactgaattc cttccacctg 300
aagcaatgtg tgaagaggta cagttctttt gatttcctaa ctgaagttgt cagcaaggta 360
ccagatcttg gtggtgctga ttcattgtga gatgaaagag tgttacctag aagaagaaag 420
tcaaattggc gtgaccacga gaatgatgaa tcaagatcta gtaaaatggc tataaganat 480
gcaaatacca ncnccagagg gacgtdggar gggtcgaggc agagggcg

(2) INFORMATION FOR SEQ ID NO:1745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..143
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1501017
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745:

Met	Arg	Lys	Lys	Leu	Gly	Thr	Arg	Phe	Pro	Ala	Ala	Arg	Ile	Lys	Lys
1			5					10					15		
Ile	Met	Gln	Ala	Asp	Glu	Asp	Val	Gly	Lys	Ile	Ala	Leu	Ala	Val	Pro
		20						25				30			
Val	Leu	Val	Ser	Arg	Ala	Leu	Glu	Leu	Phe	Leu	Gln	Asp	Leu	Ile	Asp
		35					40				45				
Arg	Thr	Tyr	Glu	Ile	Thr	Leu	Gln	Ser	Gly	Ala	Lys	Thr	Leu	Asn	Ser
	50				55					60					
Phe	His	Leu	Lys	Gln	Cys	Val	Lys	Arg	Tyr	Ser	Ser	Phe	Asp	Phe	Leu
65				70					75				80		
Thr	Glu	Val	Val	Ser	Lys	Val	Pro	Asp	Leu	Gly	Gly	Ala	Asp	Ser	Cys
			85					90					95		
Gly	Asp	Glu	Arg	Val	Leu	Pro	Arg	Arg	Arg	Lys	Ser	Asn	Gly	Ser	Asp
			100				105					110			
Pro	Glu	Asn	Asp	Glu	Ser	Arg	Ser	Lys	Met	Ala	Ile	Arg	Xaa	Ala	
		115				120					125				
Asn	Thr	Xaa	Xaa	Arg	Gly	Thr	Xaa	Xaa	Gly	Ser	Arg	Gln	Arg	Ala	
	130				135						140				

(2) INFORMATION FOR SEQ ID NO:1746:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..126
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1501018
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746:

Met	Gln	Ala	Asp	Glu	Asp	Val	Gly	Lys	Ile	Ala	Leu	Ala	Val	Pro	Val
1			5					10					15		
Leu	Val	Ser	Arg	Ala	Leu	Glu	Leu	Phe	Leu	Gln	Asp	Leu	Ile	Asp	Arg
		20					25				30				
Thr	Tyr	Glu	Ile	Thr	Leu	Gln	Ser	Gly	Ala	Lys	Thr	Leu	Asn	Ser	Phe
	35				40						45				
His	Leu	Lys	Gln	Cys	Val	Lys	Arg	Tyr	Ser	Ser	Phe	Asp	Phe	Leu	Thr
	50				55					60					
Glu	Val	Val	Ser	Lys	Val	Pro	Asp	Leu	Gly	Gly	Ala	Asp	Ser	Cys	Gly
65			70						75				80		
Asp	Glu	Arg	Val	Leu	Pro	Arg	Arg	Arg	Lys	Ser	Asn	Gly	Ser	Asp	Pro
			85				90					95			
Glu	Asn	Asp	Glu	Ser	Arg	Ser	Ser	Lys	Met	Ala	Ile	Arg	Xaa	Ala	Asn
		100				105					110				
Thr	Xaa	Xaa	Arg	Gly	Thr	Xaa	Xaa	Gly	Ser	Arg	Gln	Arg	Ala		
		115			120						125				

(2) INFORMATION FOR SEQ ID NO:1747:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 538 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..538
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501023
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747:
atccgcctcc gaaccacga gccacgacc cactactaca tcagtccacc gccaccgcgc 60
accgcgagtc cgcgacagac atccgcgcgc cggcctcact ctcaactcccc agtccccacc 120
gtgccgccac aagcgacgcg acgcagccac gcagggagag ggaaatggcc acggccgcga 180
ctgccacggc ggggagtaga gcagccgtgc tgctgctgct ctgcgtggcg ctggcgctgg 240
cgctgcggcc ctccgacgcc ggcgcggggc gcgactgcca cttcccggcc gtgttcaact 300
tcggcgactc caactcggac acgggcggcc tgtcatcgct cttcggcgcc gcaccgccgc 360
ccaacggcag gaccttcttc ggcatgcccg cmggccgcta ctgcgatggt cgcctcgtca 420
tcgacttcat cgctgaaacc tggggctgac tcacctcagt gcgtacctga actcgatcgg 480
aagcaacttc acacaggag ccaactttgc aacagctggt tcacgatca gaagacag

(2) INFORMATION FOR SEQ ID NO:1748:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 179 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..179
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501024
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748:
Ile Arg Leu Arg Thr His Glu Ala Thr Thr His Tyr Tyr Ile Ser Pro
1 5 10 15
Pro Pro Pro Arg Thr Ala Ser Pro Arg Gln Thr Ser Ala Pro Arg Pro
 20 25 30
His Ser His Ser Pro Val Pro Thr Val Pro Pro Gln Ala Thr Arg Arg
 35 40 45
Ser His Ala Gly Arg Gly Lys Trp Pro Arg Pro Arg Leu Pro Arg Arg
50 55 60
Gly Val Glu Gln Pro Cys Cys Cys Ser Arg Trp Arg Trp Arg Trp
65 70 75 80
Arg Cys Gly Pro Pro Thr Pro Ala Arg Ala Ala Thr Ala Thr Ser Arg
 85 90 95
Pro Cys Ser Thr Ser Ala Thr Pro Thr Arg Thr Arg Ala Ala Cys His
 100 105 110
Arg Ser Ser Ala Pro His Arg Arg Pro Thr Ala Gly Pro Ser Ser Ala
 115 120 125
Cys Pro Xaa Ala Ala Thr Ala Met Val Ala Ser Ser Ser Thr Ser Ser
130 135 140
Leu Lys Pro Gly Ala Asp Ser Pro Gln Cys Val Pro Glu Leu Asp Arg
145 150 155 160
Lys Gln Leu His Thr Gly Ser Gln Leu Cys Asn Ser Trp Phe Ile Asp
 165 170 175
Gln Lys Thr

(2) INFORMATION FOR SEQ ID NO:1749:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1501025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749:

```
Pro Pro Pro Asn Pro Arg Gly His Asp Pro Leu Leu His Gln Ser Thr
1      5      10      15
Ala Thr Ala His Arg Glu Ser Ala Thr Asp Ile Arg Ala Pro Ala Ser
20      25      30
Leu Ser Leu Pro Ser Pro His Arg Ala Ala Thr Ser Asp Ala Thr Gln
35      40      45
Pro Arg Arg Glu Arg Glu Met Ala Thr Ala Ala Thr Ala Thr Ala Gly
50      55      60
Ser Arg Ala Ala Val Leu Leu Leu Ser Leu Ala Leu Ala Leu Ala
65      70      75      80
Leu Arg Pro Ser Asp Ala Gly Ala Gly Gly Asp Cys His Phe Pro Ala
85      90      95
Val Phe Asn Phe Gly Asp Ser Asn Ser Asp Thr Gly Gly Leu Ser Ser
100      105      110
Leu Phe Gly Ala Ala Pro Pro Pro Asn Gly Arg Thr Phe Phe Gly Met
115      120      125
Pro Xaa Gly Arg Tyr Cys Asp Gly Arg Leu Val Ile Asp Phe Ile Ala
130      135      140
Glu Thr Trp Gly
145
```

(2) INFORMATION FOR SEQ ID NO:1750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750:

```
Met Ala Thr Ala Ala Thr Ala Thr Ala Gly Ser Arg Ala Ala Val Leu
1      5      10      15
Leu Leu Leu Ser Leu Ala Leu Ala Leu Ala Leu Arg Pro Ser Asp Ala
20      25      30
Gly Ala Gly Gly Asp Cys His Phe Pro Ala Val Phe Asn Phe Gly Asp
35      40      45
Ser Asn Ser Asp Thr Gly Gly Leu Ser Ser Leu Phe Gly Ala Ala Pro
50      55      60
Pro Pro Asn Gly Arg Thr Phe Phe Gly Met Pro Xaa Gly Arg Tyr Cys
65      70      75      80
Asp Gly Arg Leu Val Ile Asp Phe Ile Ala Glu Thr Trp Gly
85      90
```

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1501027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751:

```
acccctccag tcaggccgct ccgcccgcac gtcaacggag acgtgtcaac ggcggcggtg      60
agaagacca taaccttcta gatttttttc cgctgcctca atggatctct gggagagggc      120
```

```
ccggggccttc gccggcgagg cggcggaacgg tcgcaggaac tctccgcgga ggcgggccaag 180
cgctcgtcgg cgctgggtctc ggagacggcg aagaagtcca aggagatctt ctccgaaacc 240
gcctccaagt cgcgggagat cgccgctgag gccaccaagc aggcgcgacct cctcgccgyc 300
cagatcaagc acctcgccctc cgacctccct gtgccttcga tcccgcgccat ccccgcgatc 360
ccgcctatcc ccgcccgtgc ctgcgcggtg cccgacgcgg ccgagcttga gtgctacgyc 420
atcaccgacg acctccgcga gttcgtcaag ggcgatgacca taaacacctt ccgcgacttc 480
ccactgc
```

(2) INFORMATION FOR SEQ ID NO:1752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752:

```
Pro Ser Ser Gln Ala Val Pro Arg Arg Arg Gln Arg Arg Arg Val Asn
1          5          10          15
Gly Gly Gly Glu Lys Thr His Asn Leu Asp Phe Phe Pro Leu Pro
20          25          30
Gln Trp Ile Ser Gly Arg Gly Pro Gly Pro Ser Pro Ala Arg Arg Arg
35          40          45
Thr Val Ala Gly Thr Leu Arg Gly Gly Gly Gln Ala Leu Val Gly Ala
50          55          60
Gly Leu Gly Asp Gly Glu Glu Val Gln Gly Asp Leu Leu Arg Asn Arg
65          70          75          80
Leu Gln Val Ala Gly Asp Arg Arg
85
```

(2) INFORMATION FOR SEQ ID NO:1753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..118
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501029

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753:

```
Met Asp Leu Trp Glu Arg Ala Arg Ala Phe Ala Gly Glu Ala Ala Asn
1          5          10          15
Gly Arg Arg Asn Ser Pro Arg Arg Arg Pro Ser Ala Arg Arg Arg Trp
20          25          30
Ser Arg Arg Arg Arg Arg Ser Pro Arg Arg Ser Ser Pro Lys Pro Pro
35          40          45
Pro Ser Arg Gly Arg Ser Pro Leu Arg Pro Pro Ser Arg Pro Thr Ser
50          55          60
Ser Pro Ala Arg Ser Ser Thr Ser Pro Pro Thr Ser Leu Cys Leu Arg
65          70          75          80
Ser Arg Pro Ser Pro Arg Ser Arg Leu Ser Pro Pro Leu Pro Arg Arg
85          90          95
Cys Pro Thr Arg Pro Ser Leu Ser Ala Thr Ala Ser Pro Thr Thr Ser
100          105          110
Ala Ser Ser Ser Arg Ala
115
```

(2) INFORMATION FOR SEQ ID NO:1754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..513
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501037

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754:

gtgctgccgc	cagatctaac	caaaccccg	gccctcctca	ccgtccggcg	agctacggac	60
tcagcagatc	accgtcgctc	gagttgtacc	tgaaggcgtg	cccgagggaac	cggccgcgag	120
ataagggcgg	cggaaggcg	ggcgacgatg	ccggtggcag	cgtcggccat	ctacttcctc	180
aaccttcgcg	gggacgtcct	catcaaccgc	ctctaccgtg	atgatgttg	gggaaatatg	240
gttgatgcgt	tcagaatgca	tatcatgcaa	acaaaagaac	ttggcacatg	ccctgttcgt	300
caaataggag	gctgctcctt	ccttttatatg	aggatcagta	atgtttacat	tgtgatcgta	360
gttagcagca	atgctaattg	tgcattgtct	ttcaaatttg	ttgtcgaggc	ggtaggtctc	420
ttcaagtcct	acttcggtg	agcttttgat	gaagacgcta	tcaggaataa	ctttgttttg	480
atatatgaac	ttcttgatga	gatcatggat	ttt			

(2) INFORMATION FOR SEQ ID NO:1755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755:

Met	Pro	Val	Ala	Ala	Ser	Ala	Ile	Tyr	Phe	Leu	Asn	Leu	Arg	Gly	Asp
1			5					10						15	
Val	Leu	Ile	Asn	Arg	Leu	Tyr	Arg	Asp	Asp	Val	Gly	Gly	Asn	Met	Val
			20					25					30		
Asp	Ala	Phe	Arg	Met	His	Ile	Met	Gln	Thr	Lys	Glu	Leu	Gly	Thr	Cys
			35				40					45			
Pro	Val	Arg	Gln	Ile	Gly	Gly	Cys	Ser	Phe	Leu	Tyr	Met	Arg	Ile	Ser
			50			55					60				
Asn	Val	Tyr	Ile	Val	Ile	Val	Val	Ser	Ser	Asn	Ala	Asn	Val	Ala	Cys
						70				75				80	
Xaa	Phe	Lys	Phe	Val	Glu	Ala	Val	Ala	Leu	Phe	Lys	Ser	Tyr	Phe	
			85					90					95		
Gly	Gly	Ala	Phe	Asp	Glu	Asp	Ala	Ile	Arg	Asn	Asn	Phe	Val	Leu	Ile
			100				105						110		
Tyr	Glu	Leu	Leu	Asp	Glu	Ile	Met	Asp	Phe						
			115				120								

(2) INFORMATION FOR SEQ ID NO:1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756:

Met	Val	Asp	Ala	Phe	Arg	Met	His	Ile	Met	Gln	Thr	Lys	Glu	Leu	Gly
1				5						10				15	

Thr Cys Pro Val Arg Gln Ile Gly Gly Cys Ser Phe Leu Tyr Met Arg
20 25 30
Ile Ser Asn Val Tyr Ile Val Ile Val Val Ser Ser Asn Ala Asn Val
35 40 45
Ala Cys Xaa Phe Lys Phe Val Val Glu Ala Val Ala Leu Phe Lys Ser
50 55 60
Tyr Phe Gly Gly Ala Phe Asp Glu Asp Ala Ile Arg Asn Asn Phe Val
65 70 75 80
Leu Ile Tyr Glu Leu Leu Asp Glu Ile Met Asp Phe
85 90

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..86
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757:

Met His Ile Met Gln Thr Lys Glu Leu Gly Thr Cys Pro Val Arg Gln
1 5 10 15
Ile Gly Gly Cys Ser Phe Leu Tyr Met Arg Ile Ser Asn Val Tyr Ile
20 25 30
Val Ile Val Val Ser Ser Asn Ala Asn Val Ala Cys Xaa Phe Lys Phe
35 40 45
Val Val Glu Ala Val Ala Leu Phe Lys Ser Tyr Phe Gly Gly Ala Phe
50 55 60
Asp Glu Asp Ala Ile Arg Asn Asn Phe Val Leu Ile Tyr Glu Leu Leu
65 70 75 80
Asp Glu Ile Met Asp Phe
85

(2) INFORMATION FOR SEQ ID NO:1758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..405
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758:

accagtcccc	tttacatcca	cacacaacgc	gcaccacacc	acaccacacc	acccgacgcc	60
aacgtccgag	accaaactcc	gatccccact	atgccggcgg	acggggaggg	gctggcgccg	120
gccgtccact	tctggggcga	gcacccggcc	acggaggcgg	agttctactc	ggcgcacggc	180
acggagggcg	agccctccta	cttcaccacg	cccgcgcggg	gcgcccggcg	gctcttcacg	240
cgcgcgtgga	ggccccgcgc	gcccgcgcgc	cccagggcgc	tcgtgttcat	ggtccacggc	300
tacggcaatg	acatcagctg	gacgttccag	tccacggcgg	tcttcctcgc	gcgggtccggg	360
ttcgctgct	tcgcggccga	cctcccgggc	cacggccgct	cccac		

(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1501059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759:

Thr	Ser	Pro	Leu	Tyr	Ile	His	Thr	Gln	Arg	Ala	Pro	His	His	Thr	Thr
1				5				10						15	
Pro	Pro	Asp	Ala	Asn	Val	Arg	Asp	Gln	Thr	Pro	Ile	Pro	Thr	Met	Pro
			20					25					30		
Ala	Asp	Gly	Glu	Ala	Leu	Ala	Pro	Ala	Val	His	Phe	Trp	Gly	Glu	His
		35					40					45			
Pro	Ala	Thr	Glu	Ala	Glu	Phe	Tyr	Ser	Ala	His	Gly	Thr	Glu	Gly	Glu
	50					55					60				
Pro	Ser	Tyr	Phe	Thr	Thr	Pro	Asp	Ala	Gly	Ala	Arg	Arg	Leu	Phe	Thr
65				70					75					80	
Arg	Ala	Trp	Arg	Pro	Arg	Ala	Pro	Xaa	Arg	Pro	Arg	Ala	Leu	Val	Phe
			85					90					95		
Met	Val	His	Gly	Tyr	Gly	Asn	Asp	Ile	Ser	Trp	Thr	Phe	Gln	Ser	Thr
		100						105					110		
Ala	Val	Phe	Leu	Ala	Arg	Ser	Gly	Phe	Ala	Cys	Phe	Ala	Ala	Asp	Leu
		115					120					125			
Pro	Gly	His	Gly	Arg	Ser	His									
	130					135									

(2) INFORMATION FOR SEQ ID NO:1760:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1501060

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760:

Pro	Val	Pro	Phe	Thr	Ser	Thr	His	Asn	Ala	His	His	Thr	Thr	Pro	His
1				5				10						15	
His	Pro	Thr	Pro	Thr	Ser	Glu	Thr	Lys	Leu	Arg	Ser	Pro	Leu	Cys	Arg
			20					25					30		
Arg	Thr	Gly	Arg	Arg	Trp	Arg	Arg	Pro	Ser	Thr	Ser	Gly	Ala	Ser	Thr
		35				40						45			
Arg	Pro	Arg	Arg	Arg	Ser	Ser	Thr	Arg	Arg	Thr	Ala	Arg	Arg	Ala	Ser
	50					55					60				
Pro	Pro	Thr	Ser	Pro	Arg	Pro	Thr	Arg	Ala	Pro	Gly	Gly	Ser	Ser	Arg
65				70					75					80	
Ala	Arg	Gly	Gly	Pro	Ala	Arg	Pro	Xaa	Gly	Pro	Gly	Arg	Ser	Cys	Ser
			85					90					95		
Trp	Ser	Thr	Ala	Thr	Ala	Met	Thr	Ser	Ala	Gly	Arg	Ser	Ser	Pro	Arg
		100						105					110		
Arg	Ser	Ser	Ser	Arg	Gly	Pro	Gly	Ser	Pro	Ala	Ser	Arg	Pro	Thr	Ser
		115					120					125			
Arg	Ala	Thr	Ala	Ala	Pro										
		130													

(2) INFORMATION FOR SEQ ID NO:1761:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1501061

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761:

```
Met Pro Ala Asp Gly Glu Ala Leu Ala Pro Ala Val His Phe Trp Gly
1      5      10      15
Glu His Pro Ala Thr Glu Ala Glu Phe Tyr Ser Ala His Gly Thr Glu
20     25     30
Gly Glu Pro Ser Tyr Phe Thr Thr Pro Asp Ala Gly Ala Arg Arg Leu
35     40     45
Phe Thr Arg Ala Trp Arg Pro Arg Ala Pro Xaa Arg Pro Arg Ala Leu
50     55     60
Val Phe Met Val His Gly Tyr Gly Asn Asp Ile Ser Trp Thr Phe Gln
65     70     75     80
Ser Thr Ala Val Phe Leu Ala Arg Ser Gly Phe Ala Cys Phe Ala Ala
85     90     95
Asp Leu Pro Gly His Gly Arg Ser His
100    105
```

(2) INFORMATION FOR SEQ ID NO:1762:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..503

(D) OTHER INFORMATION: / Ceres Seq. ID 1501090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762:

```
aacttcaacg agtcccatatt tggcaaggct tcggagtacc aaactggcga attgcgacgt      60
tggcggaatt gtaatggcaa taattccttc ctcccttcgtt ccccatattct cctctttcta      120
ggtttctacc cctcatcggt cctcgctcca cggccatggt gaggatgaag caggtaaaga      180
tctcggtaaa gaaggacgtg gattcggtaca caatccgcgg cactaacaag gtcgtccatg      240
tgggcgactg cgtgctgatg cgggcgctcg actcggacaa gcagccgtat gtrgcgcggg      300
tggaagaagat ggargccgac ggacgcggca gstgncgggt rcaggtrcgc tgggtactacc      360
gccctgagga atccaagggc ggtcgcgggc agttccacgg cgccaaggag cttttccttt      420
ccgatcattt cgacctacag arcgcccaca ccatcgaggg gaaatgtgtt gtccactctt      480
tcaagaacta caccaagctt gat
```

(2) INFORMATION FOR SEQ ID NO:1763:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1501091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763:

```
Met Val Arg Met Lys Gln Val Lys Ile Ser Val Lys Lys Asp Val Asp
1      5      10      15
Ser Tyr Thr Ile Arg Gly Thr Asn Lys Val Val His Val Gly Asp Cys
20     25     30
Val Leu Met Arg Ala Ser Asp Ser Asp Lys Gln Pro Tyr Xaa Ala Arg
35     40     45
Val Glu Lys Met Xaa Ala Asp Gly Arg Gly Xaa Xaa Arg Xaa Gln Xaa
50     55     60
Arg Trp Tyr Tyr Arg Pro Glu Glu Ser Lys Gly Gly Arg Arg Gln Phe
65     70     75     80
His Gly Ala Lys Glu Leu Phe Leu Ser Asp His Phe Asp Leu Gln Xaa
```

85 90 95
Ala His Thr Ile Glu Gly Lys Cys Val Val His Ser Phe Lys Asn Tyr
100 105 110
Thr Lys Leu Asp
115

(2) INFORMATION FOR SEQ ID NO:1764:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1501092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764:

Met Lys Gln Val Lys Ile Ser Val Lys Lys Asp Val Asp Ser Tyr Thr
1 5 10 15
Ile Arg Gly Thr Asn Lys Val Val His Val Gly Asp Cys Val Leu Met
20 25 30
Arg Ala Ser Asp Ser Asp Lys Gln Pro Tyr Xaa Ala Arg Val Glu Lys
35 40 45
Met Xaa Ala Asp Gly Arg Gly Xaa Xaa Arg Xaa Gln Xaa Arg Trp Tyr
50 55 60
Tyr Arg Pro Glu Glu Ser Lys Gly Gly Arg Arg Gln Phe His Gly Ala
65 70 75 80
Lys Glu Leu Phe Leu Ser Asp His Phe Asp Leu Gln Xaa Ala His Thr
85 90 95
Ile Glu Gly Lys Cys Val Val His Ser Phe Lys Asn Tyr Thr Lys Leu
100 105 110
Asp

(2) INFORMATION FOR SEQ ID NO:1765:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1501093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765:

Met Arg Ala Ser Asp Ser Asp Lys Gln Pro Tyr Xaa Ala Arg Val Glu
1 5 10 15
Lys Met Xaa Ala Asp Gly Arg Gly Xaa Xaa Arg Xaa Gln Xaa Arg Trp
20 25 30
Tyr Tyr Arg Pro Glu Glu Ser Lys Gly Gly Arg Arg Gln Phe His Gly
35 40 45
Ala Lys Glu Leu Phe Leu Ser Asp His Phe Asp Leu Gln Xaa Ala His
50 55 60
Thr Ile Glu Gly Lys Cys Val Val His Ser Phe Lys Asn Tyr Thr Lys
65 70 75 80
Leu Asp

(2) INFORMATION FOR SEQ ID NO:1766:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 547 base pairs

(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..547
(D) OTHER INFORMATION: / Ceres Seq. ID 1501115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766:

```
acgccaccgc cacctccacc tcctcgaaac cgccgcgacc gatcgagcga abwcncccttc      60
ccgcgcccgc gccgaaaccc tagctcctct tacgccatgg ccaccgtgtc gctcactcgg      120
caggcggtct tctccaccga gtccggcggc gccctggctt ctgccaccat cctccgcttc      180
ccgccaaact tcgtacgcca gctcagcacc aaggcacgac gcaactgcag caacatcggc      240
gtcgcgcaga tcgtcgccgc cgcgtgggtc gactgcctcg ctgctcgccg cctccgcggs      300
gcggnatgtc agcgcaattc ctaacgctaa ggttgcgcas cgtccgccgt cgtattggcc      360
gagcgtaacc tgctcggttc cgacgccagc ctcgccgtcc acgcggggga raggtckgga      420
agaaggatag ccacggatgc tatcaccacg ccggtagtga acacgtcggc ctactgggtc      480
aacaactcgc aagagctaata cgactttaan gagggggargc atgctagctt cgagtatggg      540
aggtatk
```

(2) INFORMATION FOR SEQ ID NO:1767:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..107
(D) OTHER INFORMATION: / Ceres Seq. ID 1501116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767:

```
Thr Pro Pro Pro Pro Pro Pro Pro Arg Asn Arg Arg Asp Arg Ser Ser
1      5      10      15
Glu Xaa Xaa Phe Pro Arg Arg Arg Arg Asn Pro Ser Ser Ser Tyr Ala
20     25     30
Met Ala Thr Val Ser Leu Thr Pro Gln Ala Val Phe Ser Thr Glu Ser
35     40     45
Gly Gly Ala Leu Ala Ser Ala Thr Ile Leu Arg Phe Pro Pro Asn Phe
50     55     60
Val Arg Gln Leu Ser Thr Lys Ala Arg Arg Asn Cys Ser Asn Ile Gly
65     70     75     80
Val Ala Gln Ile Val Ala Ala Ala Trp Ser Asp Cys Leu Ala Ala Arg
85     90     95
Arg Leu Arg Xaa Ala Xaa Cys Gln Arg Asn Ser
100    105
```

(2) INFORMATION FOR SEQ ID NO:1768:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..142
(D) OTHER INFORMATION: / Ceres Seq. ID 1501117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768:

```
Arg His Arg His Leu His Leu Leu Glu Thr Ala Ala Thr Asp Arg Ala
1      5      10      15
Xaa Xaa Pro Ser Arg Ala Asp Ala Glu Thr Leu Ala Pro Leu Thr Pro
20     25     30
Trp Pro Pro Cys Arg Ser Leu Arg Arg Arg Ser Ser Pro Pro Ser Pro
```

35 40 45
Ala Ala Pro Trp Leu Leu Pro Pro Ser Ser Ala Ser Arg Gln Thr Ser
50 55 60
Tyr Ala Ser Ser Ala Pro Arg His Asp Ala Thr Ala Ala Thr Ser Ala
65 70 75 80
Ser Arg Arg Ser Ser Pro Pro Arg Gly Pro Thr Ala Ser Leu Leu Ala
85 90 95
Ala Ser Ala Xaa Arg Xaa Val Ser Ala Ile Pro Asn Ala Lys Val Ala
100 105 110
Xaa Arg Pro Pro Ser Tyr Trp Pro Ser Val Thr Cys Ser Ala Pro Thr
115 120 125
Pro Ala Ser Pro Ser Thr Arg Gly Xaa Gly Xaa Glu Glu Gly
130 135 140

(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..75
(D) OTHER INFORMATION: / Ceres Seq. ID 1501118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769:

Met Ala Thr Val Ser Leu Thr Pro Gln Ala Val Phe Ser Thr Glu Ser
1 5 10 15
Gly Gly Ala Leu Ala Ser Ala Thr Ile Leu Arg Phe Pro Pro Asn Phe
20 25 30
Val Arg Gln Leu Ser Thr Lys Ala Arg Arg Asn Cys Ser Asn Ile Gly
35 40 45
Val Ala Gln Ile Val Ala Ala Trp Ser Asp Cys Leu Ala Ala Arg
50 55 60
Arg Leu Arg Xaa Ala Xaa Cys Gln Arg Asn Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:1770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..921
(D) OTHER INFORMATION: / Ceres Seq. ID 1501119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770:

artagcttcr cwccrrcctc crggggctcc gcrgetccgc tagtccgctc cggcgccacg 60
gcccggctcg gaggggcggtt tcggggaggg cgaacgganc gccagcgttt ccgtttgggtt 120
ggcgtggagg cgaactgctg ctggagcgct acccgggttt cctccggttca ctacgctcg 180
cgatctgatg atcgttggct agttgctctg ccagartccc agccagcgct cctccgccat 240
gatccargcg gtgatggtga tcagcaccca ggccaagccc cgccttctca agttctacag 300
tttccagcca cccgagaagc atcaggacct cgtccgctgt gtcttccaat tactctctgc 360
aaggccccgag agcgcgagca attttgtcaa ggtggactcc atctttggcc cgggaacaaa 420
aatggtctac aagcatttgg gccacactat actttgtttt tgtctttgat agctctgaga 480
acgagcttgc catgctcgac ctctgacaag tgtttgttga aacattggac agatgcttca 540
agaatgtatg cgagcttgac atcgtattta acttcaacaa gctgcacacc attttggatg 600
agatgatata ggggggacag gtgatcgaaa caagttcaga acagataatg aaatctgttg 660
aagagattga aaggctggag aaacaatcga gcacaaccag cttcataccc aagtcgatta 720
cagagcgttt tacccggttga gcttccactc gtttccagaa caatgtgaca ttttaaggtgt 780
gaacagaact gagatatact attcagctctc attttagttc tccgataaga ccttgtatgc 840

ccccgcccc cggtgtatt ctgtaagcct gtaacctgga tatgaatgcg gcattctgcag 900
tccaataata ctgcctgcgt t

(2) INFORMATION FOR SEQ ID NO:1771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771:

Met	Ile	Xaa	Ala	Val	Met	Val	Ile	Ser	Thr	Gln	Ala	Lys	Pro	Arg	Leu
1				5					10					15	
Leu	Lys	Phe	Tyr	Ser	Phe	Gln	Pro	Pro	Glu	Lys	His	Gln	Asp	Leu	Val
		20					25						30		
Arg	Cys	Val	Phe	Gln	Leu	Leu	Ser	Ala	Arg	Pro	Glu	Ser	Ala	Ser	Asn
		35				40						45			
Phe	Val	Lys	Val	Asp	Ser	Ile	Phe	Gly	Pro	Gly	Thr	Lys	Met	Val	Tyr
	50					55					60				
Lys	His	Leu	Gly	His	Thr	Ile	Leu	Cys	Phe	Cys	Leu				
65				70						75					

(2) INFORMATION FOR SEQ ID NO:1772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772:

Met	Val	Ile	Ser	Thr	Gln	Ala	Lys	Pro	Arg	Leu	Leu	Lys	Phe	Tyr	Ser
1				5					10					15	
Phe	Gln	Pro	Pro	Glu	Lys	His	Gln	Asp	Leu	Val	Arg	Cys	Val	Phe	Gln
		20					25						30		
Leu	Leu	Ser	Ala	Arg	Pro	Glu	Ser	Ala	Ser	Asn	Phe	Val	Lys	Val	Asp
		35				40						45			
Ser	Ile	Phe	Gly	Pro	Gly	Thr	Lys	Met	Val	Tyr	Lys	His	Leu	Gly	His
	50					55					60				
Thr	Ile	Leu	Cys	Phe	Cys	Leu									
65				70											

(2) INFORMATION FOR SEQ ID NO:1773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1773:

Met	Leu	Asp	Leu	Val	Gln	Val	Phe	Val	Glu	Thr	Leu	Asp	Arg	Cys	Phe
1				5					10					15	
Lys	Asn	Val	Cys	Glu	Leu	Asp	Ile	Val	Phe	Asn	Phe	Asn	Lys	Leu	His

	20		25		30										
Thr	Ile	Leu	Asp	Glu	Met	Ile	Ser	Gly	Gly	Gln	Val	Ile	Glu	Thr	Ser
	35						40						45		
Ser	Glu	Gln	Ile	Met	Lys	Ser	Val	Glu	Glu	Ile	Glu	Arg	Leu	Glu	Lys
	50					55					60				
Gln	Ser	Ser	Thr	Thr	Ser	Phe	Ile	Pro	Lys	Ser	Ile	Thr	Glu	Arg	Phe
65					70					75				80	
Thr	Arg														

(2) INFORMATION FOR SEQ ID NO:1774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..352
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774:

acagagggat	cgatcatccgc	cccacccaca	actgctccag	atccaggcac	ggcacggcac	60
ggcagccggg	ccaacccaag	cccgtcttct	cttctctctc	gtccgtccct	cactcgccgc	120
gacgtgacaa	gacaacgcga	cgcgcgcgca	satnancgtc	gtccaaggca	cgcaggggcc	180
agccaaccaa	tcgcgtccgt	ccgggtcttg	tggtggcccg	aatgggcctc	ctcgatcagc	240
tctgggacga	gacggtggcc	ggcccgcgac	cggactccgg	cctcggcaag	ctccgcaagt	300
actctcctt	ctccccctcc	tcctcctcgt	cgtcgtccat	cctggctccc	gc	

(2) INFORMATION FOR SEQ ID NO:1775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775:

Thr	Glu	Gly	Ser	Ser	Ser	Ala	Pro	Pro	Thr	Thr	Ala	Pro	Asp	Pro	Gly
1			5						10					15	
Thr	Ala	Arg	His	Gly	Ser	Arg	Ala	Asn	Pro	Ser	Pro	Ser	Ser	Leu	Leu
			20					25					30		
Ser	Arg	Pro	Ser	Leu	Thr	Arg	Arg	Asp	Val	Thr	Arg	Gln	Arg	Asp	Ala
		35					40					45			
Arg	Ala	Xaa	Xaa	Arg	Arg	Pro	Arg	His	Ala	Gly	Ala	Ser	Gln	Pro	Ile
	50				55					60					
Ala	Ser	Val	Arg	Val	Trp	Trp	Trp	Pro	Glu	Trp	Ala	Ser	Ser	Ile	Ser
65				70						75				80	
Ser	Gly	Thr	Arg	Arg	Trp	Pro	Ala	Arg	Asp	Arg	Thr	Pro	Ala	Ser	Ala
			85					90						95	
Ser	Ser	Ala	Ser	Thr	Pro	Pro	Ser	Pro	Pro	Pro	Pro	Pro	Arg	Arg	Arg
		100					105						110		
Pro	Ser	Trp	Leu	Pro											
			115												

(2) INFORMATION FOR SEQ ID NO:1776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1501125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776:

```
Arg Gly Ile Val Ile Arg Pro Thr His Asn Cys Ser Arg Ser Arg His
1           5           10           15
Gly Thr Ala Arg Gln Pro Gly Gln Pro Lys Pro Val Phe Ser Ser Leu
          20          25          30
Ser Ser Val Pro His Ser Pro Arg Asp Lys Thr Thr Arg Arg Ala
          35          40          45
Arg Xaa Xaa Xaa Ser Ser Lys Ala Arg Arg Gly Gln Pro Thr Asn Arg
          50          55          60
Val Arg Pro Gly Leu Val Val Ala Gly Met Gly Leu Leu Asp Gln Leu
          65          70          75          80
Trp Asp Glu Thr Val Ala Gly Pro Arg Pro Asp Ser Gly Leu Gly Lys
          85          90          95
Leu Arg Lys Tyr Ser Ser Phe Ser Pro Ser Ser Ser Ser Ser Ser
          100         105         110
Ile Leu Ala Pro
          115
```

(2) INFORMATION FOR SEQ ID NO:1777:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 477 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1501137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777:

```
acaaacgaac aaggcattaa tctcctccaa tctccagtg atcccgggta accaaatcaa      60
atcagccctt tcttttgcta cggttttgta ttcatcgtg tcgccaaga aaatcgaagg      120
aacgcgccgc caccggccgc aacaaagcaa agcaggcctc cggtccctg aactgacttc      180
agaagtcacc aacgcaccca gcacagacag aagaccctcg ccggacgctc gctctcgccg      240
gggacaactc aatcccgagg ccaggatggc ccgctacgat cgcgcgatca ccgtgttctc      300
acccgacggc cacctcttcc aggtcgagta cgccctcgag gccgtccgca agggcaacgc      360
cgctgtcggc gtccgcggcg tcgacaccgt cgtcctcggc gtcgagaaga agtccacccc      420
caagctccag gactccaggt ccgtcgcgaa gatcgtkage ctggacaccc acatcgc
```

(2) INFORMATION FOR SEQ ID NO:1778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1501138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778:

```
Gln Thr Asn Lys Ala Leu Ile Ser Ser Asn Pro Pro Val Ile Pro Gly
1           5           10           15
Asn Gln Ile Lys Ser Ala Leu Ser Phe Ala Thr Val Leu Tyr Phe Ile
          20          25          30
Val Ser Pro Lys Lys Ile Glu Gly Thr Arg Arg His Arg Pro Gln Gln
          35          40          45
Ser Lys Ala Gly Leu Arg Leu Pro Glu Leu Thr Ser Glu Val Thr Asn
```

50	55	60
Ala Pro Ser Thr Asp Arg Arg Pro Ser Pro Asp Ala Arg Ser Arg Arg		
65	70	75
Gly Gln Leu Asn Pro Glu Ala Arg Met Ala Arg Tyr Asp Arg Ala Ile		80
	85	90
Thr Val Phe Ser Pro Asp Gly His Leu Phe Gln Val Glu Tyr Ala Leu		95
	100	105
Glu Ala Val Arg Lys Gly Asn Ala Ala Val Gly Val Arg Gly Val Asp		110
	115	120
Thr Val Val Leu Gly Val Glu Lys Lys Ser Thr Pro Lys Leu Gln Asp		125
	130	135
Ser Arg Ser Xaa Arg Lys Ile Xaa Ser Leu Asp Thr His Ile		140
145	150	155

(2) INFORMATION FOR SEQ ID NO:1779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..442
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779:

atcatgcatt	cttcatggcg	acggtgacca	gtttgagctt	ctcaggcagc	tgcagacacg	60
ggccacgcta	tactgcccgg	ccggcggcag	ttctcgtagt	agtcagctac	ttaatgatca	120
gctagctaga	gcatacgcgna	gattacaagt	ngcggcgggc	atggcggtgg	cggcgttccc	180
ttcctgcggc	gccttcgccc	ctccttgccct	agttagtaca	aggagagcct	tctcctcgggt	240
ggtggccatg	gcttcgcgag	ccccggtgag	agctcccagc	aggaagccct	tcgcccctcc	300
tcgcgaggta	caccgccccg	tggcgcactc	gctgcccccg	cagaagcggg	agatcttcga	360
gtcgtctgar	tcgtggggcg	cggacaacat	cctggtgctc	ctcaagcccc	tggagaggtc	420
ctggcagccg	cagactacct	gc				

(2) INFORMATION FOR SEQ ID NO:1780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780:

Ser Cys Ile Leu His Gly Asp Gly Asp Gln Phe Glu Leu Leu Arg Gln		
1	5	10
Leu Gln Thr Arg Ala Thr Leu Tyr Cys Pro Ala Gly Gly Ser Ser Arg		15
	20	25
Ser Ser Gln Leu Leu Asn Asp Gln Leu Ala Arg Ala Ser Xaa Arg Leu		30
	35	40
Gln Xaa Ala Ala Gly Met Ala Val Ala Ala Phe Pro Ser Cys Gly Ala		45
	50	55
Phe Ala Pro Pro Cys Leu Val Ser Thr Arg Arg Ala Phe Ser Ser Val		60
65	70	75
Val Ala Met Ala Ser Ala Ala Pro Val Arg Ala Pro Ser Arg Lys Pro		80
	85	90
Phe Ala Pro Pro Arg Glu Val His Arg Pro Val Ala His Ser Leu Pro		95
	100	105
Pro Gln Lys Arg Glu Ile Phe Glu Ser Leu Xaa Ser Trp Ala Ala Asp		110
	115	120
		125

Asn Ile Leu Val Leu Leu Lys Pro Val Glu Arg Ser Trp Gln Pro Gln
130 135 140
Thr Thr Cys
145

(2) INFORMATION FOR SEQ ID NO:1781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781:

Met Ala Val Ala Ala Phe Pro Ser Cys Gly Ala Phe Ala Pro Pro Cys
1 5 10 15
Leu Val Ser Thr Arg Arg Ala Phe Ser Ser Val Val Ala Met Ala Ser
20 25 30
Ala Ala Pro Val Arg Ala Pro Ser Arg Lys Pro Phe Ala Pro Pro Arg
35 40 45
Glu Val His Arg Pro Val Ala His Ser Leu Pro Pro Gln Lys Arg Glu
50 55 60
Ile Phe Glu Ser Leu Xaa Ser Trp Ala Ala Asp Asn Ile Leu Val Leu
65 70 75 80
Leu Lys Pro Val Glu Arg Ser Trp Gln Pro Gln Thr Thr Cys
85 90

(2) INFORMATION FOR SEQ ID NO:1782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..464

(D) OTHER INFORMATION: / Ceres Seq. ID 1501142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782:

atcgcccgcn gtccctctcct ctccctccccg gcccccttcac tccaccaacg aacccccacgc 60
aggcagcagc acgcgcaasc gcaaggaagg cacaaacact annngccggg catggcgacg 120
cgggcgagc tggagaaggg cgggcccggc aggaaggagc ccggcaagggt gccgtcgccg 180
ctgtaccgc agcacgargg ggagcgggag tnggtgccct ggctcgctccc cgctcatcttc 240
gtcgccagca tcaccgtctt cgctgctacc atgtacgcca acaactgcmc cgcgcgcgac 300
accaacaagt gcgtcgccc cttcctcggm cgcttctcct tccagccgct gcgacagaac 360
ccgctcttcg ggccctcctc cgccacgctc accaagatgg gggccctggt gtgggagaag 420
gtggtgcacc gccaccaggg ctggcgccctc ctctccagca tgtk

(2) INFORMATION FOR SEQ ID NO:1783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1501143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1783:

Ile Ala Arg Xaa Pro Leu Leu Ser Ser Pro Ala Pro Ser Leu His Gln

1		5		10		15									
Arg	Thr	Pro	Arg	Arg	Gln	Gln	His	Ala	Gln	Xaa	Gln	Gly	Arg	His	Lys
		20						25					30		
His	Xaa	Xaa	Pro	Gly	Met	Ala	Thr	Arg	Ala	Asp	Val	Glu	Lys	Gly	Gly
		35						40				45			
Pro	Ala	Arg	Lys	Glu	Pro	Gly	Lys	Val	Pro	Ser	Pro	Leu	Tyr	Pro	Gln
		50					55				60				
His	Xaa	Gly	Glu	Arg	Glu	Xaa	Val	Pro	Trp	Leu	Val	Pro	Val	Ile	Phe
65					70					75					80
Val	Ala	Ser	Ile	Thr	Val	Phe	Val	Val	Thr	Met	Tyr	Ala	Asn	Asn	Cys
			85						90					95	
Xaa	Ala	Arg	Asp	Thr	Asn	Lys	Cys	Val	Ala	Arg	Phe	Leu	Xaa	Arg	Phe
			100						105				110		
Ser	Phe	Gln	Pro	Leu	Arg	Gln	Asn	Pro	Leu	Phe	Gly	Pro	Ser	Ser	Ala
		115					120					125			
Thr	Leu	Thr	Lys	Met	Gly	Ala	Leu	Val	Trp	Glu	Lys	Val	Val	His	Arg
		130					135					140			
His	Gln	Gly	Trp	Arg	Leu	Leu	Ser	Ser	Met						
145					150										

(2) INFORMATION FOR SEQ ID NO:1784:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1501144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784:

Ser	Pro	Xaa	Val	Leu	Ser	Ser	Pro	Pro	Arg	Pro	Leu	His	Ser	Thr	Asn
1			5						10					15	
Glu	Pro	His	Ala	Gly	Ser	Ser	Thr	Arg	Xaa	Arg	Lys	Glu	Gly	Thr	Asn
		20						25				30			
Thr	Xaa	Xaa	Arg	Ala	Trp	Arg	Arg	Gly	Arg	Thr	Trp	Arg	Arg	Ala	Gly
		35					40				45				
Arg	Arg	Gly	Arg	Ser	Pro	Ala	Arg	Cys	Arg	Arg	Arg	Cys	Thr	Arg	Ser
		50					55				60				
Thr	Xaa	Gly	Ser	Gly	Ser	Xaa	Cys	Pro	Gly	Ser	Ser	Pro	Ser	Ser	Ser
65					70					75					80
Ser	Pro	Ala	Ser	Pro	Ser	Ser	Ser	Ser	Pro	Cys	Thr	Pro	Thr	Thr	Xaa
			85						90					95	
Pro	Arg	Ala	Thr	Pro	Thr	Ser	Ala	Ser	Pro	Ala	Ser	Ser	Xaa	Ala	Ser
		100							105				110		
Pro	Ser	Ser	Arg	Cys	Asp	Arg	Thr	Arg	Ser	Ser	Gly	Pro	Pro	Pro	Pro
		115					120					125			
Arg	Ser	Pro	Arg	Trp	Gly	Pro	Trp	Cys	Gly	Arg	Arg	Trp	Cys	Thr	Ala
		130					135					140			
Thr	Arg	Ala	Gly	Ala	Ser	Ser	Pro	Ala	Cys						
145					150										

(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1501145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785:

Arg Pro Xaa Ser Ser Pro Leu Leu Pro Gly Pro Phe Thr Pro Pro Thr
1 5 10 15
Asn Pro Thr Gln Ala Ala Ala Arg Ala Xaa Ala Arg Lys Ala Gln Thr
20 25 30
Leu Xaa Ala Gly His Gly Asp Ala Gly Gly Arg Gly Glu Gly Arg Ala
35 40 45
Gly Glu Glu Gly Ala Arg Gln Gly Ala Val Ala Ala Val Pro Ala Ala
50 55 60
Arg Xaa Gly Ala Gly Xaa Gly Ala Leu Ala Arg Pro Arg His Leu Arg
65 70 75 80
Arg Gln His His Arg Leu Arg Arg His His Val Arg Gln Gln Leu Xaa
85 90 95
Arg Ala Arg His Gln Gln Val Arg Arg Pro Leu Pro Arg Xaa Leu Leu
100 105 110
Leu Pro Ala Ala Ala Thr Glu Pro Ala Leu Arg Ala Leu Leu Arg His
115 120 125
Ala His Gln Asp Gly Gly Pro Gly Val Gly Glu Gly Gly Ala Pro Pro
130 135 140
Pro Gly Leu Ala Pro Pro Leu Gln His
145 150

(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..480
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786:

ttctcgccct accatcgccct gaccgacgcg cccgttttct cctgaaaaca gaaggctccg	60
gcctccggca tccgccaaaa aggggaaaaa aggagagata acacacacac acacaaaccc	120
caatcccctg cggcgccgat ggacccgtca tcggcgggct ccggcggcaa ctccctcccg	180
tccgtcggcc ccgacgggca gaagcggcgc gtgtgtact tctacgacc ggatgtgggc	240
aactactact acgggcagg ccattccgat aagccgcacc gcatccggat gacgcactcg	300
ctgctggcgc gctacggcct cctcaaccag atgcaggtgt accgccccaa cccggccccgc	360
gaccgcgacc tctgccgctt ccacgccgac gactacatca acttctgcg ctccgtcacg	420
ccggaaacgc agcaggacca gatccgcctg ctcaagcgct tcaacgtcgc cgaggactgc	480

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787:

Met Asp Pro Ser Ser Ala Gly Ser Gly Gly Asn Ser Leu Pro Ser Val
1 5 10 15
Gly Pro Asp Gly Gln Lys Arg Arg Val Cys Tyr Phe Tyr Asp Pro Asp
20 25 30
Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro His Arg
35 40 45

Ile Arg Met Thr His Ser Leu Leu Ala Arg Tyr Gly Leu Leu Asn Gln
50 55 60
Met Gln Val Tyr Arg Pro Asn Pro Ala Arg Asp Arg Asp Leu Cys Arg
65 70 75 80
Phe His Ala Asp Asp Tyr Ile Asn Phe Leu Arg Ser Val Thr Pro Glu
85 90 95
Thr Gln Gln Asp Gln Ile Arg Leu Leu Lys Arg Phe Asn Val Gly Glu
100 105 110
Asp Cys

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1501165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788:

Met Lys Pro His Arg Ile Arg Met Thr His Ser Leu Leu Ala Arg Tyr
1 5 10 15
Gly Leu Leu Asn Gln Met Gln Val Tyr Arg Pro Asn Pro Ala Arg Asp
20 25 30
Arg Asp Leu Cys Arg Phe His Ala Asp Asp Tyr Ile Asn Phe Leu Arg
35 40 45
Ser Val Thr Pro Glu Thr Gln Gln Asp Gln Ile Arg Leu Leu Lys Arg
50 55 60
Phe Asn Val Gly Glu Asp Cys
65 70

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1501166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789:

Met Thr His Ser Leu Leu Ala Arg Tyr Gly Leu Leu Asn Gln Met Gln
1 5 10 15
Val Tyr Arg Pro Asn Pro Ala Arg Asp Arg Asp Leu Cys Arg Phe His
20 25 30
Ala Asp Asp Tyr Ile Asn Phe Leu Arg Ser Val Thr Pro Glu Thr Gln
35 40 45
Gln Asp Gln Ile Arg Leu Leu Lys Arg Phe Asn Val Gly Glu Asp Cys
50 55 60

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..520

(D) OTHER INFORMATION: / Ceres Seq. ID 1501167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790:

atctcacttt	ctttctcgct	gcgtccgcca	tgctctcgct	ttccttctct	ctgctttgct	60
tttgtgtcgt	cgatgtcgaa	aactccttcc	agaccaagct	tcgtctgctg	tcggcttgca	120
ccagtcctca	cggcccacgt	cgagggagac	gaagggatag	gaggcggagg	cggaggttgc	180
aaaaaatggt	cgggagcatg	caggcggtgg	acccagcggg	ccggataagc	gcgttgctcg	240
cattgcgcca	stcctcgcca	tgetctagcc	gctggccctg	ctccgccctt	tcattggcgc	300
gcgtggccgg	ggcgtccgat	gttgccgctt	ccgcgttggg	gctagcggga	aaaggggaag	360
gcggcgcgct	cagtrgttct	acgggtgccg	gccgtctcgc	ccatggtcgc	cacacgaagg	420
aagatagcca	cgcgcgggac	gcaggaggcc	ggggcggggtg	tacgagctga	tccccaggta	480
gtgaacatgt	tccatctctt	gcctattctg	ttcctctctg			

(2) INFORMATION FOR SEQ ID NO:1791:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1501168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791:

Leu	Thr	Phe	Phe	Ala	Ala	Ser	Ala	Met	Leu	Ser	Leu	Ser	Phe	Ser
1			5					10					15	
Leu	Leu	Cys	Phe	Cys	Val	Val	Asp	Val	Glu	Asn	Ser	Phe	Gln	Thr
			20					25					30	Lys
Leu	Arg	Leu	Leu	Ser	Ala	Cys	Thr	Ser	Pro	His	Gly	Pro	Arg	Arg
			35				40					45		Gly
Arg	Arg	Arg	Asp	Arg	Arg	Arg	Arg	Arg	Arg	Leu	Gln	Lys	Met	Val
			50				55				60			Gly
Ser	Met	Gln	Ala	Val	Asp	Pro	Ala	Gly	Arg	Ile	Ser	Ala	Leu	Leu
			65				70			75			80	Ala
Leu	Arg	Xaa	Ser	Ser	Pro	Cys	Ser	Ser	Arg	Trp	Pro	Cys	Ser	Ala
			85						90				95	Leu
Ser	Leu	Ala	Arg	Val	Ala	Gly	Ala	Ser	Asp	Val	Ala	Ala	Ser	Ala
			100				105						110	Leu
Gly	Leu	Ala	Gly	Lys	Gly	Glu	Gly	Gly	Gly	Val	Ser	Xaa	Ser	Thr
			115				120					125		Gly
Ala	Gly	Arg	Leu	Ala	His	Gly	Arg	His	Thr	Lys	Glu	Asp	Ser	His
			130				135					140		Ala
Pro	Asp	Ala	Gly	Gly	Arg	Gly	Gly	Cys	Thr	Ser				
			145				150			155				

(2) INFORMATION FOR SEQ ID NO:1792:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1501169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792:

Met	Leu	Ser	Leu	Ser	Phe	Ser	Leu	Leu	Cys	Phe	Cys	Val	Val	Asp	Val
1			5					10						15	
Glu	Asn	Ser	Phe	Gln	Thr	Lys	Leu	Arg	Leu	Leu	Ser	Ala	Cys	Thr	Ser

20 25 30
Pro His Gly Pro Arg Arg Gly Arg Arg Arg Asp Arg Arg Arg Arg Arg
35 40 45
Arg Leu Gln Lys Met Val Gly Ser Met Gln Ala Val Asp Pro Ala Gly
50 55 60
Arg Ile Ser Ala Leu Leu Ala Leu Arg Xaa Ser Ser Pro Cys Ser Ser
65 70 75 80
Arg Trp Pro Cys Ser Ala Leu Ser Leu Ala Arg Val Ala Gly Ala Ser
85 90 95
Asp Val Ala Ala Ser Ala Leu Gly Leu Ala Gly Lys Gly Glu Gly Gly
100 105 110
Gly Val Ser Xaa Ser Thr Gly Ala Gly Arg Leu Ala His Gly Arg His
115 120 125
Thr Lys Glu Asp Ser His Ala Pro Asp Ala Gly Gly Arg Gly Gly Cys
130 135 140
Thr Ser
145

(2) INFORMATION FOR SEQ ID NO:1793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..94
(D) OTHER INFORMATION: / Ceres Seq. ID 1501170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793:

Met Val Gly Ser Met Gln Ala Val Asp Pro Ala Gly Arg Ile Ser Ala
1 5 10 15
Leu Leu Ala Leu Arg Xaa Ser Ser Pro Cys Ser Ser Arg Trp Pro Cys
20 25 30
Ser Ala Leu Ser Leu Ala Arg Val Ala Gly Ala Ser Asp Val Ala Ala
35 40 45
Ser Ala Leu Gly Leu Ala Gly Lys Gly Glu Gly Gly Val Ser Xaa
50 55 60
Ser Thr Gly Ala Gly Arg Leu Ala His Gly Arg His Thr Lys Glu Asp
65 70 75 80
Ser His Ala Pro Asp Ala Gly Gly Arg Gly Gly Cys Thr Ser
85 90

(2) INFORMATION FOR SEQ ID NO:1794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..462
(D) OTHER INFORMATION: / Ceres Seq. ID 1501203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794:

arctgcagcc agagccaccc accttatcgt catcctcgct cgctcctcat cgccagcgcc 60
tcctcctcct cctccttctt ccccaccgct gccgacatgg ctgcgcaaga agagaagacc 120
gctgttggtg ttgctgctgc tgccgatgtc gcgacagagg agcctacgcc ggcggsgagc 180
agcaacctca gccggtggtg gcggcgcgca ggcgaggacc atcgggcgcc ggcggggctc 240
cgccaacccc ttcgacttct ccaccatgat gaaccttctc aatgacccta gcatcaagga 300
gatggcagag cagatcgcca aggaccggc gttcacggag atggcgasa gctgcagaag 360
acgggtggtgt cccgcgggca gcaacagcag cagcaggcgc ggcagcagca gcagcagctg 420
gaccgcgaga agtacgtggc gacgatgcag cagctgatgc ag

(2) INFORMATION FOR SEQ ID NO:1795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795:

Xaa Cys Ser Gln Ser His Pro Pro Tyr Arg His Pro Arg Ser Leu Leu
1 5 10 15
Ile Ala Ser Ala Ser Ser Ser Ser Phe Phe Pro Thr Ala Ala Asp
20 25 30
Met Ala Ala Gln Glu Glu Lys Thr Ala Val Val Val Ala Ala Ala
35 40 45
Asp Val Ala Thr Glu Glu Pro Thr Pro Ala Xaa Ser Ser Asn Leu Ser
50 55 60
Arg Leu Gly Arg Arg Ala Gly Gln Asp His Arg Arg Pro Ala Gly Leu
65 70 75 80
Arg Gln Pro Leu Arg Leu Leu His His Asp Glu Pro Ser Gln
85 90

(2) INFORMATION FOR SEQ ID NO:1796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1501205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796:

Xaa Ala Ala Arg Ala Thr His Leu Ile Val Ile Leu Ala Arg Ser Ser
1 5 10 15
Ser Pro Ala Pro Pro Pro Pro Pro Pro Ser Ser Pro Pro Leu Pro Thr
20 25 30
Trp Leu Arg Lys Lys Arg Arg Pro Leu Leu Leu Leu Leu Leu Pro
35 40 45
Met Ser Arg Gln Arg Ser Leu Arg Arg Arg Xaa Ala Ala Thr Ser Ala
50 55 60
Gly Trp Gly Gly Ala Gln Gly Arg Thr Ile Gly Ala Arg Arg Gly Ser
65 70 75 80
Ala Asn Pro Phe Asp Phe Ser Thr Met Met Asn Leu Leu Asn Asp Pro
85 90 95
Ser Ile Lys Glu Met Ala Glu Gln Ile Ala Lys Asp Pro Ala Phe Thr
100 105 110
Glu Met Ala Xaa Ser Cys Arg Arg Trp Cys Pro Arg Gly Ser Asn
115 120 125
Ser Ser Ser Arg Arg Gly Ser Ser Ser Ser Trp Thr Arg Arg Ser
130 135 140
Thr Trp Arg Arg Cys Ser Ser
145 150

(2) INFORMATION FOR SEQ ID NO:1797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..103
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501206
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1797:
Met Ser Arg Gln Arg Ser Leu Arg Arg Arg Xaa Ala Ala Thr Ser Ala
1 5 10 15
Gly Trp Gly Gly Ala Gln Gly Arg Thr Ile Gly Ala Arg Arg Gly Ser
 20 25 30
Ala Asn Pro Phe Asp Phe Ser Thr Met Met Asn Leu Leu Asn Asp Pro
 35 40 45
Ser Ile Lys Glu Met Ala Glu Gln Ile Ala Lys Asp Pro Ala Phe Thr
 50 55 60
Glu Met Ala Xaa Ser Cys Arg Arg Arg Trp Cys Pro Arg Gly Ser Asn
65 70 75 80
Ser Ser Ser Arg Arg Gly Ser Ser Ser Ser Ser Trp Thr Arg Arg Ser
 85 90 95
Thr Trp Arg Arg Cys Ser Ser
 100

(2) INFORMATION FOR SEQ ID NO:1798:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..509
(D) OTHER INFORMATION: / Ceres Seq. ID 1501245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1798:

aataaatcgc	ggaattccca	acgccgcacc	ttcaccgccg	ggctccccag	tccaatccaa	60
cccaacccca	gtccggcgac	ggttccgggc	agcgcgcgat	cggatcgctc	cgggttcggc	120
ttctcgtcga	acggcgcgga	ttcctgcccc	cgatcggagg	gcgtyggctg	cggcgsctcg	180
gcgtctgata	tgctgcggtc	ggcttcttct	tgggararga	gtgggatgga	cggggaagcg	240
atccggatgg	gtggcgga	cttggcgccc	gcctacctct	ccggcgccgc	caccgcmacc	300
gccatcacca	tgcaggatcc	gaaccagaac	cagaaccaga	accagaacca	gaaccaaagc	360
cagttcctgt	tcagcgccaa	ctccacggcg	ctgcagctgt	tcggaagcrc	cgcggtcccc	420
acggttggtc	ctgctgggta	tataavttac	actgggaaac	accacacttc	ctgttatgaa	480
ccaagcaagt	acttcaaaca	tcggcgag				

(2) INFORMATION FOR SEQ ID NO:1799:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..169
(D) OTHER INFORMATION: / Ceres Seq. ID 1501246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1799:

Asn Lys Ser Arg Asn Ser Gln Arg Arg Thr Phe Thr Ala Gly Leu Pro	
1 5 10 15	
Ser Pro Ile Gln Pro Asn Pro Ser Pro Ala Thr Val Pro Gly Ser Ala	
20 25 30	
Arg Ser Asp Arg Arg Gly Phe Gly Phe Ser Ser Asn Gly Ala Asp Ser	
35 40 45	
Cys Pro Arg Ser Glu Gly Xaa Gly Cys Gly Xaa Ser Ala Ser Asp Leu	

50	55	60
Leu Arg Ser Ala Ser Ser Trp Xaa Xaa Ser Gly Met Asp Gly Glu Ala		
65	70	75
Ile Arg Met Gly Gly Gly Asn Leu Ala Pro Ala Tyr Leu Ser Gly Ala		80
	85	90
Ala Thr Xaa Thr Ala Ile Thr Met Gln Asp Pro Asn Gln Asn Gln Asn		95
	100	105
Gln Asn Gln Asn Gln Asn Gln Ser Gln Phe Leu Phe Ser Ala Asn Ser		110
	115	120
Thr Ala Leu Gln Leu Phe Gly Ser Xaa Ala Val Pro Thr Val Gly Pro		125
	130	135
Ala Gly Tyr Ile Xaa Tyr Thr Gly Lys His Pro Pro Ser Cys Tyr Glu		140
145	150	155
Pro Ser Lys Tyr Phe Lys His Arg Arg		160
	165	

(2) INFORMATION FOR SEQ ID NO:1800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1800:

Ile Asn Arg Gly Ile Pro Asn Ala Ala Pro Ser Pro Pro Gly Ser Pro		
1	5	10
Val Gln Ser Asn Pro Thr Pro Val Arg Arg Arg Phe Arg Ala Ala Arg		15
	20	25
Asp Arg Ile Val Ala Gly Ser Ala Ser Arg Arg Thr Ala Arg Ile Pro		30
	35	40
Ala Pro Asp Arg Arg Ala Xaa Ala Ala Ala Xaa Arg Arg Leu Ile Cys		45
	50	55
Cys Gly Arg Leu Leu Leu Gly Xaa Xaa Val Gly Trp Thr Gly Lys Arg		60
65	70	75
Ser Gly Trp Val Ala Thr Trp Arg Pro Pro Thr Ser Pro Ala Pro		80
	85	90
Pro Pro Xaa Pro Pro Ser Pro Cys Arg Ile Arg Thr Arg Thr Arg Thr		95
	100	105
Arg Thr Arg Thr Arg Thr Lys Ala Ser Ser Cys Ser Ala Pro Thr Pro		110
	115	120
Arg Arg Cys Ser Cys Ser Glu Xaa Pro Arg Ser Pro Arg Leu Val Leu		125
	130	135
		140
Leu Val Ile		
145		

(2) INFORMATION FOR SEQ ID NO:1801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1801:

Met Asp Gly Glu Ala Ile Arg Met Gly Gly Gly Asn Leu Ala Pro Ala		
1	5	10
		15

Tyr Leu Ser Gly Ala Ala Thr Xaa Thr Ala Ile Thr Met Gln Asp Pro
20 25 30
Asn Gln Asn Gln Asn Gln Asn Gln Asn Gln Asn Gln Ser Gln Phe Leu
35 40 45
Phe Ser Ala Asn Ser Thr Ala Leu Gln Leu Phe Gly Ser Xaa Ala Val
50 55 60
Pro Thr Val Gly Pro Ala Gly Tyr Ile Xaa Tyr Thr Gly Lys His Pro
65 70 75 80
Pro Ser Cys Tyr Glu Pro Ser Lys Tyr Phe Lys His Arg Arg
85 90

(2) INFORMATION FOR SEQ ID NO:1802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..476
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1802:

aacggaactt	agctgccgag	cgcccaaagc	cccaccgccg	ctcccatcaa	gcggcgctaa	60
aggtttcctc	gcccgcacg	cgatgccgaa	gaacaaggga	aaggagggca	agaaccggaa	120
gcggggcaag	aacgargcgg	acgacgagaa	gcgggagctg	gntgttcaag	gaggacgggc	180
aggagtacgc	gcaggtgacg	cggatgctgg	gcaacggccg	ctgcgaggcg	ccgtcttcct	240
gaacacccgt	tccgatcttt	gcccagaagg	tctacttggg	catcaataag	aaactctttc	300
ccctcaaaact	gattgtgggt	ccatcctctt	ctgtctggaa	aatgttgtca	ccaaactacc	360
ctatttcctg	ttccagtttg	gcatggaagt	ataagttgtg	tacttctatt	ctcaagttgt	420
tgtctttgta	ttatgaaatg	tttccaataa	tcagcagttt	ttgatgtatg	gtcgtg	

(2) INFORMATION FOR SEQ ID NO:1803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1803:

Thr Glu Leu Ser Cys Arg Ala Pro Lys Ala Pro Pro Pro Leu Pro Ser
1 5 10 15
Ser Gly Ala Lys Gly Phe Leu Ala Arg Asn Ala Met Pro Lys Asn Lys
20 25 30
Gly Lys Gly Gly Lys Asn Arg Lys Arg Gly Lys Asn Xaa Ala Asp Asp
35 40 45
Glu Lys Arg Glu Leu Xaa Val Gln Gly Gly Arg Ala Gly Val Arg Ala
50 55 60
Gly Asp Ala Asp Ala Gly Gln Arg Pro Leu Arg Gly Ala Val Phe Leu
65 70 75 80
Asn Thr Arg Ser Asp Leu Cys Pro Glu Gly Leu Leu Gly His Gln
85 90 95

(2) INFORMATION FOR SEQ ID NO:1804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1501261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1804:

```
Arg Asn Leu Ala Ala Glu Arg Pro Lys Pro His Arg Arg Ser His Gln
1          5          10          15
Ala Ala Leu Lys Val Ser Ser Pro Ala Thr Arg Cys Arg Arg Thr Arg
20          25          30
Glu Arg Glu Ala Arg Thr Gly Ser Gly Ala Arg Thr Xaa Arg Thr Thr
35          40          45
Arg Ser Gly Ser Trp Xaa Phe Lys Glu Asp Gly Gln Glu Tyr Ala Gln
50          55          60
Val Thr Arg Met Leu Gly Asn Gly Arg Cys Glu Ala Pro Ser Ser
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:1805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1501262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1805:

```
Met Pro Lys Asn Lys Gly Lys Gly Lys Lys Asn Arg Lys Arg Gly Lys
1          5          10          15
Asn Xaa Ala Asp Asp Glu Lys Arg Glu Leu Xaa Val Gln Gly Gly Arg
20          25          30
Ala Gly Val Arg Ala Gly Asp Ala Asp Ala Gly Gln Arg Pro Leu Arg
35          40          45
Gly Ala Val Phe Leu Asn Thr Arg Ser Asp Leu Cys Pro Glu Gly Leu
50          55          60
Leu Gly His Gln
65
```

(2) INFORMATION FOR SEQ ID NO:1806:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 479 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..479

(D) OTHER INFORMATION: / Ceres Seq. ID 1501268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1806:

```
acgatccac tctcccgcgt cacctcaagg agtcaagggtg caaagctaag cttagctcat 60
tgctcaagct tccgtctctt tctctctgcg agactgcaca ctgccaccac gcgcaatggc 120
ggcattccac catttggttg cggccttgct ccttctactc ctgctccctt ccaccctga 180
ggcgacgtcc tcggcgctgc ttggcatcag ctacgggtcgc gttgggaaca acctccctgc 240
agctacatca gtgccgcaga ttgtggcttc cctgggcgtc ggccgcgtcc gactctacga 300
tgctgacagc accaccattc ggccttcgc caacacgggc gtcgagctcg tcgtcggcgt 360
ccctgacgag tgcctcgcca ctgtctccac cccgacgggc gcmgcctcct gggtcgcgtc 420
caacatttcc ccctgcgtc cggccacaa agatcgcctt cctcacagtc ggcaacgag
```

(2) INFORMATION FOR SEQ ID NO:1807:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..159
(D) OTHER INFORMATION: / Ceres Seq. ID 1501269
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1807:

Asp Pro Thr Leu Pro Ala His Leu Lys Glu Ser Arg Cys Lys Ala Lys
1 5 10 15
Leu Ser Ser Leu Leu Lys Leu Pro Ser Leu Ser Leu Cys Glu Thr Ala
20 25 30
His Cys His His Ala Gln Trp Arg His Ser Thr Ile Cys Cys Arg Pro
35 40 45
Cys Ser Phe Tyr Ser Cys Ser Leu Pro Pro Leu Arg Arg Pro Arg
50 55 60
Arg Cys Leu Ala Ser Ala Thr Val Ala Leu Ala Thr Thr Ser Leu Gln
65 70 75 80
Leu His Gln Cys Arg Arg Leu Trp Leu Pro Trp Ala Ser Ala Ala Ser
85 90 95
Asp Ser Thr Met Leu Thr Ala Pro Pro Phe Ala Pro Ser Pro Thr Arg
100 105 110
Ala Ser Ser Ser Ser Ser Ala Ser Leu Thr Ser Ala Ser Pro Leu Ser
115 120 125
Pro Pro Arg Arg Ala Xaa Pro Pro Gly Ser Ala Pro Thr Phe Pro Pro
130 135 140
Ala Leu Pro Ala Thr Lys Ile Ala Phe Leu Thr Val Gly Asn Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:1808:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..121
(D) OTHER INFORMATION: / Ceres Seq. ID 1501270
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1808:

Met Ala Ala Phe His His Leu Leu Pro Ala Leu Leu Leu Leu Leu
1 5 10 15
Leu Pro Ser Thr Pro Glu Ala Thr Ser Ser Ala Leu Leu Gly Ile Ser
20 25 30
Tyr Gly Arg Val Gly Asn Asn Leu Pro Ala Ala Thr Ser Val Pro Gln
35 40 45
Ile Val Ala Ser Leu Gly Val Gly Arg Val Arg Leu Tyr Asp Ala Asp
50 55 60
Ser Thr Thr Ile Arg Ala Phe Ala Asn Thr Gly Val Glu Leu Val Val
65 70 75 80
Gly Val Pro Asp Glu Cys Leu Ala Thr Val Ser Thr Pro Thr Gly Xaa
85 90 95
Ala Ser Trp Val Arg Ser Asn Ile Ser Pro Cys Ala Pro Gly His Lys
100 105 110
Asp Arg Leu Pro His Ser Arg Gln Arg
115 120

(2) INFORMATION FOR SEQ ID NO:1809:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 422 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..422
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1809:

aaggagagag	agagagggcag	agggagagat	tggagggagg	cccctgcccc	aggcaagaga	60
aaccgcggcg	cgcggagaga	gggtgagggt	gagttctcag	aagcccgtga	ggacttggct	120
gctcttgaga	aggactatga	ggaagtcggt	gcagaggggtg	ccgatgacga	gggtgacgag	180
ggagacgact	attgagtagc	tggctaataa	gtagttctct	gggtggtaaat	ggttgggtta	240
ttttgagtat	atactctatg	gttccactcc	attggatact	gctgctgtgt	gtgtttccat	300
tttgactat	gtagtaaatt	gttcgtagcc	ccctattggc	catgattgtt	catatcatcc	360
ttctttggtt	tgaacgcta	ttcgtccaat	ttcgggtgat	atgctataat	gctattatgt	420

tg

(2) INFORMATION FOR SEQ ID NO:1810:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..64
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1810:

Lys	Glu	Arg	Glu	Arg	Gly	Arg	Gly	Arg	Trp	Arg	Glu	Ala	Pro	Ala	
1			5				10				15				
Gln	Gly	Lys	Arg	Asn	Arg	Gly	Ala	Arg	Arg	Glu	Gly	Glu	Gly	Glu	Phe
			20				25				30				
Ser	Glu	Ala	Arg	Glu	Asp	Leu	Ala	Ala	Leu	Glu	Lys	Asp	Tyr	Glu	Glu
			35				40				45				
Val	Gly	Ala	Glu	Gly	Ala	Asp	Asp	Glu	Gly	Asp	Glu	Gly	Asp	Asp	Tyr
			50				55				60				

(2) INFORMATION FOR SEQ ID NO:1811:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..65
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1811:

Arg	Arg	Glu	Arg	Glu	Ala	Glu	Gly	Glu	Ile	Gly	Gly	Arg	Pro	Leu	Pro
1					5				10				15		
Lys	Ala	Arg	Glu	Thr	Ala	Ala	Arg	Gly	Glu	Arg	Val	Arg	Val	Ser	Ser
			20				25				30				
Gln	Lys	Pro	Val	Arg	Thr	Trp	Leu	Leu	Arg	Arg	Thr	Met	Arg	Lys	
			35				40				45				
Ser	Val	Gln	Arg	Val	Pro	Met	Thr	Arg	Val	Thr	Arg	Glu	Thr	Thr	Ile
			50				55				60				

Glu
65

(2) INFORMATION FOR SEQ ID NO:1812:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..570
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1812:

ataaagcacc	ctctccttgc	gcgaattcgg	acacggccac	cacacatccc	ttcctctctt	60
tctcctcgag	gctcgagcat	tcgtgctgct	ccgacccccc	cgccacaggc	tcggcgggtcc	120
ggcgatctcg	ctcaccggcg	ggaacatgac	tacttcaagg	cgcccttgctg	acaggaagac	180
cgcaaagtgc	cagaagaaca	tcaccaggag	gggttctgtg	cctgaaacca	ctgtcaagaa	240
gggaaatgac	taccctgttg	gccctctagt	gcttgggttc	ttcatctttg	tcgtcattgg	300
atcatcggtg	tttcagatca	tcaggacggc	aaccagcggc	ggggtggctt	gagagccggc	360
ccacatctaa	tccccagtat	agagagttgc	ttgttataca	tgcatccagc	taggattggg	420
tagcagctaa	aatgttaaac	gtgacaagac	tgccctgcat	tccgttcatt	tggtgggcct	480
tgaatctgga	actgaacat	aaggcagaat	catgtacctt	atataaagtg	ttaaatgggt	540
aactggatct	cagtgtttca	tttaattctt				

(2) INFORMATION FOR SEQ ID NO:1813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..56
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1813:

Ile	Lys	His	Pro	Leu	Ala	Arg	Ile	Arg	Thr	Arg	Pro	Pro	His	Ile
1			5				10						15	
Pro	Ser	Ser	Leu	Ser	Pro	Arg	Gly	Ser	Ser	Ile	Arg	Ala	Ala	Pro
			20				25					30		Thr
Pro	Pro	Pro	Gln	Ala	Arg	Arg	Ser	Gly	Asp	Leu	Ala	His	Arg	Arg
			35				40					45		Glu
His	Asp	Tyr	Phe	Lys	Ala	Pro	Cys							
50						55								

(2) INFORMATION FOR SEQ ID NO:1814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..48
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1814:

Lys	Ala	Pro	Ser	Pro	Cys	Ala	Asn	Ser	Asp	Thr	Ala	Thr	Thr	His	Pro
1			5				10							15	
Phe	Leu	Ser	Phe	Ser	Ser	Arg	Leu	Glu	His	Ser	Cys	Cys	Ser	Asp	Pro
			20				25					30			
Thr	Ala	Thr	Gly	Ser	Ala	Val	Arg	Arg	Ser	Arg	Ser	Pro	Ala	Gly	Thr
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:1815:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..68
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501309
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815:

Met Thr Thr Ser Arg Leu Ala Asp Arg Lys Thr Ala Lys Phe Gln
1 5 10 15
Lys Asn Ile Thr Arg Arg Gly Ser Val Pro Glu Thr Thr Val Lys Lys
 20 25 30
Gly Asn Asp Tyr Pro Val Gly Pro Leu Val Leu Gly Phe Phe Ile Phe
 35 40 45
Val Val Ile Gly Ser Ser Leu Phe Gln Ile Ile Arg Thr Ala Thr Ser
50 55 60
Gly Gly Val Ala
65

- (2) INFORMATION FOR SEQ ID NO:1816:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1036 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1036
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501310
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816:

aacccaagag cgaaaatgga tccgcaccag ttcgccccct cccagcagtc ggcgctgacc 60
atggaatcgg cggagatcac ggccgccgcc gccgcgcgc gcgcacccaa cggcgctgcc 120
cgggctatcg tcgaggacga cgacgaggac gacgacgtcc ccgaggtggc cgcctgcata 180
tcgacgatgc tcgaccgcgg gggtagcgtg gagagccacc gcctcttctt cgcgcgcgcgc 240
accgcgctgg agatgctccg cgaccgcggt acgccgttcc ggaggaagag ctgcgccgga 300
ccctcccga gttccgcgcc tgggtgggaat acaggccaga rctcgaacgc ctgccttct 360
ccactaccct cgcctccgac ccgtccagca aggtgaaagt tgtgttctgt ccacctggac 420
ctgtcaaaat cgcagctatc cggctgatat ataccgaagt caaagatgag aacttgtcca 480
gactgattct gatactgcag ggcaaaataa tgtctacaac cagagaatcc atcaaggagw 540
tctttcgatt taaagttgac acattccaga tcacggaatt actggtgaac atcactaagc 600
atgtcctcaa gcccaagcat gaagtgttga ctgcagaggg gaaagctaag ctccctgaagg 660
agtacaatgt ggttgattca cagttgcctc gcatgctgga gaatgatgct gttgctcgct 720
attacgggct aggcaaggga actggttcta aggttatata cgacagcgag cttaccggga 780
accatgtgac gtaccgatgc attacctgag gggcccatgt gtttcgggtg atgaagtgtc 840
gtaagcagtc tgtaaaaaat tacctctaag aggggcaggt gacactgttc tgctaggcct 900
ttgtaagcac ccaattatgc aggatgaagc tcgctgtgta ctattggtaa aatcatcttg 960
cgccattgcc gtaccttaag tgcttggtgt taatcttgga aacagtgaga caactaatcc 1020
tgtagtgagt tatctc

- (2) INFORMATION FOR SEQ ID NO:1817:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1501311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817:

Asn Pro Arg Ala Lys Met Asp Pro His Gln Phe Ala Pro Ser Gln Gln
1 5 10 15
Ser Ala Leu Thr Met Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala
20 25 30
Ala Arg Ala Pro Asn Gly Ala Ala Arg Ala Ile Val Glu Asp Asp Asp
35 40 45
Glu Asp Asp Asp Val Pro Glu Val Ala Ala Cys Ile Ser Thr Met Leu
50 55 60
Asp Arg Gly Gly Ser Val Glu Ser His Arg Leu Phe Leu Ala Arg Arg
65 70 75 80
Thr Ala Leu Glu Met Leu Arg Asp Arg Gly Thr Pro Phe Arg Arg Lys
85 90 95
Ser Ser Pro Gly Pro Ser Arg Ser Ser Ala Pro Gly Gly Asn Thr Gly
100 105 110
Gln Xaa Ser Asn Ala Ser Pro Ser Pro Leu Pro Ser Pro Pro Thr Arg
115 120 125
Pro Ala Arg
130

(2) INFORMATION FOR SEQ ID NO:1818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1501312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818:

Met Asp Pro His Gln Phe Ala Pro Ser Gln Gln Ser Ala Leu Thr Met
1 5 10 15
Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala Ala Arg Ala Pro Asn
20 25 30
Gly Ala Ala Arg Ala Ile Val Glu Asp Asp Asp Glu Asp Asp Val
35 40 45
Pro Glu Val Ala Ala Cys Ile Ser Thr Met Leu Asp Arg Gly Gly Ser
50 55 60
Val Glu Ser His Arg Leu Phe Leu Ala Arg Arg Thr Ala Leu Glu Met
65 70 75 80
Leu Arg Asp Arg Gly Thr Pro Phe Arg Arg Lys Ser Ser Pro Gly Pro
85 90 95
Ser Arg Ser Ser Ala Pro Gly Gly Asn Thr Gly Gln Xaa Ser Asn Ala
100 105 110
Ser Pro Ser Pro Leu Pro Ser Pro Pro Thr Arg Pro Ala Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:1819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111

(D) OTHER INFORMATION: / Ceres Seq. ID 1501313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819:

Met Glu Ser Ala Glu Ile Thr Ala Ala Ala Ala Ala Arg Ala Pro

1 5 10 15
Asn Gly Ala Ala Arg Ala Ile Val Glu Asp Asp Asp Glu Asp Asp Asp
20 25 30
Val Pro Glu Val Ala Ala Cys Ile Ser Thr Met Leu Asp Arg Gly Gly
35 40 45
Ser Val Glu Ser His Arg Leu Phe Leu Ala Arg Arg Thr Ala Leu Glu
50 55 60
Met Leu Arg Asp Arg Gly Thr Pro Phe Arg Arg Lys Ser Ser Pro Gly
65 70 75 80
Pro Ser Arg Ser Ser Ala Pro Gly Gly Asn Thr Gly Gln Xaa Ser Asn
85 90 95
Ala Ser Pro Ser Pro Leu Pro Ser Pro Pro Thr Arg Pro Ala Arg
100 105 110

(2) INFORMATION FOR SEQ ID NO:1820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..458
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501318

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1820:

atagagacav ggaggggggag tgggtccgagg tcaataggat ataactccag gactcctctc 60
catcagaatc agagacgagt cgagtgagg ggcagaggcc acaaaacaga gagtacccaa 120
acgatcgatc tgtgcatctc ccggtccgctc ccgcaaccat ctaattcaga agcagacatc 180
aatggcgagc hacggctgca acggcaacgg caacggcaac ggcaacggca aggcggctcc 240
ggcgggtgtg gtggtaccgg agatcaagtt caccaagctc ttcattcaacg gcgagtctgt 300
cgacgccgcc tccggcaaga cattcgatac cagggaacca ggtaccaggg ctacacgctc 360
aaggagccta tcggcgctcgt gggcgctcatc atcccctgga acttccccac catgatgttc 420
ttcctcaagg tcagcccggc gctcgccrcg ggctgcac

(2) INFORMATION FOR SEQ ID NO:1821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821:

Met Ala Ser Xaa Gly Cys Asn Gly Asn Gly Asn Gly Asn Gly Asn Gly
1 5 10 15
Lys Ala Ala Pro Ala Gly Val Val Val Pro Glu Ile Lys Phe Thr Lys
20 25 30
Leu Phe Ile Asn Gly Glu Phe Val Asp Ala Ala Ser Gly Lys Thr Phe
35 40 45
Asp Thr Arg Asp Pro Gly Thr Arg Ala Thr Arg Ser Arg Ser Leu Ser
50 55 60
Ala Ser Trp Ala Ser Ser Pro Gly Thr Ser Pro Pro
65 70 75

(2) INFORMATION FOR SEQ ID NO:1822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..543

(D) OTHER INFORMATION: / Ceres Seq. ID 1501324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822:

gcctcgcgca	ctcgcaactta	acctagccgc	cagccctcga	cgaccgacgc	gacgtcgccct	60
tcgccccctgc	tccaacccct	gcccccttcg	tcgctccggc	ctcggcagga	agatcctcca	120
tcgacgggtcc	tgctgatgcc	tctgctgtca	tcgttctgag	gagagcctca	gtggtcggat	180
ccttgatgtg	ttgggccccg	tcgaggcgat	tgtcaccact	tcacacaggg	gcaaagtgcg	240
gtcggtcctc	ccccctctgga	tcctccaccg	ccaatgctcg	atgcctgcat	cgacaaagct	300
cccgtccgaa	gtctccccct	ttcggatcct	tccccctgcc	gtgcttgctt	cctcgtcctg	360
ggatactccg	ccggccccctt	catcgtccag	agaacctggc	atgagacacg	ccaccagagc	420
ttgtttacag	ttcagcccag	ttggccatta	ctttgctagt	gcttcacatg	acaggactgc	480
tagaatttgg	tcaattgata	aaatccagcc	tttgcggaata	atggctgggc	atcttttctga	540
tgt						

(2) INFORMATION FOR SEQ ID NO:1823:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

(D) OTHER INFORMATION: / Ceres Seq. ID 1501325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823:

Pro	Arg	Ala	Leu	Ala	Leu	Asn	Leu	Ala	Ala	Ser	Pro	Arg	Arg	Pro	Thr	
1			5					10						15		
Arg	Arg	Arg	Leu	Arg	Pro	Cys	Ser	Asn	Pro	Cys	Pro	Leu	Arg	Arg	Ser	
			20					25					30			
Gly	Leu	Gly	Arg	Lys	Ile	Leu	His	Arg	Arg	Ser	Cys	Arg	Cys	Leu	Cys	
			35				40					45				
Cys	His	Arg	Ser	Glu	Glu	Ser	Leu	Ser	Gly	Arg	Ile	Leu	Asp	Val	Leu	
	50					55				60						
Gly	Pro	Val	Glu	Ala	Ile	Val	Thr	Thr	Ser	His	Arg	Gly	Lys	Val	Arg	
65					70					75				80		
Ser	Val	Leu	Pro	Leu	Trp	Ile	Leu	His	Arg	Gln	Cys	Ser	Met	Pro	Ala	
			85					90					95			
Ser	Thr	Lys	Leu	Pro	Ser	Glu	Val	Ser	Pro	Phe	Arg	Ile	Leu	Pro	Leu	
			100					105					110			
Pro	Val	Leu	Ala	Ser	Ser	Ser	Trp	Asp	Thr	Pro	Pro	Ala	Pro	Ser	Ser	
			115				120					125				
Ser	Arg	Glu	Pro	Gly	Met	Arg	His	Ala	Thr	Arg	Ala	Cys	Leu	Gln	Phe	
	130					135					140					
Ser	Pro	Val	Gly	His	Tyr	Phe	Ala	Ser	Ala	Ser	His	Asp	Arg	Thr	Ala	
145					150					155				160		
Arg	Ile	Trp	Ser	Ile	Asp	Lys	Ile	Gln	Pro	Leu	Arg	Ile	Met	Ala	Gly	
			165					170					175			
His	Leu	Ser	Asp													
			180													

(2) INFORMATION FOR SEQ ID NO:1824:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 536 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

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(B) LOCATION: 1..536

(D) OTHER INFORMATION: / Ceres Seq. ID 1501326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824:

aatcaccttc	ttcgtttcat	cctctgattc	wccccctgcw	ggtctgctct	gctcccatcc	60
catggagccc	gacgccgccc	aaaaccctag	ccccagcccc	gtccccccgc	ccatctccgc	120
ctactaccag	acgcgcgccc	aacaccacgc	cgtcgtaact	agcgactggc	tcgcccacgc	180
cgccgcgcga	gocgcagcct	tccccggcgc	cgataccgcc	gatgcmgcmc	cgcccccgtc	240
ccccgggggc	ggcggcggtga	tcgaggagtt	caacttctgg	cgccgcaagc	ccgaggccgc	300
cgaggcggtg	gocgccatca	tggctctcgc	cgcmgtcatc	cgctccagca	gggccaccac	360
catgatggag	ctcgagatcg	agctcaagaa	ggcatctgac	aagctcaagt	cctgggatgc	420
tacatccatt	tctctttctg	ctgcttgtga	ttgttcatg	cggtttgtaa	cgaggacctc	480
acatctggag	catgagaagt	ttgatgcagc	aaaatcgcg	ctaattgagc	gaggag	

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1501327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825:

Ile	Thr	Phe	Phe	Val	Ser	Ser	Ser	Asp	Xaa	Pro	Pro	Xaa	Gly	Leu	Leu	
1				5				10						15		
Cys	Ser	His	Pro	Met	Glu	Pro	Asp	Ala	Ala	Gln	Asn	Pro	Ser	Pro	Ser	
			20					25					30			
Pro	Val	Pro	Pro	Pro	Ile	Ser	Ala	Tyr	Tyr	Gln	Thr	Arg	Ala	Glu	His	
		35					40					45				
His	Ala	Val	Val	Thr	Ser	Asp	Trp	Leu	Ala	His	Ala	Ala	Ala	Ala	Ala	
	50					55					60					
Ala	Ala	Phe	Pro	Gly	Ala	Asp	Thr	Ala	Asp	Xaa	Xaa	Pro	Pro	Pro	Ser	
65				70					75						80	
Pro	Gly	Gly	Gly	Gly	Val	Ile	Glu	Glu	Phe	Asn	Phe	Trp	Arg	Arg	Lys	
			85					90					95			
Pro	Glu	Ala	Ala	Glu	Ala	Val	Ala	Ala	Ile	Met	Ala	Leu	Ala	Xaa	Val	
		100						105				110				
Ile	Arg	Ser	Ser	Arg	Ala	Thr	Thr	Met	Met	Glu	Leu	Glu	Ile	Glu	Leu	
	115					120					125					
Lys	Lys	Ala	Ser	Asp	Lys	Leu	Lys	Ser	Trp	Asp	Ala	Thr	Ser	Ile	Ser	
	130					135					140					
Leu	Ser	Ala	Ala	Cys	Asp	Leu	Phe	Met	Arg	Phe	Val	Thr	Arg	Thr	Ser	
145				150						155					160	
His	Leu	Glu	His	Glu	Lys	Phe	Asp	Ala	Ala	Lys	Ser	Arg	Leu	Ile	Glu	
			165					170						175		
Arg	Gly															

(2) INFORMATION FOR SEQ ID NO:1826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1501328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826:

Met Glu Pro Asp Ala Ala Gln Asn Pro Ser Pro Ser Pro Val Pro Pro

1					5					10					15		
Pro	Ile	Ser	Ala	Tyr	Tyr	Gln	Thr	Arg	Ala	Glu	His	His	Ala	Val	Val		
			20					25					30				
Thr	Ser	Asp	Trp	Leu	Ala	His	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Phe	Pro		
		35					40					45					
Gly	Ala	Asp	Thr	Ala	Asp	Xaa	Xaa	Pro	Pro	Pro	Ser	Pro	Gly	Gly	Gly		
	50					55					60						
Gly	Val	Ile	Glu	Glu	Phe	Asn	Phe	Trp	Arg	Arg	Lys	Pro	Glu	Ala	Ala		
65					70					75					80		
Glu	Ala	Val	Ala	Ala	Ile	Met	Ala	Leu	Ala	Xaa	Val	Ile	Arg	Ser	Ser		
				85				90						95			
Arg	Ala	Thr	Thr	Met	Met	Glu	Leu	Glu	Ile	Glu	Leu	Lys	Lys	Ala	Ser		
			100					105					110				
Asp	Lys	Leu	Lys	Ser	Trp	Asp	Ala	Thr	Ser	Ile	Ser	Leu	Ser	Ala	Ala		
		115					120					125					
Cys	Asp	Leu	Phe	Met	Arg	Phe	Val	Thr	Arg	Thr	Ser	His	Leu	Glu	His		
	130					135					140						
Glu	Lys	Phe	Asp	Ala	Ala	Lys	Ser	Arg	Leu	Ile	Glu	Arg	Gly				
145					150					155							

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..492
(D) OTHER INFORMATION: / Ceres Seq. ID 1501329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827:

acactcgctc	tcgccactgt	cgtcaccga	tccgtcatgg	cgactgctgc	gccattgttg	60
ctcttccacg	gtctctctct	cctctctctc	ctggcgctcg	gcccattggcg	tgaacgtgaa	120
gcccggggag	caccacatacc	tcaacaggca	gagcttcccc	ccggggttcg	tcttcggcac	180
ggcgtcttcg	gcgtaccag	tggaggggaa	cacgcacagg	tacgggcgcg	ggccctgcac	240
ctgggacacc	ttcctcaagt	atccaggcac	tactcctgat	aacgcgaccg	cggacgtgac	300
agtcgacgag	tacaatcgct	acatggatga	tgtggacaat	atggtccggg	ttggcttcga	360
cgcgtaccgc	ttctcgatct	catggtcgcg	tattttcccc	agtgggattg	ggagggttaa	420
caaggatggt	tgggactatt	accacaggct	catcaactac	ttgctggcga	accatattac	480
tccctacgtg	gt					

(2) INFORMATION FOR SEQ ID NO:1828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1501330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828:

Thr	Leu	Ala	Leu	Ala	Thr	Val	Val	His	Arg	Ser	Val	Met	Ala	Thr	Ala
1				5					10					15	
Ala	Pro	Leu	Leu	Leu	Phe	His	Gly	Leu	Leu	Leu	Leu	Leu	Ser	Leu	Ala
			20					25					30		
Leu	Gly	Pro	Trp	Arg	Glu	Arg	Glu	Ala	Arg	Gly	Ala	Pro	His	Pro	Gln
		35					40					45			
Gln	Ala	Glu	Leu	Pro	Pro	Gly	Val	Arg	Leu	Arg	His	Gly	Val	Phe	Gly
	50					55					60				
Val	Pro	Gly	Gly	Gly	Glu	His	Ala	Gln	Val	Arg	Ala	Arg	Ala	Leu	His

80

90

- ```
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
```

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1829:

(2) INFORMATION FOR SEQ ID NO:1830:

- ```
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
```

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1830:

(2) INFORMATION FOR SEQ ID NO:1831:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..136
(D) OTHER INFORMATION: / Ceres Seq. ID 1501340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831:

Val	Glu	Ser	Arg	Thr	Phe	Leu	Pro	Arg	Ser	Arg	Xaa	Gln	Ser	Ala	Thr
1				5					10					15	
Thr	His	Thr	Pro	Thr	Asn	Thr	Met	Asp	Ala	Ala	Ala	Lys	Glu	Ala	
			20				25					30			
Leu	Ile	Leu	Asp	Leu	His	Ala	Val	Glu	Ala	Val	Lys	Leu	Gly	Thr	Phe
		35				40					45				
Val	Leu	Lys	Ser	Gly	Ile	Thr	Ser	Pro	Ile	Tyr	Leu	Asp	Leu	Arg	Val
	50				55					60					
Leu	Val	Ser	His	Pro	Arg	Leu	Leu	Ala	Ser	Val	Ala	Ser	Leu	Leu	Gly
65					70				75					80	
Ala	Leu	Pro	Ala	Thr	Arg	Pro	Tyr	Asp	Leu	Leu	Cys	Gly	Val	Pro	Xaa
			85					90					95		
Thr	Ala	Leu	Pro	Phe	Ala	Ala	Ala	Leu	Ser	Val	Ala	Xaa	Ser	Val	Pro
			100					105					110		
Met	Leu	Leu	Ser	Arg	Tyr	Asp	Thr	Lys	Arg	Val	Glu	Gly	Ala	Phe	Arg
		115				120						125			
Xaa	Ala	Gln	Xaa	Val	Leu	Ile	Val								
	130				135										

(2) INFORMATION FOR SEQ ID NO:1832:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1501341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832:

Arg	Val	Lys	Asn	Phe	Ser	Pro	Pro	Phe	Ala	Xaa	Thr	Val	Gly	His	Tyr
1				5					10					15	
Thr	His	Ala	Ala	His	Gln	His	His	Gly	Arg	Arg	Arg	Glu	Gly	Gly	Ala
			20					25					30		
Asp	Pro	Gly	Pro	Ala	Arg	Gly	Gly	Arg	Glu	Ala	Gly	His	Leu	Arg	
		35				40					45				
Ala	Gln	Val	Arg	Asp	His	Leu	Pro	Asp	Leu	Pro	Gly	Pro	Ala	Arg	Ala
	50				55					60					
Arg	Leu	Pro	Pro	Ala	Pro	Ala	Arg	Leu	Arg	Arg	Val	Pro	Pro	Arg	Arg
65					70				75					80	
Ala	Pro	Gly	His	Ala	Pro	Leu	Arg	Pro	Ser	Leu	Arg	Arg	Ala	Leu	Xaa
			85					90					95		
Ser	Ala	Ala	Leu	Arg	Gly	Arg	Ala	Leu	Arg	Arg	Xaa	Leu	Arg	Ala	His
			100					105					110		
Ala	Ala	Gln	Pro	Leu	Arg	His	Gln	Ala	Arg	Arg	Gly	Arg	Leu	Pro	Xaa
		115				120						125			
Arg	Pro	Xaa	Arg	Ala	His	Arg									
	130				135										

(2) INFORMATION FOR SEQ ID NO:1833:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..112
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833:

```
Met Asp Ala Ala Ala Lys Glu Ala Leu Ile Leu Asp Leu His Ala Val
1          5          10          15
Glu Ala Val Lys Leu Gly Thr Phe Val Leu Lys Ser Gly Ile Thr Ser
20          25          30
Pro Ile Tyr Leu Asp Leu Arg Val Leu Val Ser His Pro Arg Leu Leu
35          40          45
Ala Ser Val Ala Ser Leu Leu Gly Ala Leu Pro Ala Thr Arg Pro Tyr
50          55          60
Asp Leu Leu Cys Gly Val Pro Xaa Thr Ala Leu Pro Phe Ala Ala Ala
65          70          75          80
Leu Ser Val Ala Xaa Ser Val Pro Met Leu Leu Ser Arg Tyr Asp Thr
85          90          95
Lys Arg Val Glu Gly Ala Phe Arg Xaa Ala Gln Xaa Val Leu Ile Val
100          105          110
```

(2) INFORMATION FOR SEQ ID NO:1834:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 539 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..539
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1834:

```
agcagcccat cccagcagc actgcctcgt cgtctcgcgt attggcggtg gcatcacccgt      60
cggcattgtg cccattacca tgccgcgcgt gccgcgcgcc gacgatttac tcattctcga      120
gttcacgcgc agcaaccgcc gtatccccca cgccgtgttc aactccttca tcgcctccca      180
atccccaccc tccgccttct cccgcacctc acagcgcttc cgaaaagccc tagtgctccg      240
cgccctcgac gccgcctctt acaccgtggg cgctctctgc tcctccagcc tcctcctcca      300
caaggcgcg aaggtcctcg ccgaccccca cgcagccgcc tgcttcccc accagattcc      360
ttttacagaa aatgaagaaa acgatgaggg tagggctgcg gtggccgatc tcaagcgcc      420
cctcgacctt gagtggggcca acctcccgcg ctccacgctc gagctcgtmg ccggggacgg      480
gtcccaccag actggtgcmg ctgccgacca caccatgcgt acaaagcttc gcctgttcg
```

(2) INFORMATION FOR SEQ ID NO:1835:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..124
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835:

```
Ser Ser Pro Ser Pro Ala Ala Leu Pro Arg Arg Leu Ala Tyr Trp Arg
1          5          10          15
Trp His His Arg Arg His Cys Ala His Tyr His Ala Ala Ala Ala Arg
20          25          30
Gly Arg Arg Phe Thr His Ser Arg Val His Arg Glu Gln Pro Pro Tyr
35          40          45
```

Pro Pro Arg Arg Val Gln Leu Leu His Arg Leu Pro Ile Pro Thr Leu
50 55 60
Arg Leu Leu Pro His Leu Thr Ala Pro Pro Lys Ser Pro Ser Ala Pro
65 70 75 80
Arg Pro Arg Arg Arg Pro Leu His Arg Gly Arg Leu Leu Leu Leu Gln
85 90 95
Pro Pro Pro Pro Gln Gly Ala Lys Gly Pro Arg Arg Pro Arg Arg Ser
100 105 110
Arg Leu Leu Pro Pro Pro Asp Ser Phe Tyr Arg Lys
115 120

(2) INFORMATION FOR SEQ ID NO:1836:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1501347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836:

Ala Ala His Pro Gln Gln His Cys Leu Val Val Ser His Ile Gly Val
1 5 10 15
Gly Ile Thr Val Gly Ile Val Pro Ile Thr Met Pro Pro Leu Pro Ala
20 25 30
Ala Asp Asp Leu Leu Ile Leu Glu Phe Ile Ala Ser Asn Arg Arg Ile
35 40 45
Pro His Ala Val Phe Asn Ser Phe Ile Ala Ser Gln Ser Pro Pro Ser
50 55 60
Ala Phe Ser Arg Thr Ser Gln Arg Leu Arg Lys Ala Leu Val Leu Arg
65 70 75 80
Ala Leu Asp Ala Ala Leu Tyr Thr Val Gly Ala Ser Cys Ser Ser Ser
85 90 95
Leu Leu Leu His Lys Ala Arg Lys Val Leu Ala Asp Pro Asp Ala Ala
100 105 110
Ala Cys Phe Pro His Gln Ile Pro Phe Thr Glu Asn Glu Asn Asp
115 120 125
Glu Ala Arg Ala Ala Val Ala Asp Leu Lys Arg Leu Leu Asp Leu Glu
130 135 140
Trp Ala Asn Leu Pro Xaa Ser Thr Leu Glu Leu Xaa Ala Gly Asp Gly
145 150 155 160
Ser His Gln Thr Gly Xaa Ala Ala Asp His Thr Met Arg Thr Lys Leu
165 170 175
Arg Leu Phe

(2) INFORMATION FOR SEQ ID NO:1837:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1501348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837:

Met Pro Pro Leu Pro Ala Ala Asp Asp Leu Leu Ile Leu Glu Phe Ile
1 5 10 15
Ala Ser Asn Arg Arg Ile Pro His Ala Val Phe Asn Ser Phe Ile Ala

20 25 30
Ser Gln Ser Pro Pro Ser Ala Phe Ser Arg Thr Ser Gln Arg Leu Arg
35 40 45
Lys Ala Leu Val Leu Arg Ala Leu Asp Ala Ala Leu Tyr Thr Val Gly
50 55 60
Ala Ser Cys Ser Ser Ser Leu Leu His Lys Ala Arg Lys Val Leu
65 70 75 80
Ala Asp Pro Asp Ala Ala Ala Cys Phe Pro His Gln Ile Pro Phe Thr
85 90 95
Glu Asn Glu Glu Asn Asp Glu Ala Arg Ala Ala Val Ala Asp Leu Lys
100 105 110
Arg Leu Leu Asp Leu Glu Trp Ala Asn Leu Pro Xaa Ser Thr Leu Glu
115 120 125
Leu Xaa Ala Gly Asp Gly Ser His Gln Thr Gly Xaa Ala Ala Asp His
130 135 140
Thr Met Arg Thr Lys Leu Arg Leu Phe
145 150

(2) INFORMATION FOR SEQ ID NO:1838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..511
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838:

agccttccaa	tctctaggag	aaacgtcttg	ccctccactc	caacatcgac	acgactactc	60
gtccgactag	aaccaaaactt	ttcaatccat	cgttcgcagt	tcagttcaca	cttcacaggc	120
gagcgcgacc	atggataccc	aagcacgtcc	ggttccccgc	gtcaagctcg	gcacccaggg	180
attcgagggtg	tccaagctgg	ggttcgggtg	catggggctg	acgggcgcat	acaactcccc	240
gctggacgac	gaggccggca	tcgccgtcat	cgcgcacgct	ttcagcccg	gagtcacctt	300
gttcgacacc	tccgacgtat	acgggcccct	caccaacgaa	atcctcctcg	gcaaggcgct	360
gaagcagctg	cgcggggagc	aggtgcaggt	ggccaccaag	ttcggggatam	ggcgtgacga	420
gagcggcacs	ggnaccgtgt	gcggccggcc	ggagtagctt	cgtrcctgct	gcgaggccag	480
cctgcgcgcg	ctcggcacgc	actgcatcga	c			

(2) INFORMATION FOR SEQ ID NO:1839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..138
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839:

Ser Leu Pro Ile Ser Arg Arg Asn Val Leu Pro Ser Thr Pro Thr Ser
1 5 10 15
Thr Arg Leu Leu Val Arg Leu Glu Pro Asn Phe Ser Ile His Arg Ser
20 25 30
Gln Phe Ser Ser His Phe Thr Gly Glu Arg Asp His Gly Tyr Pro Ser
35 40 45
Thr Ser Gly Ser Pro Arg Gln Ala Arg His Pro Gly Ile Arg Gly Val
50 55 60
Gln Ala Gly Val Arg Val His Gly Ala Asp Gly Arg Ile Gln Leu Pro
65 70 75 80
Ala Gly Arg Arg Gly Arg His Arg Arg His Arg Ala Arg Phe Gln Pro

85 90 95
Arg Ser His Leu Val Arg His Leu Arg Arg Ile Arg Ala Pro His Gln
100 105 110
Arg Asn Pro Arg Gln Gly Ala Glu Ala Ala Ala Ala Gly Ala Gly
115 120 125
Ala Gly Gly His Gln Val Arg Asp Xaa Ala
130 135

(2) INFORMATION FOR SEQ ID NO:1840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1501366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840:

Met Asp Thr Gln Ala Arg Pro Val Pro Arg Val Lys Leu Gly Thr Gln
1 5 10 15
Gly Phe Glu Val Ser Lys Leu Gly Phe Gly Cys Met Gly Leu Thr Gly
20 25 30
Ala Tyr Asn Ser Pro Leu Asp Asp Glu Ala Gly Ile Ala Val Ile Ala
35 40 45
His Ala Phe Ser Arg Gly Val Thr Leu Phe Asp Thr Ser Asp Val Tyr
50 55 60
Gly Pro Leu Thr Asn Glu Ile Leu Leu Gly Lys Ala Leu Lys Gln Leu
65 70 75 80
Pro Arg Glu Gln Val Gln Val Ala Thr Lys Phe Gly Ile Xaa Arg Asp
85 90 95
Glu Ser Gly Xaa Xaa Thr Val Cys Gly Arg Pro Glu Tyr Val Arg Xaa
100 105 110
Cys Cys Glu Ala Ser Leu Arg Arg Leu Gly Ile Asp Cys Ile Asp
115 120 125

(2) INFORMATION FOR SEQ ID NO:1841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1501367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841:

Met Gly Leu Thr Gly Ala Tyr Asn Ser Pro Leu Asp Asp Glu Ala Gly
1 5 10 15
Ile Ala Val Ile Ala His Ala Phe Ser Arg Gly Val Thr Leu Phe Asp
20 25 30
Thr Ser Asp Val Tyr Gly Pro Leu Thr Asn Glu Ile Leu Leu Gly Lys
35 40 45
Ala Leu Lys Gln Leu Pro Arg Glu Gln Val Gln Val Ala Thr Lys Phe
50 55 60
Gly Ile Xaa Arg Asp Glu Ser Gly Xaa Xaa Thr Val Cys Gly Arg Pro
65 70 75 80
Glu Tyr Val Arg Xaa Cys Cys Glu Ala Ser Leu Arg Arg Leu Gly Ile
85 90 95
Asp Cys Ile Asp
100

(2) INFORMATION FOR SEQ ID NO:1842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..516
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842:

```
atctataaca gccgccacct tcccccttat actcgccgga ggcaaccagt actcgtgccca      60
cgactgccac cctcctctt ccttgtgatc tccgaatacc catctcagat tccaagggcc      120
gcgccgtgta atccccggct ctccccaccc accatatatc tagtatccgc gcctcaaatac      180
cctcgcgaaa cgccccgccg taagcagttg ttgtctgccg tgatttgagc cgggcggagc      240
gattgatccc gggacgaggt gtctcagctc ttgatcttga tcctgacccg gggaggcggt      300
cctggtttat tgggtgggagc gaagaagcca tgataccttc cgtgaggctc tctcctggtc      360
ctgcagcctt ctacagctcc agcctacgct caaaattacc gtcaattcca tccatctcca      420
gtctcaaacc ctccaaatat gtggtctcct cgctgaaacc actctaccta gcaccgctag      480
atggtccgcg cactgccgag cttaagtctc ggagac
```

(2) INFORMATION FOR SEQ ID NO:1843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843:

```
Ile Tyr Asn Ser Arg His Leu Pro Pro Tyr Thr Arg Arg Arg Gln Pro
1          5          10          15
Val Leu Val Pro Arg Leu Pro Pro Leu Leu Phe Leu Val Ile Ser Glu
20          25          30
Tyr Pro Ser Gln Ile Pro Arg Ala Ala Pro Cys Asn Pro Arg Leu Ser
35          40          45
Pro Pro Thr Ile Tyr Leu Val Ser Ala Pro Gln Ile Pro Arg Glu Thr
50          55          60
Pro Arg Arg Lys Gln Leu Ser Ala Val Ile
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:1844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..62
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844:

```
Met Ile Pro Ser Val Arg Leu Ser Pro Gly Pro Ala Ala Phe Ser Gly
1          5          10          15
Ser Ser Leu Arg Ser Lys Leu Pro Ser Ile Pro Ser Ile Ser Ser Leu
20          25          30
Lys Pro Ser Lys Tyr Val Val Ser Ser Leu Lys Pro Leu Tyr Leu Ala
35          40          45
```

Pro Leu Asp Gly Pro Arg Thr Ala Glu Leu Lys Ser Arg Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..529
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845:

aattctgcaa agcacgarcc cggttcgttc tcgacctttc gtctcgctct cgcccgcmcg	60
accccgcgga scctagccta gccttgcccc cgaccgcgga ttccccctcg gccgccgcgc	120
gcccgcaccc gcacccgcga tgatgaactg cgccggaggg nangaccccg tggaggactt	180
cctgatctcc ggcgcgctcg acgacgaaga tctagccatc ttctgcgacg gaggacttgg	240
gattgarggt gtcaatggag atgcttgtgg atttgagcag tctaatttgg gcaaaaggag	300
tagagatgaa ccatgttcat ctggtctaaa atccaaagct tgtcgtgaaa aaatgaggag	360
ggacaagctg aatgacaggt tcctggaatt aarttcggtt atgaatcctg gaaaacaagc	420
aaagttggat aaagccaata tcttgarcga mgcagcccg atggtggcac aacttagagg	480
tgaggcagaa aagcttaaaag aatcaaatga gaagctgcgg grgaatatc	

(2) INFORMATION FOR SEQ ID NO:1846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501417

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846:

Met Met Asn Cys Ala Gly Gly Xaa Asp Pro Val Glu Asp Phe Leu Ile	
1 5 10 15	
Ser Gly Ala Val Asp Asp Glu Asp Leu Ala Ile Phe Cys Asp Gly Gly	
20 25 30	
Leu Gly Ile Xaa Gly Val Asn Gly Asp Ala Cys Gly Phe Glu Gln Ser	
35 40 45	
Asn Leu Gly Lys Arg Ser Arg Asp Glu Pro Cys Ser Ser Gly Leu Lys	
50 55 60	
Ser Lys Ala Cys Arg Glu Lys Met Arg Arg Asp Lys Leu Asn Asp Arg	
65 70 75 80	
Phe Leu Glu Leu Xaa Ser Val Met Asn Pro Gly Lys Gln Ala Lys Leu	
85 90 95	
Asp Lys Ala Asn Ile Leu Xaa Xaa Ala Ala Arg Met Val Ala Gln Leu	
100 105 110	
Arg Gly Glu Ala Glu Lys Leu Lys Glu Ser Asn Glu Lys Leu Arg Xaa	
115 120 125	
Asn Ile	
130	

(2) INFORMATION FOR SEQ ID NO:1847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1501418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847:

Met Asn Cys Ala Gly Gly Xaa Asp Pro Val Glu Asp Phe Leu Ile Ser
1 5 10 15
Gly Ala Val Asp Asp Glu Asp Leu Ala Ile Phe Cys Asp Gly Gly Leu
20 25 30
Gly Ile Xaa Gly Val Asn Gly Asp Ala Cys Gly Phe Glu Gln Ser Asn
35 40 45
Leu Gly Lys Arg Ser Arg Asp Glu Pro Cys Ser Ser Gly Leu Lys Ser
50 55 60
Lys Ala Cys Arg Glu Lys Met Arg Arg Asp Lys Leu Asn Asp Arg Phe
65 70 75 80
Leu Glu Leu Xaa Ser Val Met Asn Pro Gly Lys Gln Ala Lys Leu Asp
85 90 95
Lys Ala Asn Ile Leu Xaa Xaa Ala Ala Arg Met Val Ala Gln Leu Arg
100 105 110
Gly Glu Ala Glu Lys Leu Lys Glu Ser Asn Glu Lys Leu Arg Xaa Asn
115 120 125
Ile

(2) INFORMATION FOR SEQ ID NO:1848:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 546 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..546

(D) OTHER INFORMATION: / Ceres Seq. ID 1501439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848:

gaggcgatcg	catcgagac	tcggagccgg	caaaacccta	aggggaaggt	ttctgcaagg	60
aggagggaga	tgcagggcgc	cagcacatgc	tcctggagga	gcccttccgc	ctcgctcccg	120
tcctctcccc	cgccaagcct	aaagtattcc	catcactcac	caagatagtt	gggacgctcg	180
ggcccaattc	acactcgggt	gagattattc	aggaatgcct	cactgctgga	atgtcagttg	240
cacgatttga	tttctcatgg	atggatgctg	cgtatcacca	ggagaccctt	gataatttga	300
ggaaagcggc	acagaatgtg	aagaagttgt	gccctgtaat	gttggatact	cttgggtccag	360
aaattcaggt	tcacaattcc	actggtgagc	caattgagtt	gaaagctggg	aatcatgtta	420
tcataactcc	agatatttct	aaagctctct	ctgctgagat	cctaccaatt	aagtttggtg	480
atctggcaaa	agctgtgaag	aagggkgata	ctctttttat	gggccaatat	ctcttcacag	540
gaagtg						

(2) INFORMATION FOR SEQ ID NO:1849:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1501440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849:

Met Leu Leu Glu Glu Pro Phe Arg Leu Ala Ser Val Leu Ser Pro Ala
1 5 10 15
Lys Pro Lys Val Phe Pro Ser Leu Thr Lys Ile Val Gly Thr Leu Gly
20 25 30
Pro Asn Ser His Ser Val Glu Ile Ile Gln Glu Cys Leu Thr Ala Gly

35 40 45
Met Ser Val Ala Arg Phe Asp Phe Ser Trp Met Asp Ala Ala Tyr His
50 55 60
Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala Ala Gln Asn Val Lys Lys
65 70 75 80
Leu Cys Pro Val Met Leu Asp Thr Leu Gly Pro Glu Ile Gln Val His
85 90 95
Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys Ala Gly Asn His Val Ile
100 105 110
Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser Ala Glu Ile Leu Pro Ile
115 120 125
Lys Phe Gly Asp Leu Ala Lys Ala Val Lys Lys Xaa Asp Thr Leu Phe
130 135 140
Met Gly Gln Tyr Leu Phe Thr Gly Ser
145 150

(2) INFORMATION FOR SEQ ID NO:1850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850:

Met Ser Val Ala Arg Phe Asp Phe Ser Trp Met Asp Ala Ala Tyr His
1 5 10 15
Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala Ala Gln Asn Val Lys Lys
20 25 30
Leu Cys Pro Val Met Leu Asp Thr Leu Gly Pro Glu Ile Gln Val His
35 40 45
Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys Ala Gly Asn His Val Ile
50 55 60
Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser Ala Glu Ile Leu Pro Ile
65 70 75 80
Lys Phe Gly Asp Leu Ala Lys Ala Val Lys Lys Xaa Asp Thr Leu Phe
85 90 95
Met Gly Gln Tyr Leu Phe Thr Gly Ser
100 105

(2) INFORMATION FOR SEQ ID NO:1851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851:

Met Asp Ala Ala Tyr His Gln Glu Thr Leu Asp Asn Leu Arg Lys Ala
1 5 10 15
Ala Gln Asn Val Lys Lys Leu Cys Pro Val Met Leu Asp Thr Leu Gly
20 25 30
Pro Glu Ile Gln Val His Asn Ser Thr Gly Glu Pro Ile Glu Leu Lys
35 40 45
Ala Gly Asn His Val Ile Ile Thr Pro Asp Ile Ser Lys Ala Leu Ser
50 55 60

Ala Glu Ile Leu Pro Ile Lys Phe Gly Asp Leu Ala Lys Ala Val Lys
65 70 75 80
Lys Xaa Asp Thr Leu Phe Met Gly Gln Tyr Leu Phe Thr Gly Ser
85 90 95

(2) INFORMATION FOR SEQ ID NO:1852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 552 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..552
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852:

tgcgatacgg	gagcttgcc	ttctaaatcc	tgagctaaca	ataatcttga	caaaggaaga	60
agggcacaca	gttcaacgca	acgaatattg	ttatgctgg	ggccttggtg	aatatgttaa	120
atgggtgaat	actgacaaga	aacccttgca	tgacccgatt	gcgttcagaa	aggagttgga	180
tggtataaca	gtggatgtct	cccttcaatg	gtcctctgat	tcctactctg	atacagtgtc	240
aggatacgca	aacagtatcc	gcactattga	tggtgggtact	catattgatg	gtctaaaggc	300
ttcattgacg	agaaccatta	ataaccttgc	aaagaagtcg	aagmtattaa	ggataaggat	360
attaccttga	gtggggagca	tgtaagagaa	ggaatgacat	gcatcatttc	agtgaaggtc	420
cctagtccag	agtttgaggg	tcaaacaaag	acaaggttgg	gaaatccaga	agtacggaga	480
atagttgagc	agtctgttca	agaaaactta	acagagtact	tagagcttca	tccagatggt	540
ctggattcaa	tc					

(2) INFORMATION FOR SEQ ID NO:1853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853:

Arg	Ile	Arg	Glu	Leu	Ala	Phe	Leu	Asn	Pro	Glu	Leu	Thr	Ile	Ile	Leu	
1				5				10						15		
Thr	Lys	Glu	Glu	Gly	His	Thr	Val	Gln	Arg	Asn	Glu	Tyr	Cys	Tyr	Ala	
		20						25					30			
Gly	Gly	Leu	Val	Glu	Tyr	Val	Lys	Trp	Leu	Asn	Thr	Asp	Lys	Lys	Pro	
		35					40					45				
Leu	His	Asp	Pro	Ile	Ala	Phe	Arg	Lys	Glu	Leu	Asp	Gly	Ile	Thr	Val	
	50					55					60					
Asp	Val	Ser	Leu	Gln	Trp	Ser	Ser	Asp	Ser	Tyr	Ser	Asp	Thr	Val	Leu	
65				70						75					80	
Gly	Tyr	Ala	Asn	Ser	Ile	Arg	Thr	Ile	Asp	Gly	Gly	Thr	His	Ile	Asp	
			85					90						95		
Gly	Leu	Lys	Ala	Ser	Leu	Thr	Arg	Thr	Ile	Asn	Asn	Leu	Ala	Lys	Lys	
		100					105						110			
Ser	Lys	Xaa	Leu	Arg	Ile	Arg	Ile	Leu	Pro							
		115					120									

(2) INFORMATION FOR SEQ ID NO:1854:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 1501485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854:

actaccgag	ttcacttcac	actcgtgcac	ccatccgggt	cactgggtca	ctgacaccgc	60
gccccaatca	cgcgcgcgc	acccgcgatg	atggcggcgg	cggcgatctc	cggctccagc	120
ggccacctcg	tcgtctcttc	cccccgcttc	aggcagccgc	tcacgctccc	ttctcgcagc	180
ggtcgcccaa	tcgcgcgcgc	cgctcgggcc	gtggcccgcg	gcggggtcgc	ggtcgccgccc	240
gtgtccagcc	ccgctgtgtc	ggccgctcgc	gggaaggatg	ccaaacaggc	tcctaaggat	300
ttccttcata	tcaatgattt	tgacaaggat	acaataatga	atatccttaa	tcgagcgatc	360
gaggttaagg	cagcgataaa	gtctggagac	aggagcttcc	aaccattcaa	tgggaaatca	420
atggcgatga	tttttgccaa	gccatcaatg	aggacccgtg	tttcatttga	ggcgggattc	480
ttcttacttg	gtgggcgatg	tatttatttg	ggtcc			

(2) INFORMATION FOR SEQ ID NO:1855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1501486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855:

Tyr	Pro	Ser	Ser	His	Thr	Arg	Ala	Pro	Ile	Arg	Val	Thr	Gly	Ser	
1			5					10					15		
Leu	Thr	Pro	Arg	Pro	Asn	His	Ala	Arg	Ala	Thr	Arg	Asp	Asp	Gly	Gly
			20					25					30		
Gly	Gly	Asp	Leu	Arg	Leu	Gln	Arg	Pro	Pro	Arg	Arg	Leu	Leu	Pro	Pro
		35					40					45			
Leu	Gln	Ala	Ala	Ala	His	Ala	Pro	Phe	Ser	Gln	Arg	Ser	Pro	Asn	Arg
	50					55				60					
Arg	Arg	Arg	Leu	Gly	Arg	Gly	Pro	Arg	Arg	Gly	Arg	Gly	Arg	Arg	Arg
65					70				75					80	
Val	Gln	Pro	Arg	Cys	Val	Gly	Arg	Arg	Gly	Glu	Gly	Cys	Gln	Thr	Gly
			85					90						95	
Ser															

(2) INFORMATION FOR SEQ ID NO:1856:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1501487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856:

Met	Met	Ala	Ala	Ala	Ala	Ile	Ser	Gly	Ser	Ser	Gly	His	Leu	Val	Val
1					5				10					15	
Ser	Ser	Pro	Arg	Phe	Arg	Gln	Pro	Leu	Thr	Leu	Pro	Ser	Arg	Ser	Gly
			20					25					30		
Arg	Pro	Ile	Ala	Ala	Ala	Ala	Ser	Ala	Val	Ala	Arg	Gly	Gly	Val	Ala
			35				40					45			
Val	Ala	Ala	Val	Ser	Ser	Pro	Ala	Val	Ser	Ala	Val	Ala	Gly	Lys	Asp
	50					55					60				
Ala	Lys	Gln	Ala	Pro	Lys	Asp	Phe	Leu	His	Ile	Asn	Asp	Phe	Asp	Lys

(2) INFORMATION FOR SEQ ID NO:1857:

(A) LENGTH: 141 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1501488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857:

(2) INFORMATION FOR SEQ ID NO:1858:

(A) LENGTH: 577 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -

(B) LOCATION: 1..577

(D) OTHER INFORMATION: / Ceres Seq. ID 1501489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858:

aacctctcctg	ctcctcctcc	cacggtcccg	ccatttcgtc	ccccgctcac	caactcaaac	60
ccctcctcgt	ctcaaacctt	aaccctagcc	ctagcccgct	ccggcgagac	cgacgatgcc	120
gaagaggtcg	gcggggcggc	ggacgaagag	gagttccgcg	ccgaggtgga	ggagcgcttc	180
atcaacgagg	agtacaagat	ctggaagaag	aacacaccct	tcctctacga	cctcgtcatc	240
accacgcgc	tcgaatggcc	ctcccttacc	gtgcagtggc	tccccgaccg	caccgagccg	300
ccggggaagg	accactccgt	ccagaagatg	atccttggca	cgcacacctc	tgacaacgag	360
cccaactacc	tcatgctcgc	gcagggtccag	ctgccccctg	acgacgccga	ggccgacgcc	420
cgyactacg	acgatgacca	cgccgacatc	ggtggttttg	gcgcmgsctc	cggsaargtg	480
caaattgttc	agcagataaa	tcatgatgga	gaggccaatc	gagctcgcta	tatgccccaa	540
aattcatttta	taattqctac	taagacagtt	agcgcgag			

(2) INFORMATION FOR SEQ ID NO:1859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1501490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859:

Asn Pro Pro Ala Pro Pro Pro Thr Val Pro Pro Phe Arg Pro Pro Leu
1 5 10 15
Thr Asn Ser Asn Pro Leu Arg Ser Gln Thr Leu Thr Leu Ala Leu Ala
20 25 30
Arg Ser Arg Arg Thr Asp Asp Ala Glu Glu Val Gly Gly Ala Ala Asp
35 40 45
Glu Glu Glu Phe Arg Ala Glu Val Glu Glu Arg Leu Ile Asn Glu Glu
50 55 60
Tyr Lys Ile Trp Lys Lys Asn Thr Pro Phe Leu Tyr Asp Leu Val Ile
65 70 75 80
Thr His Ala Leu Glu Trp Pro Ser Leu Thr Val Gln Trp Leu Pro Asp
85 90 95
Arg Thr Glu Pro Pro Gly Lys Asp His Ser Val Gln Lys Met Ile Leu
100 105 110
Gly Thr His Thr Ser Asp Asn Glu Pro Asn Tyr Leu Met Leu Ala Gln
115 120 125
Val Gln Leu Pro Leu Asp Asp Ala Glu Ala Asp Ala Arg Xaa Tyr Asp
130 135 140
Asp Asp His Ala Asp Ile Gly Gly Phe Gly Xaa Xaa Ser Xaa Xaa Val
145 150 155 160
Gln Ile Val Gln Gln Ile Asn His Asp Gly Glu Val Asn Arg Ala Arg
165 170 175
Tyr Met Pro Gln Asn Ser Phe Ile Ile Ala Thr Lys Thr Val Ser Ala
180 185 190

(2) INFORMATION FOR SEQ ID NO:1860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 1501491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860:

Pro Ser Cys Ser Ser Ser His Gly Pro Ala Ile Ser Ser Pro Ala His
1 5 10 15
Gln Leu Lys Pro Pro Pro Leu Ser Asn Pro Asn Pro Ser Pro Ser Pro
20 25 30
Leu Pro Ala Asp Arg Arg Cys Arg Arg Gly Arg Arg Gly Gly Gly Arg
35 40 45
Arg Gly Val Pro Arg Arg Gly Gly Gly Ala Pro His Gln Arg Gly Val
50 55 60
Gln Asp Leu Glu Glu Glu His Thr Leu Pro Leu Arg Pro Arg His His
65 70 75 80
Pro Arg Ala Arg Met Ala Leu Pro Tyr Arg Ala Val Ala Pro Arg Pro

85 90 95
His Arg Ala Ala Gly Glu Gly Pro Leu Arg Pro Glu Asp Asp Pro Trp
100 105 110
His Ala His Leu
115

(2) INFORMATION FOR SEQ ID NO:1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..967
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861:

aaaaaactct	ctgtctctct	aggttttttg	atttttagccg	ccgccgctgc	tcattctcaca	60
tccctcgaga	agacgcctgc	tcctcgccga	tcgatacgat	ggcgcgtctc	tccgacctcc	120
acaccgccga	cggcctcaag	tcctcgagg	ctcacctcgc	cggcaaaacc	tatgtgtctg	180
gtgactccat	tactaaggat	gacattaagg	tcttcgccgc	ggtgccgctc	aagcctggcg	240
ctgagtttcc	taatgccgcc	cgctggtacg	agaccgtctc	tgccgctgta	gcctcaagat	300
tccttggtaa	ggctggttgg	gtaaatctgc	ctgcgggatc	agctcctgcg	gcagctgctc	360
ctgcggatga	ggctgaggat	gatgatgacc	ttgatctttt	tggtgatgaa	actgaggagg	420
acaagaaggc	agctgatgag	cgtgccgccg	ctgccaaagg	ctcttctaaa	aagaaagaaa	480
gtggtaaatc	ctccgtcctt	atggatgtca	aaccatggga	cgatgagact	gatatgaaga	540
agctggagga	ggctgtccgc	agtgtccaga	tggagggtct	gacttgggga	gcatcaaagc	600
ttgtgcctgt	tggatacggc	atcaagaaga	tgactatcat	gttgacaatt	gtcgacgatc	660
ttgtgtccat	cgacactcta	attgaggacc	accttacgca	agagcccatc	aatgagtacg	720
tccagagttg	cgacattgtg	gctttcaaca	agatctagag	ttcagtttct	gagattgggc	780
aacggcagcg	gctcagctcg	tcaagtttgt	gctgggatgc	cagtttatcc	cttctagtct	840
attacagaaa	tgttgttcgg	agctgagtc	attataaaca	tcttggtctg	agtttattgt	900
tgagtgggtc	cagttttttt	caatatacat	ttatcttaaa	aacagcggta	ctgatgtttt	960
ttgtct						

(2) INFORMATION FOR SEQ ID NO:1862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862:

Lys	Thr	Leu	Cys	Leu	Ser	Arg	Phe	Phe	Asp	Phe	Ser	Arg	Arg	Cys
1			5						10				15	
Ser	Ser	His	Ile	Pro	Arg	Glu	Asp	Ala	Cys	Ser	Ser	Pro	Ile	Asp
		20						25				30		Thr
Met	Ala	Val	Phe	Ser	Asp	Leu	His	Thr	Ala	Asp	Gly	Leu	Lys	Ser
	35					40					45			Leu
Glu	Ala	His	Leu	Ala	Gly	Lys	Thr	Tyr	Val	Ser	Gly	Asp	Ser	Ile
	50					55					60			Thr
Lys	Asp	Asp	Ile	Lys	Val	Phe	Ala	Ala	Val	Pro	Ser	Lys	Pro	Gly
65					70				75				80	Ala
Glu	Phe	Pro	Asn	Ala	Ala	Arg	Trp	Tyr	Glu	Thr	Val	Ser	Ala	Val
			85					90					95	
Ala	Ser	Arg	Phe	Pro	Gly	Lys	Ala	Val	Gly	Val	Asn	Leu	Pro	Ala
	100							105				110		Gly
Ser	Ala	Pro	Ala	Ala	Ala	Ala	Pro	Ala	Asp	Glu	Ala	Glu	Asp	Asp

115	120	125
Asp Leu Asp Leu Phe Gly	Asp Glu Thr Glu Glu	Asp Lys Lys Ala Ala
130	135	140
Asp Glu Arg Ala Ala Ala	Lys Ala Ser Ser	Lys Lys Lys Glu Ser
145	150	155
Gly Lys Ser Ser Val Leu	Met Asp Val Lys	Pro Trp Asp Asp Glu Thr
165	170	175
Asp Met Lys Lys Leu Glu	Glu Ala Val Arg	Ser Val Gln Met Glu Gly
180	185	190
Leu Thr Trp Gly Ala Ser	Lys Leu Val Pro	Val Gly Tyr Gly Ile Lys
195	200	205
Lys Met Thr Ile Met Leu	Thr Ile Val Asp	Asp Leu Val Ser Ile Asp
210	215	220
Thr Leu Ile Glu Asp His	Leu Thr Gln Glu	Pro Ile Asn Glu Tyr Val
225	230	235
Gln Ser Cys Asp Ile Val	Ala Phe Asn Lys	Ile
245	250	

(2) INFORMATION FOR SEQ ID NO:1863:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1501517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863:

Met	Ala	Val	Phe	Ser	Asp	Leu	His	Thr	Ala	Asp	Gly	Leu	Lys	Ser	Leu
1			5						10					15	
Glu	Ala	His	Leu	Ala	Gly	Lys	Thr	Tyr	Val	Ser	Gly	Asp	Ser	Ile	Thr
		20						25					30		
Lys	Asp	Asp	Ile	Lys	Val	Phe	Ala	Ala	Val	Pro	Ser	Lys	Pro	Gly	Ala
	35					40						45			
Glu	Phe	Pro	Asn	Ala	Ala	Arg	Trp	Tyr	Glu	Thr	Val	Ser	Ala	Ala	Val
	50				55						60				
Ala	Ser	Arg	Phe	Pro	Gly	Lys	Ala	Val	Gly	Val	Asn	Leu	Pro	Ala	Gly
65			70						75					80	
Ser	Ala	Pro	Ala	Ala	Ala	Ala	Pro	Ala	Asp	Glu	Ala	Glu	Asp	Asp	Asp
		85							90					95	
Asp	Leu	Asp	Leu	Phe	Gly	Asp	Glu	Thr	Glu	Glu	Asp	Lys	Lys	Ala	Ala
	100							105					110		
Asp	Glu	Arg	Ala	Ala	Ala	Ala	Lys	Ala	Ser	Ser	Lys	Lys	Lys	Glu	Ser
	115							120				125			
Gly	Lys	Ser	Ser	Val	Leu	Met	Asp	Val	Lys	Pro	Trp	Asp	Asp	Glu	Thr
	130					135					140				
Asp	Met	Lys	Lys	Leu	Glu	Ala	Val	Arg	Ser	Val	Gln	Met	Glu	Gly	
145				150					155					160	
Leu	Thr	Trp	Gly	Ala	Ser	Lys	Leu	Val	Pro	Val	Gly	Tyr	Gly	Ile	Lys
		165							170					175	
Lys	Met	Thr	Ile	Met	Leu	Thr	Ile	Val	Asp	Asp	Leu	Val	Ser	Ile	Asp
	180							185					190		
Thr	Leu	Ile	Glu	Asp	His	Leu	Thr	Gln	Glu	Pro	Ile	Asn	Glu	Tyr	Val
	195						200					205			
Gln	Ser	Cys	Asp	Ile	Val	Ala	Phe	Asn	Lys	Ile					
	210					215									

(2) INFORMATION FOR SEQ ID NO:1864:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 584 base pairs

(B) TYPE: nucleic acid

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864:

(2) INFORMATION FOR SEO ID NO:1865:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1501544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865:

(2) INFORMATION FOR SEQ ID NO:1866:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..151
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866:

```
Met Ser Asp Ser His Glu Thr Asp Arg Asn Ile Glu Ile Trp Lys Ile
1      5      10      15
Lys Lys Leu Ile Lys Ala Leu Glu Ser Ala Arg Gly Asn Gly Thr Ser
20      25      30
Met Ile Ser Leu Ile Met Pro Pro Arg Asp Gln Val Ala Arg Val Ala
35      40      45
Lys Met Leu Gly Asp Glu Tyr Gly Thr Ala Ser Asn Ile Lys Ser Arg
50      55      60
Val Asn Arg Gln Ser Val Leu Ala Ala Ile Thr Ser Ala Gln Gln Arg
65      70      75      80
Leu Lys Leu Tyr Asn Lys Val Pro Pro Asn Gly Leu Val Leu Tyr Thr
85      90      95
Gly Thr Ile Val Thr Glu Asp Gly Lys Glu Lys Lys Val Thr Ile Asp
100     105     110
Phe Glu Pro Phe Lys Pro Ile Asn Val Ser Leu Tyr Leu Cys Asp Asn
115     120     125
Lys Phe His Thr Glu Ala Leu Asn Glu Leu Leu Glu Ser Asp Asp Lys
130     135     140
Phe Gly Phe Ile Val Met Asp
145     150
```

(2) INFORMATION FOR SEQ ID NO:1867:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..119

 (D) OTHER INFORMATION: / Ceres Seq. ID 1501546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867:

```
Met Ile Ser Leu Ile Met Pro Pro Arg Asp Gln Val Ala Arg Val Ala
1      5      10      15
Lys Met Leu Gly Asp Glu Tyr Gly Thr Ala Ser Asn Ile Lys Ser Arg
20      25      30
Val Asn Arg Gln Ser Val Leu Ala Ala Ile Thr Ser Ala Gln Gln Arg
35      40      45
Leu Lys Leu Tyr Asn Lys Val Pro Pro Asn Gly Leu Val Leu Tyr Thr
50      55      60
Gly Thr Ile Val Thr Glu Asp Gly Lys Glu Lys Lys Val Thr Ile Asp
65      70      75      80
Phe Glu Pro Phe Lys Pro Ile Asn Val Ser Leu Tyr Leu Cys Asp Asn
85      90      95
Lys Phe His Thr Glu Ala Leu Asn Glu Leu Leu Glu Ser Asp Asp Lys
100     105     110
Phe Gly Phe Ile Val Met Asp
115
```

(2) INFORMATION FOR SEQ ID NO:1868:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1030 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1030

(D) OTHER INFORMATION: / Ceres Seq. ID 1501547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868:

aaaaggaacc	ctagccatga	gcgccgcctc	caagaagctc	ttccaggccg	ccaggtcctc	60
cgtcctctcc	gcttctaacc	gctccgtcct	cgccgccgag	ggccgcaccg	ccgcgctcgc	120
cacgctcacc	aactttggca	ggaagaccct	ccccaccgcc	tacttatcct	accacaagca	180
gggatcccac	catgccgcgt	cgggggtggg	agccatcgcc	gccgcagtc	cagctgmagt	240
ttacatgctc	caggaccagg	aggctcatgc	tgcagagatg	gagcgcacct	tcattgccat	300
caagcctgat	ggtgtccaaa	gaggcctgat	ttctgagatt	atgagccgat	ttgagagaaa	360
aggctataag	cttggttgcca	tcaagctgat	tgttccatcc	aaagaatttg	ctgagaagca	420
ctaccatgat	ctcaaggaaa	ggcctttctt	cagtgggttg	tgtgattttc	tcagctctgg	480
ccctgtgctt	gcaatggttt	gggaaggaga	gggtgtcatc	aagtatggga	gaaaactaat	540
tggtgccaca	gacccacaga	aatctgaacc	aggaaccatc	aggggtgatc	ttgccattgt	600
tgttgaaga	aacatcattc	atggaagtga	tggcccagag	acagcgaagg	atgagatcgc	660
tttatggttt	gaacccaagg	agctggtctc	ttacaccagc	aatgcggaga	agtggatcta	720
tgggggtgaat	taacgagaga	gtcaatctgt	tttttttctt	tcttttgatc	tcggttttca	780
cataattgcc	gacagacct	ggcacaagga	tgtataaaag	tcgctaccgt	cacttctgag	840
ttggattgtg	accttcaggt	gtagtaaggc	acaaggaagg	atggaaagga	aaggaatata	900
ccgtgaaata	tagagcgtgc	actgagtagt	cgcgatgttc	aaatcaaact	atatatcacc	960
gtcactggag	tcattgaatc	caagatgggt	atgcagatgt	ttctttggat	ctatttctct	1020
agatatcccc						

(2) INFORMATION FOR SEQ ID NO:1869:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..243

(D) OTHER INFORMATION: / Ceres Seq. ID 1501548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869:

Lys	Gly	Thr	Leu	Ala	Met	Ser	Ala	Ala	Ser	Lys	Lys	Leu	Phe	Gln	Ala
1			5					10						15	
Ala	Arg	Ser	Leu	Val	Leu	Ser	Ala	Ser	Asn	Arg	Ser	Val	Leu	Ala	Ala
			20					25					30		
Glu	Gly	Arg	Thr	Ala	Ala	Leu	Ala	Thr	Leu	Thr	Asn	Phe	Gly	Arg	Lys
			35				40					45			
Thr	Leu	Pro	Thr	Ala	Tyr	Leu	Ser	Tyr	His	Lys	Gln	Gly	Ser	His	His
			50				55				60				
Ala	Ala	Ser	Gly	Trp	Gly	Ala	Ile	Ala	Ala	Ala	Val	Pro	Ala	Xaa	Val
65					70				75					80	
Tyr	Met	Leu	Gln	Asp	Gln	Glu	Ala	His	Ala	Ala	Glu	Met	Glu	Arg	Thr
			85					90						95	
Phe	Ile	Ala	Ile	Lys	Pro	Asp	Gly	Val	Gln	Arg	Gly	Leu	Ile	Ser	Glu
			100				105						110		
Ile	Met	Ser	Arg	Phe	Glu	Arg	Lys	Gly	Tyr	Lys	Leu	Val	Ala	Ile	Lys
			115				120					125			
Leu	Ile	Val	Pro	Ser	Lys	Glu	Phe	Ala	Glu	Lys	His	Tyr	His	Asp	Leu
			130				135				140				
Lys	Glu	Arg	Pro	Phe	Phe	Ser	Gly	Leu	Cys	Asp	Phe	Leu	Ser	Ser	Gly
145					150				155					160	
Pro	Val	Leu	Ala	Met	Val	Trp	Glu	Gly	Glu	Gly	Val	Ile	Lys	Tyr	Gly
			165					170						175	
Arg	Lys	Leu	Ile	Gly	Ala	Thr	Asp	Pro	Gln	Lys	Ser	Glu	Pro	Gly	Thr
			180					185					190		
Ile	Arg	Gly	Asp	Leu	Ala	Ile	Val	Val	Gly	Arg	Asn	Ile	Ile	His	Gly

	195					200						205					
Ser	Asp	Gly	Pro	Glu	Thr	Ala	Lys	Asp	Glu	Ile	Ala	Leu	Trp	Phe	Glu		
	210						215					220					
Pro	Lys	Glu	Leu	Val	Ser	Tyr	Thr	Ser	Asn	Ala	Glu	Lys	Trp	Ile	Tyr		
	225					230					235				240		
Gly	Val	Asn															

(2) INFORMATION FOR SEQ ID NO:1870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..238

(D) OTHER INFORMATION: / Ceres Seq. ID 1501549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870:

Met	Ser	Ala	Ala	Ser	Lys	Lys	Leu	Phe	Gln	Ala	Ala	Arg	Ser	Leu	Val		
1				5					10					15			
Leu	Ser	Ala	Ser	Asn	Arg	Ser	Val	Leu	Ala	Ala	Glu	Gly	Arg	Thr	Ala		
			20					25					30				
Ala	Leu	Ala	Thr	Leu	Thr	Asn	Phe	Gly	Arg	Lys	Thr	Leu	Pro	Thr	Ala		
		35				40						45					
Tyr	Leu	Ser	Tyr	His	Lys	Gln	Gly	Ser	His	His	Ala	Ala	Ser	Gly	Trp		
	50				55						60						
Gly	Ala	Ile	Ala	Ala	Ala	Val	Pro	Ala	Xaa	Val	Tyr	Met	Leu	Gln	Asp		
65				70					75					80			
Gln	Glu	Ala	His	Ala	Ala	Glu	Met	Glu	Arg	Thr	Phe	Ile	Ala	Ile	Lys		
			85						90					95			
Pro	Asp	Gly	Val	Gln	Arg	Gly	Leu	Ile	Ser	Glu	Ile	Met	Ser	Arg	Phe		
			100					105					110				
Glu	Arg	Lys	Gly	Tyr	Lys	Leu	Val	Ala	Ile	Lys	Leu	Ile	Val	Pro	Ser		
		115				120						125					
Lys	Glu	Phe	Ala	Glu	Lys	His	Tyr	His	Asp	Leu	Lys	Glu	Arg	Pro	Phe		
	130				135						140						
Phe	Ser	Gly	Leu	Cys	Asp	Phe	Leu	Ser	Ser	Gly	Pro	Val	Leu	Ala	Met		
145				150						155					160		
Val	Trp	Glu	Gly	Glu	Gly	Val	Ile	Lys	Tyr	Gly	Arg	Lys	Leu	Ile	Gly		
			165						170					175			
Ala	Thr	Asp	Pro	Gln	Lys	Ser	Glu	Pro	Gly	Thr	Ile	Arg	Gly	Asp	Leu		
		180						185					190				
Ala	Ile	Val	Val	Gly	Arg	Asn	Ile	Ile	His	Gly	Ser	Asp	Gly	Pro	Glu		
	195					200						205					
Thr	Ala	Lys	Asp	Glu	Ile	Ala	Leu	Trp	Phe	Glu	Pro	Lys	Glu	Leu	Val		
	210					215						220					
Ser	Tyr	Thr	Ser	Asn	Ala	Glu	Lys	Trp	Ile	Tyr	Gly	Val	Asn				
225				230						235							

(2) INFORMATION FOR SEQ ID NO:1871:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1501550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871:

Met Leu Gln Asp Gln Glu Ala His Ala Ala Glu Met Glu Arg Thr Phe
1 5 10 15
Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly Leu Ile Ser Glu Ile
20 25 30
Met Ser Arg Phe Glu Arg Lys Gly Tyr Lys Leu Val Ala Ile Lys Leu
35 40 45
Ile Val Pro Ser Lys Glu Phe Ala Glu Lys His Tyr His Asp Leu Lys
50 55 60
Glu Arg Pro Phe Phe Ser Gly Leu Cys Asp Phe Leu Ser Ser Gly Pro
65 70 75 80
Val Leu Ala Met Val Trp Glu Gly Glu Gly Val Ile Lys Tyr Gly Arg
85 90 95
Lys Leu Ile Gly Ala Thr Asp Pro Gln Lys Ser Glu Pro Gly Thr Ile
100 105 110
Arg Gly Asp Leu Ala Ile Val Val Gly Arg Asn Ile Ile His Gly Ser
115 120 125
Asp Gly Pro Glu Thr Ala Lys Asp Glu Ile Ala Leu Trp Phe Glu Pro
130 135 140
Lys Glu Leu Val Ser Tyr Thr Ser Asn Ala Glu Lys Trp Ile Tyr Gly
145 150 155 160
Val Asn

(2) INFORMATION FOR SEQ ID NO:1872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..563
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872:

attggcgac	aaatcagcaa	caggcgcggc	gaacaaatgg	ggcgtctgta	gtccggaggc	60
cttcttagtt	taggggctct	ggcccgatc	gacctgttt	ttttttcca	atagcggatt	120
arcccaacag	agaacctttc	acggccctgc	tagagagagt	ttaacaatca	aaatagaaaa	180
cagaaacaaa	attcatcaga	gtgagagttc	atcttcttct	ccaagctgat	ttctgcttgt	240
tagctactca	cgtcaacaga	aaatctcgcg	ttcagctcct	ctccagtctc	tccgcctccc	300
gcttacttct	ctgactctgt	cctctttcgt	ttctttcttg	tcggcgacgg	ctggcggtcg	360
gggtgctgcg	ccgctctcac	cttcaccgcc	gacgagcatt	cacaagtagt	ggtctcttac	420
wggtggcggc	gtagaggtga	cgaaaaagcc	ttgacaatga	gcagcatagg	cacaggttat	480
gatctgtctg	tcaccacctt	ctctccccgat	ggccgcgtct	tccaggtcga	gtatgccacg	540
aargctgtcg	acaacagcgg	gac				

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873:

Met Ser Ser Ile Gly Thr Gly Tyr Asp Leu Ser Val Thr Thr Phe Ser
1 5 10 15
Pro Asp Gly Arg Val Phe Gln Val Glu Tyr Ala Thr Xaa Ala Val Asp
20 25 30
Asn Ser Gly

35

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 567 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..567
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874:

agggcaaaag	aggaaatttc	tttgggctgg	gtctaataaa	ccctaattggg	ctgcggcctc	60
gtagataaac	cagcactact	catccgctgc	cccacggaag	tttcggcggc	gcsgcgtgct	120
cgtgatctca	accaaggcgt	gtctccgctc	cggtcacccg	tactccacg	caaacatgtc	180
gaggaggaag	accagggagc	ccaaggagga	gaacgtcacc	cttggaacca	ctgtccgtga	240
aggagagtat	gtcttttgtg	tcgctcacat	ctttgcatcc	ttcaatgaca	ccttcattca	300
tatcactgat	ttgtctggga	gggaaactct	ggttcggatc	accggtggca	tgaaggtgaa	360
ggctgaccgt	gacgagtcgt	caccttacgc	tgctatgctt	gctgctcaag	acgtcgcaca	420
gcgctgcaag	gagcttggca	ttactgcact	gcacattaag	cttcgtgcca	ccggaggcaa	480
caagaccaag	acccccggac	ctggtgcccc	gtctgccctc	agggcgcttg	ctcgtttctg	540
gatgaaaatc	ggacgcattg	aggacgt				

(2) INFORMATION FOR SEQ ID NO:1875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875:

Met	Gly	Cys	Gly	Leu	Val	Asp	Lys	Pro	Ala	Leu	Leu	Ile	Arg	Arg	Pro
1			5				10				15				
Thr	Glu	Val	Ser	Ala	Ala	Xaa	Arg	Ala	Arg	Asp	Leu	Asn	Gln	Gly	Val
			20				25				30				
Ser	Pro	Leu	Arg	Ser	Pro	Val	Thr	Pro	Arg	Lys	His	Val	Glu	Glu	Glu
			35				40				45				
Asp	Gln	Gly	Ala	Gln	Gly	Gly	Glu	Arg	His	Pro	Trp	Thr	His	Cys	Pro
			50				55				60				

(2) INFORMATION FOR SEQ ID NO:1876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876:

Met	Ser	Arg	Arg	Lys	Thr	Arg	Glu	Pro	Lys	Glu	Glu	Asn	Val	Thr	Leu
1				5			10				15				
Gly	Pro	Thr	Val	Arg	Glu	Gly	Glu	Tyr	Val	Phe	Xaa	Val	Ala	His	Ile
			20				25				30				

Phe Ala Ser Phe Asn Asp Thr Phe Ile His Ile Thr Asp Leu Ser Gly
35 40 45
Arg Glu Thr Leu Val Arg Ile Thr Gly Gly Met Lys Val Lys Ala Asp
50 55 60
Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met Leu Ala Ala Gln Asp Val
65 70 75 80
Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr Ala Leu His Ile Lys Leu
85 90 95
Arg Ala Thr Gly Gly Asn Lys Thr Lys Thr Pro Gly Pro Gly Ala Gln
100 105 110
Ser Ala Leu Arg Ala Leu Ala Arg Ser Gly Met Lys Ile Gly Arg Ile
115 120 125
Glu Asp
130

(2) INFORMATION FOR SEQ ID NO:1877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877:

Met Lys Val Lys Ala Asp Arg Asp Glu Ser Pro Tyr Ala Ala Met
1 5 10 15
Leu Ala Ala Gln Asp Val Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr
20 25 30
Ala Leu His Ile Lys Leu Arg Ala Thr Gly Gly Asn Lys Thr Lys Thr
35 40 45
Pro Gly Pro Gly Ala Gln Ser Ala Leu Arg Ala Leu Ala Arg Ser Gly
50 55 60
Met Lys Ile Gly Arg Ile Glu Asp
65 70

(2) INFORMATION FOR SEQ ID NO:1878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878:

gtcatcaatc	aaataactcag	acaaccatgg	ggcaccagca	ggcgcasacg	gcaaggacga	60
caccgaggag	ctgcttgcag	cccaccggca	gctgtrgtgc	catgccctgg	gctacgtcaa	120
gtccatggcg	ctcaagtgcg	ccctggacct	gcgcattccc	gacaccatcg	accgctgcgg	180
cgggagcgcc	accctgggcg	agctgctcgc	cgccagcgag	atcccggcgt	ccaaccacga	240
ctacctccgg	cggttcctgc	gcacgctgac	agccatgcgc	atcttcgcgg	ccagccacga	300
ccccgccaag	gccgacgacg	cgccgcccac	ctcctaccag	ctgaccccgg	cgccccggct	360
gctcgtcagc	agcagcagca	gcgtcgacga	cgccgcccgg	cctcgaagga	gaacactact	420
accccgagca	tcctcccca	catcgcccac	ctggtccgcc	ccaacaccat	ctccctgctg	480
ttcagcatgg	gcgag					

(2) INFORMATION FOR SEQ ID NO:1879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..165
(D) OTHER INFORMATION: / Ceres Seq. ID 1501572
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879:

Val Ile Asn Gln Ile Leu Arg Gln Pro Trp Gly Thr Ser Arg Arg Xaa
1 5 10 15
Arg Gln Gly Arg His Arg Gly Ala Ala Cys Ser Pro Pro Ala Ala Xaa
20 25 30
Val Pro Cys Pro Gly Leu Arg Gln Val His Gly Ala Gln Val Arg Pro
35 40 45
Gly Pro Ala His Pro Arg His His Arg Pro Leu Arg Arg Glu Arg His
50 55 60
Pro Gly Arg Ala Ala Arg Arg Gln Arg Asp Pro Gly Val Gln Pro Arg
65 70 75 80
Leu Pro Pro Ala Gly His Ala His Ala Asp Ser His Ala His Leu Arg
85 90 95
Gly Gln Pro Arg Pro Arg Gln Gly Arg Arg Arg Gly Arg His Leu Leu
100 105 110
Pro Ala Asp Pro Gly Val Pro Ala Ala Arg Gln Gln Gln Gln Arg
115 120 125
Arg Arg Arg Arg Arg Ala Ser Lys Glu Asn Thr Thr Thr Pro Ser Ile
130 135 140
Leu Pro Asn Ile Ala His Leu Val Arg Pro Asn Thr Ile Ser Leu Leu
145 150 155 160
Phe Ser Met Gly Glu
165

(2) INFORMATION FOR SEQ ID NO:1880:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..164
(D) OTHER INFORMATION: / Ceres Seq. ID 1501573
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1880:

Ser Ser Ile Lys Tyr Ser Asp Asn His Gly Ala Pro Ala Gly Ala Xaa
1 5 10 15
Gly Lys Asp Asp Thr Glu Glu Leu Leu Ala Ala His Arg Gln Leu Xaa
20 25 30
Cys His Ala Leu Gly Tyr Val Lys Ser Met Ala Leu Lys Cys Ala Leu
35 40 45
Asp Leu Arg Ile Pro Asp Thr Ile Asp Arg Cys Gly Gly Ser Ala Thr
50 55 60
Leu Gly Glu Leu Leu Ala Ala Ser Glu Ile Pro Ala Ser Asn His Asp
65 70 75 80
Tyr Leu Arg Arg Val Met Arg Thr Leu Thr Ala Met Arg Ile Phe Ala
85 90 95
Ala Ser His Asp Pro Ala Lys Ala Asp Asp Ala Ala Ala Ile Ser Tyr
100 105 110
Gln Leu Thr Pro Ala Ser Arg Leu Leu Val Ser Ser Ser Ser Val
115 120 125
Asp Asp Ala Ala Gly Pro Arg Arg Arg Thr Leu Leu Pro Arg Ala Ser
130 135 140
Ser Pro Thr Ser Pro Thr Trp Ser Ala Pro Thr Pro Ser Pro Cys Cys

145
Ser Ala Trp Ala

150

155

160

(2) INFORMATION FOR SEQ ID NO:1881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881:

Met Ala Leu Lys Cys Ala Leu Asp Leu Arg Ile Pro Asp Thr Ile Asp
1 5 10 15
Arg Cys Gly Gly Ser Ala Thr Leu Gly Glu Leu Leu Ala Ala Ser Glu
20 25 30
Ile Pro Ala Ser Asn His Asp Tyr Leu Arg Arg Val Met Arg Thr Leu
35 40 45
Thr Ala Met Arg Ile Phe Ala Ala Ser His Asp Pro Ala Lys Ala Asp
50 55 60
Asp Ala Ala Ala Ile Ser Tyr Gln Leu Thr Pro Ala Ser Arg Leu Leu
65 70 75 80
Val Ser Ser Ser Ser Ser Val Asp Asp Ala Ala Gly Pro Arg Arg Arg
85 90 95
Thr Leu Leu Pro Arg Ala Ser Ser Pro Thr Ser Pro Thr Trp Ser Ala
100 105 110
Pro Thr Pro Ser Pro Cys Cys Ser Ala Trp Ala
115 120

(2) INFORMATION FOR SEQ ID NO:1882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..500
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1882:

atcttaacag ccaggaagct ggcgctcttg ttgtccttgt tcttttccca cccggctacc 60
cccgtcgtcg ccgccgcttt ccccggtggt tcagagctcg agtcggctag ctaggccgcc 120
tggttaatct ccctgccttc tataagtaca gggtcattgt gtgctgtgct cccagctcca 180
tactgacac aagagagcac gctactactc atcactcgcc aacgtgcaga gatcaggag 240
gcggcacact ccattccactg accgctcatg gcgaagggtcc acctctacgt cgccgcggcc 300
tgccgcgtcg tccctcgctg cgccgccccg gccctcgccg gcgacccccga catgctgcag 360
gacgtctgcc cggctgacta cgccctcccc gtgaagctga acgggttcgc gtgcaaggcg 420
aacttttcgg cggacgactt cttcttcgac gggctgagga accccggcaa caccaacaac 480
ccggcgggct ccgtggtgac

(2) INFORMATION FOR SEQ ID NO:1883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1501583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883:

Met Ala Lys Val His Leu Tyr Val Ala Ala Cys Ala Val Val Leu
1 5 10 15
Ala Leu Ala Ala Pro Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp
20 25 30
Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu Asn Gly Phe Ala
35 40 45
Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe Asp Gly Leu Arg
50 55 60
Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:1884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1501584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884:

Met Leu Gln Asp Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu
1 5 10 15
Asn Gly Phe Ala Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe
20 25 30
Asp Gly Leu Arg Asn Pro Gly Asn Thr Asn Asn Pro Ala Gly Ser Val
35 40 45
Val

(2) INFORMATION FOR SEQ ID NO:1885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 515 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 1501589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885:

agtggacagg tggcatcttc tgcgctcgca acacctcggc gcccaaacgt aaccgtccca 60
acaaactcct ctccctcccc ttcccagcag aagtaccagc gccggccatg gacatgcagt 120
tcttccccga caggcgact tgcgcctgcg gascgctggc acggcatgta ccttcacgcc 180
gaggaagacg gggtaggat caccctgcgc cggcgccgtg ggacgctgaa cgaggcgtgg 240
gtrgtgcacc acctcgagcg caacggcgctc aactacgtcc tcctccacag cgccgcctac 300
ggccggtacc tcgccatcgt aagcatggaa gcgactccgg cgccgtcttc gggccaaggt 360
caaggcgccc gccgcacctg cctcgccgtc cagcgccctt acgacgcccc agggcagaac 420
gacgtcctgt ggcagttccg cttcgcgacg acgggtccga cgatgtcgtc atgcgcaatc 480
gcgtgtacgg cacctggcac aactacggcg acgag

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1501590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886:

Ser	Gly	Gln	Val	Ala	Ser	Ser	Ala	Leu	Ala	Thr	Pro	Arg	Arg	Pro	Asn	
1					5				10					15		
Val	Thr	Val	Pro	Thr	Asn	Ser	Ser	Pro	Ser	Pro	Ser	Gln	Gln	Lys	Tyr	
			20					25					30			
Gln	Arg	Arg	Pro	Trp	Thr	Cys	Ser	Ser	Ser	Pro	Thr	Gly	Ala	Leu	Ala	
			35				40					45				
Pro	Ala	Xaa	Arg	Trp	His	Gly	Met	Tyr	Leu	His	Ala	Glu	Glu	Asp	Gly	
			50			55					60					
Val	Arg	Ile	Thr	Leu	Arg	Arg	Arg	Arg	Gly	Thr	Leu	Asn	Glu	Ala	Trp	
65					70				75						80	
Xaa	Val	His	His	Leu	Glu	Arg	Asn	Gly	Val	Asn	Tyr	Val	Leu	Leu	His	
				85					90					95		
Ser	Ala	Ala	Tyr	Gly	Arg	Tyr	Leu	Ala	Ile	Val	Ser	Met	Glu	Ala	Thr	
			100					105					110			
Pro	Ala	Pro	Ser	Ser	Gly	Gln	Gly	Gln	Gly	Ala	Arg	Arg	Thr	Cys	Leu	
			115				120						125			
Ala	Val	Gln	Arg	Leu	Tyr	Asp	Ala	Pro	Gly	Gln	Asn	Asp	Val	Leu	Trp	
			130				135					140				
Gln	Phe	Arg	Phe	Ala	Thr	Thr	Gly	Pro	Thr	Met	Ser	Ser	Cys	Ala	Ile	
145					150				155						160	
Ala	Cys	Thr	Ala	Pro	Gly	Thr	Thr	Thr	Ala	Thr						
				165					170							

(2) INFORMATION FOR SEQ ID NO:1887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1501591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887:

Trp	Thr	Gly	Gly	Ile	Phe	Cys	Ala	Arg	Asn	Thr	Ser	Ala	Pro	Lys	Arg	
1				5					10					15		
Asn	Arg	Pro	Asn	Lys	Leu	Leu	Ser	Leu	Pro	Phe	Pro	Ala	Glu	Val	Pro	
			20					25					30			
Ala	Pro	Ala	Met	Asp	Met	Gln	Phe	Pro	Asp	Arg	Arg	Thr	Cys	Ala		
			35				40					45				
Cys	Gly	Xaa	Leu	Ala	Arg	His	Val	Pro	Ser	Arg	Arg	Gly	Arg	Arg	Gly	
			50			55					60					
Glu	Asp	His	Pro	Ala	Pro	Ala	Pro	Trp	Asp	Ala	Glu	Arg	Gly	Val	Gly	
65				70					75						80	
Xaa	Ala	Pro	Pro	Arg	Ala	Gln	Arg	Arg	Gln	Leu	Arg	Pro	Pro	Pro	Gln	
				85					90					95		
Arg	Arg	Leu	Arg	Pro	Leu	Pro	Arg	His	Arg	Lys	His	Gly	Ser	Asp	Ser	
			100					105					110			
Gly	Ala	Val	Phe	Gly	Pro	Arg	Ser	Arg	Arg	Pro	Pro	His	Leu	Pro	Arg	
			115				120					125				
Arg	Pro	Ala	Pro	Leu	Arg	Arg	Pro	Arg	Ala	Glu	Arg	Arg	Pro	Val	Ala	
			130				135					140				
Val	Pro	Leu	Arg	Asp	Asp	Gly	Ser	Asp	Asp	Val	Met	Arg	Asn	Arg		
145				150					155						160	
Val	Tyr	Gly	Thr	Trp	His	Asn	Tyr	Gly	Asp	Glu						
				165					170							

(2) INFORMATION FOR SEQ ID NO:1888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1501592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888:

Met Asp Met Gln Phe Phe Pro Asp Arg Arg Thr Cys Ala Cys Gly Xaa
1 5 10 15
Leu Ala Arg His Val Pro Ser Arg Arg Gly Arg Arg Gly Glu Asp His
20 25 30
Pro Ala Pro Ala Pro Trp Asp Ala Glu Arg Gly Val Gly Xaa Ala Pro
35 40 45
Pro Arg Ala Gln Arg Arg Gln Leu Arg Pro Pro Pro Gln Arg Arg Leu
50 55 60
Arg Pro Leu Pro Arg His Arg Lys His Gly Ser Asp Ser Gly Ala Val
65 70 75 80
Phe Gly Pro Arg Ser Arg Arg Pro Pro His Leu Pro Arg Arg Pro Ala
85 90 95
Pro Leu Arg Arg Pro Arg Ala Glu Arg Arg Pro Val Ala Val Pro Leu
100 105 110
Arg Asp Asp Gly Ser Asp Asp Val Val Met Arg Asn Arg Val Tyr Gly
115 120 125
Thr Trp His Asn Tyr Gly Asp Glu
130 135

(2) INFORMATION FOR SEQ ID NO:1889:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889:

atcacaagca atcgatcaag ctagcatggc ggtgaagggtg tgggtgttcg ccgtggcact 60
gatgatgtgc gctggtgtag ggcttggagc tgacgacgac ggcggcagsc cttattagcc 120
gctgtcgtct garctcgccc aactaccgcg gcgccttggc aaaggccatc ctcttcttcg 180
argggcagcg gtcggggcgg ctgccggcaa accagagagt caggtggcgc ggggactcgg 240
cgctcaccga cggccaaccc gaaaacgtga acttgacggg tggctactac gacgccggag 300
acaacgtcaa gttcgggtttc ccgatggcgt tcagcgtcac cctcctgarc tggagcrccg 360
tcgagtaccg cbacgagggtg gcggcggcgg gtcagctccg cmacctccgg tccgccatcc 420
agtkgggcgc cgacttcctt ctccgtdecc ac

(2) INFORMATION FOR SEQ ID NO:1890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501610

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890:

Ser Gln Ala Ile Asp Gln Ala Ser Met Ala Val Lys Val Trp Val Phe
1 5 10 15
Ala Val Ala Leu Met Met Cys Ala Gly Val Gly Leu Gly Ala Asp Asp
20 25 30
Asp Gly Gly Xaa Pro Tyr
35

(2) INFORMATION FOR SEQ ID NO:1891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..30
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891:

Met Ala Val Lys Val Trp Val Phe Ala Val Ala Leu Met Met Cys Ala
1 5 10 15
Gly Val Gly Leu Gly Ala Asp Asp Asp Gly Gly Xaa Pro Tyr
20 25 30

(2) INFORMATION FOR SEQ ID NO:1892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892:

Met Ala Phe Ser Val Thr Leu Leu Xaa Trp Ser Xaa Val Glu Tyr Arg
1 5 10 15
Xaa Glu Val Ala Ala Gly Gln Leu Arg Xaa Leu Arg Ser Ala Ile
20 25 30
Gln Xaa Gly Ala Asp Phe Leu Leu Arg Xaa His
35 40

(2) INFORMATION FOR SEQ ID NO:1893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..501
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893:

aaactgctgg aatatactta caccgggaag aaggcgaagg ccgtcgcgct ctcggcrgcg	60
gcggcggcgg cggcagcggc gatgcttgcg ttcgagcagc aggtgttggc ggatctggtg	120
gaagatccga acggaggtct ggtggtgctc tcctcgggtc tccctctcgc ttccctagcc	180
gctaccctcc tcctccatct ccaccagacc cccggcaacg cggctggagg aggatgtctc	240
ctcgtcctct ccgccaccga taccctcaag gcccggtacc ggccgcgcct ccaagacaag	300
ctgcaggttc acgacgtgcc cccctgacct gccgcgcasa gcgcgcnmam cctttacgcc	360
tctgggctgc tctcttcctc tctcccgcgc cmctcgcmgc cgacctctc amctcccgcg	420
tcctcccctc ccgcgtccaa gccctactcc tcctctccgc cccacmgctc camcgatacc	480

tcctccgatg ccttcacatcg c

(2) INFORMATION FOR SEQ ID NO:1894:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 1501625

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894:

Lys	Leu	Leu	Glu	Tyr	Thr	Tyr	Thr	Gly	Lys	Lys	Ala	Lys	Ala	Val	Ala
1			5					10						15	
Leu	Ser	Xaa	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Met	Leu	Ala	Phe	Glu	
		20						25				30			
Gln	Gln	Val	Leu	Ala	Asp	Leu	Val	Glu	Asp	Pro	Asn	Gly	Gly	Leu	Val
		35					40					45			
Val	Leu	Ser	Ser	Gly	Leu	Pro	Leu	Ala	Ser	Leu	Ala	Ala	Thr	Leu	Leu
	50					55					60				
Leu	His	Leu	His	Gln	Thr	Pro	Gly	Asn	Ala	Ala	Gly	Gly	Gly	Cys	Leu
65					70					75				80	
Leu	Val	Leu	Ser	Ala	Thr	Asp	Thr	Leu	Lys	Ala	Arg	Ile	Arg	Arg	Arg
			85					90					95		
Leu	Gln	Asp	Lys	Leu	Gln	Val	His	Asp	Val	Pro	Pro	Asp	Leu	Ala	Ala
		100						105				110			
Xaa	Ser	Ala	Xaa	Xaa	Leu	Tyr	Ala	Ser	Gly	Leu	Leu	Ser	Ser	Ser	Leu
		115					120					125			
Pro	Ala	Xaa	Ser	Xaa	Pro	Thr	Ser	Ser	Xaa	Pro	Xaa	Ser	Ser	Pro	Pro
	130					135					140				
Ala	Ser	Lys	Pro	Tyr	Ser	Ser	Ser	Pro	Pro	His	Xaa	Ser	Xaa	Asp	Thr
145					150					155					160
Ser	Ser	Asp	Ala	Phe	Ile	Cys									
						165									

(2) INFORMATION FOR SEQ ID NO:1895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1501626

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1895:

Thr	Ala	Gly	Ile	Tyr	Leu	His	Arg	Glu	Gly	Gly	Arg	Arg	Ala		
1				5					10				15		
Leu	Gly	Xaa	Gly	Gly	Gly	Gly	Gly	Ser	Gly	Asp	Ala	Cys	Val	Arg	Ala
		20						25				30			
Ala	Gly	Val	Gly	Gly	Ser	Gly	Gly	Arg	Ser	Glu	Arg	Arg	Ser	Gly	Gly
		35				40						45			
Ala	Leu	Gly	Ser	Pro	Ser	Arg	Phe	Pro	Ser	Arg	Tyr	Pro	Pro	Pro	
	50					55				60					
Pro	Ser	Pro	Pro	Asp	Pro	Arg	Gln	Arg	Gly	Trp	Arg	Arg	Met	Ser	Pro
65					70					75				80	
Arg	Pro	Leu	Arg	His	Arg	Tyr	Pro	Gln	Gly	Pro	Asp	Pro	Ala	Pro	Pro
			85					90						95	
Pro	Arg	Gln	Ala	Ala	Gly	Ser	Arg	Arg	Ala	Pro					
		100						105							

(2) INFORMATION FOR SEQ ID NO:1896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896:

Met	Leu	Ala	Phe	Glu	Gln	Gln	Val	Leu	Ala	Asp	Leu	Val	Glu	Asp	Pro	
1				5				10					15			
Asn	Gly	Gly	Leu	Val	Val	Leu	Ser	Ser	Gly	Leu	Pro	Leu	Ala	Ser	Leu	
			20					25					30			
Ala	Ala	Thr	Leu	Leu	Leu	His	Leu	His	Gln	Thr	Pro	Gly	Asn	Ala	Ala	
		35					40					45				
Gly	Gly	Gly	Cys	Leu	Leu	Val	Leu	Ser	Ala	Thr	Asp	Thr	Leu	Lys	Ala	
		50				55					60					
Arg	Ile	Arg	Arg	Arg	Leu	Gln	Asp	Lys	Leu	Gln	Val	His	Asp	Val	Pro	
65					70				75					80		
Pro	Asp	Leu	Ala	Ala	Xaa	Ser	Ala	Xaa	Xaa	Leu	Tyr	Ala	Ser	Gly	Leu	
			85					90						95		
Leu	Ser	Ser	Ser	Leu	Pro	Ala	Xaa	Ser	Xaa	Pro	Thr	Ser	Ser	Xaa	Pro	
			100					105						110		
Xaa	Ser	Ser	Pro	Pro	Ala	Ser	Lys	Pro	Tyr	Ser	Ser	Ser	Pro	Pro	His	
			115				120						125			
Xaa	Ser	Xaa	Asp	Thr	Ser	Ser	Asp	Ala	Phe	Ile	Cys					
			130				135				140					

(2) INFORMATION FOR SEQ ID NO:1897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..427
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897:

aaactctgct	gcattcttctt	ccactctcca	gtctccacta	gcattcagtcg	ccgctgccta		60
tcctcgagca	ccatttccat	caacagcatc	cgcctctggc	aagctagcga	casaactcat		120
ggcactccgc	gcgctcgaca	acacgatgcc	cgcmgccgtc	gaggagcggc	ccaagaaggt		180
ggctaagggtg	ggcgctccccg	cmgcmgccgc	caaggccgcm	gcctcccccg	ggagtggcgg		240
caagaagaag	aaggggaacg	acgagaactc	ggcgccaagg	gccacggccg	cggcggcgga		300
gcaggcmgtg	gagtacatct	cgtcggagga	gctggaggcg	gcggccaacc	ctaaggccaa		360
ggccgcgggg	ctggtcgcg	gccttgactc	caaggactgg	gtcaggacct	gcraggcct		420
caacgac							

(2) INFORMATION FOR SEQ ID NO:1898:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898:

Asn Ser Ala Ala Ser Ser Ser Thr Leu Gln Ser Pro Leu Ala Ser Val
1 5 10 15
Ala Ala Ala Tyr Pro Arg Ala Pro Phe Pro Ser Thr Ala Ser Ala Ser
20 25 30
Gly Lys Leu Ala Thr Xaa Leu Met Ala Leu Arg Ala Leu Asp Asn Thr
35 40 45
Met Pro Xaa Ala Val Glu Glu Arg Pro Lys Lys Val Ala Lys Val Gly
50 55 60
Val Pro Xaa Xaa Ala Ala Lys Ala Xaa Ala Ser Pro Gly Ser Gly Gly
65 70 75 80
Lys Lys Lys Lys Gly Asn Asp Glu Asn Ser Ala Pro Arg Ala Thr Ala
85 90 95
Ala Ala Ala Glu Gln Xaa Val Glu Tyr Ile Ser Ser Glu Glu Leu Glu
100 105 110
Ala Ala Ala Asn Pro Lys Ala Lys Ala Ala Gly Leu Val Ala Gly Leu
115 120 125
Asp Ser Lys Asp Trp Val Arg Thr Cys Xaa Ala Leu Asn Asp
130 135 140

(2) INFORMATION FOR SEQ ID NO:1899:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501634

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899:

Met Ala Leu Arg Ala Leu Asp Asn Thr Met Pro Xaa Ala Val Glu Glu
1 5 10 15
Arg Pro Lys Lys Val Ala Lys Val Gly Val Pro Xaa Xaa Ala Ala Lys
20 25 30
Ala Xaa Ala Ser Pro Gly Ser Gly Gly Lys Lys Lys Lys Gly Asn Asp
35 40 45
Glu Asn Ser Ala Pro Arg Ala Thr Ala Ala Ala Ala Glu Gln Xaa Val
50 55 60
Glu Tyr Ile Ser Ser Glu Glu Leu Glu Ala Ala Ala Asn Pro Lys Ala
65 70 75 80
Lys Ala Ala Gly Leu Val Ala Gly Leu Asp Ser Lys Asp Trp Val Arg
85 90 95
Thr Cys Xaa Ala Leu Asn Asp
100

(2) INFORMATION FOR SEQ ID NO:1900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900:

Met Pro Xaa Ala Val Glu Glu Arg Pro Lys Lys Val Ala Lys Val Gly
1 5 10 15
Val Pro Xaa Xaa Ala Ala Lys Ala Xaa Ala Ser Pro Gly Ser Gly Gly
20 25 30

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Lys Lys Lys Lys Gly Asn Asp Glu Asn Ser Ala Pro Arg Ala Thr Ala
35 40 45
Ala Ala Ala Glu Gln Xaa Val Glu Tyr Ile Ser Ser Glu Glu Leu Glu
50 55 60
Ala Ala Ala Asn Pro Lys Ala Lys Ala Ala Gly Leu Val Ala Gly Leu
65 70 75 80
Asp Ser Lys Asp Trp Val Arg Thr Cys Xaa Ala Leu Asn Asp
85 90

(2) INFORMATION FOR SEQ ID NO:1901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..541
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501639

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901:

ccggaacgcc	cgtcccgtcc	gtcctctccc	catccacatc	catcccgtgt	gctcctactg	60
ctcctcgatt	tgatcaccca	ttaggggagg	cggtttacca	gtgagcacgc	gcgagarata	120
ggataggagg	aaagggaagc	tagcggsttc	gctctcgcg	ggagatggcg	cargcggtkg	180
aggagtggta	ccggcagatg	cccatcatca	cgcgctccta	cctcamcgcc	gctgtcgtca	240
ccaccgtcgg	ctgcamcctc	gaaatcattt	cgccgtatca	cctgtacctt	aaccggaagc	300
tcgtgggtgca	gcactacgag	atttrgcgcc	tcgtcaccaa	sttsctctan	yttccgcaaa	360
gatggatttg	gattttctat	tccacatgtw	ctttcttgca	cgatactgca	agcttctgga	420
ggaaaactca	tttagaggaa	gaactgctga	ctttttttac	atgcwcttgt	ttggtgctac	480
tgtcctaact	ggcattgggt	ctgatcggag	ggatgatacc	ttacatttct	gagacatttg	540

(2) INFORMATION FOR SEQ ID NO:1902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902:

Met	Ala	Xaa	Ala	Xaa	Glu	Glu	Trp	Tyr	Arg	Gln	Met	Pro	Ile	Ile	Thr
1			5						10					15	
Arg	Ser	Tyr	Leu	Xaa	Ala	Ala	Val	Val	Thr	Thr	Val	Gly	Cys	Xaa	Leu
			20					25					30		
Glu	Ile	Ile	Ser	Pro	Tyr	His	Leu	Tyr	Leu	Asn	Pro	Lys	Leu	Val	Val
			35				40					45			
Gln	His	Tyr	Glu	Ile	Xaa	Arg	Leu	Val	Thr	Xaa	Xaa	Leu	Xaa	Xaa	Pro
			50			55					60				
Gln	Arg	Trp	Ile	Trp	Ile	Phe	Tyr	Ser	Thr	Cys	Xaa	Phe	Leu	His	Asp
65				70					75					80	
Thr	Ala	Ser	Phe	Trp	Arg	Lys	Thr	His	Leu	Glu	Glu	Glu	Leu	Leu	Thr
				85				90						95	
Phe	Phe	Thr	Cys	Xaa	Cys	Leu	Val	Leu	Leu	Ser					
				100					105						

(2) INFORMATION FOR SEQ ID NO:1903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..96
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501641
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903:
Met Pro Ile Ile Thr Arg Ser Tyr Leu Xaa Ala Ala Val Val Thr Thr
1 5 10 15
Val Gly Cys Xaa Leu Glu Ile Ile Ser Pro Tyr His Leu Tyr Leu Asn
 20 25 30
Pro Lys Leu Val Val Gln His Tyr Glu Ile Xaa Arg Leu Val Thr Xaa
 35 40 45
Xaa Leu Xaa Xaa Pro Gln Arg Trp Ile Trp Ile Phe Tyr Ser Thr Cys
50 55 60
Xaa Phe Leu His Asp Thr Ala Ser Phe Trp Arg Lys Thr His Leu Glu
65 70 75 80
Glu Glu Leu Leu Thr Phe Phe Thr Cys Xaa Cys Leu Val Leu Leu Ser
 85 90 95

(2) INFORMATION FOR SEQ ID NO:1904:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..56
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501642
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904:
Met Asp Leu Asp Phe Leu Phe His Met Xaa Phe Leu Ala Arg Tyr Cys
1 5 10 15
Lys Leu Leu Glu Glu Asn Ser Phe Arg Gly Arg Thr Ala Asp Phe Phe
 20 25 30
Tyr Met Xaa Leu Phe Gly Ala Thr Val Leu Thr Gly Ile Gly Ser Asp
35 40 45
Arg Arg Asp Asp Thr Leu His Phe
50 55

(2) INFORMATION FOR SEQ ID NO:1905:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1144
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501643
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905:
tttacaggca cagctaaagc aagagtcact gctaaggcaa caggagcaac aacaattagc 60
tgaacaatcc cagctgaggc aacaagagca agaaaaacta gccaaagagc aaaccggtat 120
tgcttctctg gaggttgaaa agcaacagtt ggaagaccaa attactatgt tgacaaagaa 180
agctacagag gacgcttctg agtttgctgc acgcaaggca ttttcaatgc aagataggga 240
aaaacttgaa cagcagttgc atgacatggc tttgatgatt gagaggctag aggggagtcg 300
tcaaaaactg ctaatggaga ttgattctca atcgtcagaa atagagaaac tgtttgagga 360
gaactcagcc ttatctgctt cttatcaaga agccattgat gttactgtac aatgggaaaa 420
ccagaaaatt tcagggttaga gactgtctga agcaaaatga agagctccgt tctcacttgg 480

agaaactaag acttgaacaa gttagcctgt tgaaagtaag caatatcgct acccaatcag 540
atggggcaaac tgaaaacagt atctcaaacc caccacaaat ggatcatcgag aatattttctc 600
taaarggwtc agcttataaa agwacagwgc agatctgagg ggttgctcggc agagataatg 660
aaacttttcag ctgagcttag gaaagcagtc catgcacaga ataaccttgc acgcttatac 720
agacctgtat taagagacat tgagagcaat ctgatgaaaa tgaaacaaga aacttatgcg 780
acgatccagt gatacatgtt gacatgttgt gaaactcagt cctctggcat ggccgcatgg 840
gctccacgtt actgattttc gtcgtggatg tatttatctc atgccatctt caagatgctg 900
gtgcaaagca gttctttttc tggccaccat ttataagtag agttcagtcg agatcggtgt 960
acttgatca tactcatgta taccgcatc ccagactggt tcatctcgta aattggaagc 1020
gatgtttgga tgcctatgta tcaagtggat cataaacatc caaacaacgc cttaaaatag 1080
atcgtttcga cattattatt ttctgcttg caatccaggc tctaacaact tctcggtctt 1140
gttt

(2) INFORMATION FOR SEQ ID NO:1906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906:

Leu Gln Ala Gln Leu Lys Gln Glu Ser Leu Leu Arg Gln Gln Glu Gln
1 5 10 15
Gln Gln Leu Ala Glu Gln Ser Gln Leu Arg Gln Gln Glu Gln Lys
20 25 30
Leu Ala Lys Glu Gln Thr Arg Ile Ala Ser Leu Glu Ala Glu Lys Gln
35 40 45
Gln Leu Glu Asp Gln Ile Thr Met Leu Thr Lys Lys Ala Thr Glu Asp
50 55 60
Ala Ser Glu Phe Ala Ala Arg Lys Ala Phe Ser Met Gln Asp Arg Glu
65 70 75 80
Lys Leu Glu Gln Gln Leu His Asp Met Ala Leu Met Ile Glu Arg Leu
85 90 95
Glu Gly Ser Arg Gln Lys Leu Leu Met Glu Ile Asp Ser Gln Ser Ser
100 105 110
Glu Ile Glu Lys Leu Phe Glu Glu Asn Ser Ala Leu Ser Ala Ser Tyr
115 120 125
Gln Glu Ala Ile Asp Val Thr Val Gln Trp Glu Asn Gln Lys Ile Ser
130 135 140
Gly
145

(2) INFORMATION FOR SEQ ID NO:1907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..90
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907:

Met Leu Thr Lys Lys Ala Thr Glu Asp Ala Ser Glu Phe Ala Ala Arg
1 5 10 15
Lys Ala Phe Ser Met Gln Asp Arg Glu Lys Leu Glu Gln Gln Leu His
20 25 30
Asp Met Ala Leu Met Ile Glu Arg Leu Glu Gly Ser Arg Gln Lys Leu

35 40 45
Leu Met Glu Ile Asp Ser Gln Ser Ser Glu Ile Glu Lys Leu Phe Glu
50 55 60
Glu Asn Ser Ala Leu Ser Ala Ser Tyr Gln Glu Ala Ile Asp Val Thr
65 70 75 80
Val Gln Trp Glu Asn Gln Lys Ile Ser Gly
85 90

(2) INFORMATION FOR SEQ ID NO:1908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908:

Met Leu Leu Tyr Asn Gly Lys Thr Arg Lys Phe Gln Val Arg Asp Cys
1 5 10 15
Leu Lys Gln Asn Glu Glu Leu Arg Ser His Leu Glu Lys Leu Arg Leu
20 25 30
Glu Gln Val Ser Leu Leu Lys Val Ser Asn Ile Ala Thr Gln Ser Asp
35 40 45
Gly Gln Thr Glu Asn Ser Ile Ser Asn Pro Pro Gln Met Val Ile Glu
50 55 60
Asn Ile Ser Leu Xaa Xaa Ser Ala Tyr Lys Xaa Thr Xaa Gln Ile
65 70 75

(2) INFORMATION FOR SEQ ID NO:1909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..597
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909:

tttttttcgcc	tataattact	cttccccgtg	cgccctcgcg	aggtcgaacc	cccaaggcga	60
ggcgacgaaa	ccctcgccag	tccccaactc	gaacctcagt	caggcggcgt	gagggagga	120
gagttcgagg	accgaggcgg	cgtcgggcga	gatgaagctt	aacgtcaaga	ccctcaaggg	180
caccaacttc	gagatcgagg	cgagccccga	tgcgtcggtt	gctgacgtga	agaggatcat	240
tgagaccact	cagggtcaga	gtacctaccg	ggcggaccag	caaagtctta	tataccaagg	300
gaaaattctc	aaggatgaga	ccactttgga	aagcaacgga	gttctganga	acagcttcct	360
tggtataatg	ttgtccaagg	ctaaggcatc	gtcgagtgga	gcttctacca	ctactgctgc	420
aaaagctcct	gcaactctgg	cccaacctgc	tgccccctgtg	ccccctgctg	catcagttgc	480
aagaacacca	acacaggctc	ctggtgccac	agctgaaacg	gcacctccaa	gtgcccgaacc	540
tcaggctgct	cagctgctac	ggttgctgct	actgatgatg	ctgatgtgta	cagtcag	

(2) INFORMATION FOR SEQ ID NO:1910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1501690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910:

Met Lys Leu Asn Val Lys Thr Leu Lys Gly Thr Asn Phe Glu Ile Glu
1 5 10 15
Ala Ser Pro Asp Ala Ser Val Ala Asp Val Lys Arg Ile Ile Glu Thr
20 25 30
Thr Gln Gly Gln Ser Thr Tyr Arg Ala Asp Gln Gln Met Leu Ile Tyr
35 40 45
Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu Ser Asn Gly Val
50 55 60
Leu Xaa Asn Ser Phe Leu Val Ile Met Leu Ser Lys Ala Lys Ala Ser
65 70 75 80
Ser Ser Gly Ala Ser Thr Thr Thr Ala Ala Lys Ala Pro Ala Thr Leu
85 90 95
Ala Gln Pro Ala Ala Pro Val Pro Pro Ala Ala Ser Val Ala Arg Thr
100 105 110
Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala Pro Pro Ser Ala
115 120 125
Gln Pro Gln Ala Ala Gln Leu Leu Arg Leu Leu Leu Leu Met Met Leu
130 135 140
Met Cys Thr Val
145

(2) INFORMATION FOR SEQ ID NO:1911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1501691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1911:

Met Leu Ile Tyr Gln Gly Lys Ile Leu Lys Asp Glu Thr Thr Leu Glu
1 5 10 15
Ser Asn Gly Val Leu Xaa Asn Ser Phe Leu Val Ile Met Leu Ser Lys
20 25 30
Ala Lys Ala Ser Ser Ser Gly Ala Ser Thr Thr Thr Ala Ala Lys Ala
35 40 45
Pro Ala Thr Leu Ala Gln Pro Ala Ala Pro Val Pro Pro Ala Ala Ser
50 55 60
Val Ala Arg Thr Pro Thr Gln Ala Pro Val Ala Thr Ala Glu Thr Ala
65 70 75 80
Pro Pro Ser Ala Gln Pro Gln Ala Ala Gln Leu Leu Arg Leu Leu Leu
85 90 95
Leu Met Met Leu Met Cys Thr Val
100

(2) INFORMATION FOR SEQ ID NO:1912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1501692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912:

Met Leu Ser Lys Ala Lys Ala Ser Ser Ser Gly Ala Ser Thr Thr Thr

1 5 10 15
Ala Ala Lys Ala Pro Ala Thr Leu Ala Gln Pro Ala Ala Pro Val Pro
20 25 30
Pro Ala Ala Ser Val Ala Arg Thr Pro Thr Gln Ala Pro Val Ala Thr
35 40 45
Ala Glu Thr Ala Pro Pro Ser Ala Gln Pro Gln Ala Ala Gln Leu Leu
50 55 60
Arg Leu Leu Leu Leu Met Met Leu Met Cys Thr Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:1913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..272
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1913:

ccgctcgatc ggcggcccat caatcaatca atcaattctc gacctcacta ctcgatctct	60
cgtctcatca gtgtgactgt gtgagtgtcc gagcacgcta gcacgcgcaa tggacgctct	120
gctcgtgact accttctctg tccccgtggg ggcgctcctc ctcggttccg ggtccgggtc	180
cgcggcaccg ctgcmgcgcg ccttcttctg gtctcggtgac tccctcgtgg acaacggcaa	240
caacaactac ctgatgacga cggcgcgcgcg cg	

(2) INFORMATION FOR SEQ ID NO:1914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914:

Ala Arg Ser Arg Pro His Gln Ser Ile Asn Gln Phe Ser Thr Ser Leu	
1 5 10 15	
Leu Asp Leu Ser Ser His Gln Cys Asp Cys Val Ser Val Arg Ala Arg	
20 25 30	

(2) INFORMATION FOR SEQ ID NO:1915:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915:

Met Asp Ala Leu Leu Val Thr Thr Phe Leu Val Pro Val Val Ala Leu	
1 5 10 15	
Leu Leu Gly Ser Gly Ser Gly Ser Ala Ala Pro Leu Xaa Arg Ala Phe	
20 25 30	
Phe Val Phe Gly Asp Ser Leu Val Asp Asn Gly Asn Asn Asn Tyr Leu	

35 40 45
Met Thr Thr Ala Arg Ala
50
(2) INFORMATION FOR SEQ ID NO:1916:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 562 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..562
(D) OTHER INFORMATION: / Ceres Seq. ID 1501710
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916:
gacgaccgca ttctctttcc tctctctcgc agtctcgcct cgcccaaccc agtccctcgc 60
gcgcgctctc tctcctgcaa ggaccgccag ggaaggacct gctgtttcaa agtattgtgc 120
gagacaccta cacgctgagc ttcgccgaca tgaaagtgtt cgggataatc tccagactgc 180
aattgagaga acgttcttaa ggatggatga gatgatgaga gacaggaggg cagggagggg 240
attatctggg tacggtgtaa tgacaattgg aaagcatata gaaaggctat caacatgagt 300
ctatttctac ccttctgtca gaagccagct tatcaggggc cagtaatgga tggatgtacc 360
gcgtgtgtgg ttctcattag agacaaccga atcattgtgg gaaatgctgg tgattctcgt 420
tgtgtactct caaggaataa tcaggcgatt gatctatcca ccgattttta accaaacctt 480
ccagacgaaa gacaaagaat agaagctgca rgacatgtgg taacttttag cgagagagga 540
aatgtgcacg gtattgatga tg

(2) INFORMATION FOR SEQ ID NO:1917:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 98 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..98
(D) OTHER INFORMATION: / Ceres Seq. ID 1501711
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917:
Thr Thr Ala Phe Ser Phe Leu Ser Leu Ala Val Ser Pro Arg Pro Thr
1 5 10 15
Gln Ser Leu Ala Arg Ala Leu Ser Pro Ala Arg Thr Ala Arg Glu Gly
20 25 30
Pro Ala Val Ser Lys Tyr Cys Ala Arg His Leu His Ala Glu Leu Arg
35 40 45
Arg His Glu Ser Phe Arg Asp Asn Leu Gln Thr Ala Ile Glu Arg Thr
50 55 60
Phe Leu Arg Met Asp Glu Met Met Arg Asp Arg Arg Ala Gly Arg Glu
65 70 75 80
Leu Ser Gly Tyr Gly Val Met Thr Ile Gly Lys His Ile Glu Arg Leu
85 90 95
Ser Thr

(2) INFORMATION FOR SEQ ID NO:1918:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1501712

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1918:

Met Ser Leu Phe Leu Pro Phe Cys Gln Lys Pro Ala Tyr Gln Gly Pro
1 5 10 15
Val Met Asp Gly Cys Thr Ala Cys Val Val Leu Ile Arg Asp Asn Arg
20 25 30
Ile Ile Val Gly Asn Ala Gly Asp Ser Arg Cys Val Leu Ser Arg Asn
35 40 45
Asn Gln Ala Ile Asp Leu Ser Thr Asp Phe Lys Pro Asn Leu Pro Asp
50 55 60
Glu Arg Gln Arg Ile Glu Ala Ala Xaa His Val Val Thr Phe Ser Glu
65 70 75 80
Arg Gly Asn Val His Arg Ile Asp Asp
85

(2) INFORMATION FOR SEQ ID NO:1919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1501713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1919:

Met Asp Gly Cys Thr Ala Cys Val Val Leu Ile Arg Asp Asn Arg Ile
1 5 10 15
Ile Val Gly Asn Ala Gly Asp Ser Arg Cys Val Leu Ser Arg Asn Asn
20 25 30
Gln Ala Ile Asp Leu Ser Thr Asp Phe Lys Pro Asn Leu Pro Asp Glu
35 40 45
Arg Gln Arg Ile Glu Ala Ala Xaa His Val Val Thr Phe Ser Glu Arg
50 55 60
Gly Asn Val His Arg Ile Asp Asp
65 70

(2) INFORMATION FOR SEQ ID NO:1920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..508

(D) OTHER INFORMATION: / Ceres Seq. ID 1501718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1920:

aaggcagcaa	ggccactaac	actagttatc	acatccacca	taacgaccat	ggctaccacc	60
tcagctttgc	tagctcttgt	cttggttagcc	agcctccttg	caggcacggt	gttcagtgat	120
gatatcgtac	ccatccatat	acccttggtg	gatcggttcc	aagcctggca	ggccgaatac	180
aaccgcacat	atgcgacccc	agaggaattc	cagcaacgct	tcatgggtcta	tagcgagaat	240
gtcaagttca	tcgagaccat	gaaccagcct	gggagctcat	atgagctcgg	tgagaaccga	300
ttcgctgacc	tcaccgagga	ggagttcaag	gacacgtatc	ttatgaagct	tgacaacgtg	360
gcctcgtccc	ctgaggccat	ggcactgacc	gtcgatacca	tgaatagagc	aggcacatct	420
ggcggcagca	acaccaacga	ggctcccaat	agtgtggact	ggaggaccaa	gggagcagtg	480
acgccggtca	agagccagca	acattgtg				

(2) INFORMATION FOR SEQ ID NO:1921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..169
(D) OTHER INFORMATION: / Ceres Seq. ID 1501719
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921:

Lys Ala Ala Arg Pro Leu Thr Leu Val Ile Thr Ser Thr Ile Thr Thr
1 5 10 15
Met Ala Thr Thr Ser Ala Leu Leu Ala Leu Val Leu Leu Ala Ser Leu
20 25 30
Leu Ala Gly Thr Val Phe Ser Asp Asp Ile Val Pro Ile His Ile Pro
35 40 45
Leu Leu Asp Arg Phe Gln Ala Trp Gln Ala Glu Tyr Asn Arg Thr Tyr
50 55 60
Ala Thr Pro Glu Glu Phe Gln Gln Arg Phe Met Val Tyr Ser Glu Asn
65 70 75 80
Val Lys Phe Ile Glu Thr Met Asn Gln Pro Gly Ser Ser Tyr Glu Leu
85 90 95
Gly Glu Asn Arg Phe Ala Asp Leu Thr Glu Glu Glu Phe Lys Asp Thr
100 105 110
Tyr Leu Met Lys Leu Asp Asn Val Ala Ser Ser Pro Glu Ala Met Ala
115 120 125
Leu Thr Val Asp Thr Met Asn Arg Ala Gly Thr Ser Gly Gly Ser Asn
130 135 140
Thr Asn Glu Ala Pro Asn Ser Val Asp Trp Arg Thr Lys Gly Ala Val
145 150 155 160
Thr Pro Val Lys Ser Gln Gln His Cys
165

(2) INFORMATION FOR SEQ ID NO:1922:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..153
(D) OTHER INFORMATION: / Ceres Seq. ID 1501720
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922:

Met Ala Thr Thr Ser Ala Leu Leu Ala Leu Val Leu Leu Ala Ser Leu
1 5 10 15
Leu Ala Gly Thr Val Phe Ser Asp Asp Ile Val Pro Ile His Ile Pro
20 25 30
Leu Leu Asp Arg Phe Gln Ala Trp Gln Ala Glu Tyr Asn Arg Thr Tyr
35 40 45
Ala Thr Pro Glu Glu Phe Gln Gln Arg Phe Met Val Tyr Ser Glu Asn
50 55 60
Val Lys Phe Ile Glu Thr Met Asn Gln Pro Gly Ser Ser Tyr Glu Leu
65 70 75 80
Gly Glu Asn Arg Phe Ala Asp Leu Thr Glu Glu Glu Phe Lys Asp Thr
85 90 95
Tyr Leu Met Lys Leu Asp Asn Val Ala Ser Ser Pro Glu Ala Met Ala
100 105 110
Leu Thr Val Asp Thr Met Asn Arg Ala Gly Thr Ser Gly Gly Ser Asn
115 120 125
Thr Asn Glu Ala Pro Asn Ser Val Asp Trp Arg Thr Lys Gly Ala Val
130 135 140
Thr Pro Val Lys Ser Gln Gln His Cys

145

150

(2) INFORMATION FOR SEQ ID NO:1923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1501721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923:

Met	Val	Tyr	Ser	Glu	Asn	Val	Lys	Phe	Ile	Glu	Thr	Met	Asn	Gln	Pro
1				5					10					15	
Gly	Ser	Ser	Tyr	Glu	Leu	Gly	Glu	Asn	Arg	Phe	Ala	Asp	Leu	Thr	Glu
			20					25					30		
Glu	Glu	Phe	Lys	Asp	Thr	Tyr	Leu	Met	Lys	Leu	Asp	Asn	Val	Ala	Ser
		35					40				45				
Ser	Pro	Glu	Ala	Met	Ala	Leu	Thr	Val	Asp	Thr	Met	Asn	Arg	Ala	Gly
	50					55				60					
Thr	Ser	Gly	Gly	Ser	Asn	Thr	Asn	Glu	Ala	Pro	Asn	Ser	Val	Asp	Trp
65				70					75					80	
Arg	Thr	Lys	Gly	Ala	Val	Thr	Pro	Val	Lys	Ser	Gln	Gln	His	Cys	
			85					90						95	

(2) INFORMATION FOR SEQ ID NO:1924:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 911 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..911

(D) OTHER INFORMATION: / Ceres Seq. ID 1501722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924:

gacgccgaca	tatgggcccc	gcttgagaag	taaggggccac	atgtcgggtgg	gaactctccc	60
ggagtgcggca	actaatcgac	cccgtgcgcc	ggctccaccc	gaagcgcaag	aggaagaggt	120
ggccatacgc	aacaagcaaa	gcatancccc	aaatccccaa	tccccaatcc	ccaatcccca	180
aaccctaggt	tatctcggcg	cggcagcgan	tggcggcggc	gggcctgagg	aaggggaatg	240
cgcgcctccc	gccggaggtg	aaccgggtgc	tctacgtgcg	gaacctgccg	ttcaacatct	300
cgagcgagga	gatgtacgac	atcttcggca	agtacggcgc	gatccggcag	atccgtcttg	360
gcaacgccaa	ggacacgcgc	gggaccgctt	acgttgctta	csaggacatc	tacgacgcca	420
agaacgccgt	cgaccacctc	tmcggcttca	acgtcgccaa	ccgctacctt	atcgtgctct	480
actaccagcc	cgccaagats	tccaagaagy	cggatatcam	gaagaaggag	gacgagatcc	540
accaggctcc	aggagaagta	cggaatcggg	tccaagacgc	ccggcccggg	ctccagcgac	600
tgagcggcca	gggtattgcc	tctgcagcct	cttgtatgat	gaagagcaat	caaaaggaac	660
aaattggttg	cgctgtgctg	tgttacatcc	agcgtcgcta	attactctgt	tgttattcag	720
gctccataac	aattgaatag	atatgtgctt	gtctaatcgc	cagcgataat	gtttagtttc	780
taccaaaaac	aagaggaatg	agtagtgtac	acctcacacc	tgtggctatg	cttgaattgt	840
tgatctatat	tctgttgtga	gactgagagt	agcatggtta	ggctgttaaa	tttgtgcttc	900
tattattggt	t					

(2) INFORMATION FOR SEQ ID NO:1925:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1501723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925:

Thr	Pro	Thr	Tyr	Gly	Pro	Arg	Leu	Arg	Ser	Lys	Gly	His	Met	Ser	Val
1				5					10					15	
Gly	Thr	Leu	Pro	Glu	Ser	Ala	Thr	Asn	Arg	Pro	Arg	Ala	Pro	Ala	Pro
			20					25					30		
Pro	Glu	Ala	Gln	Glu	Glu	Glu	Val	Ala	Ile	Arg	Asn	Lys	Gln	Ser	Ile
		35					40					45			
Xaa	Pro	Asn	Pro	Gln	Ser	Pro	Ile	Pro	Asn	Pro	Gln	Thr	Leu	Gly	Tyr
	50					55					60				
Leu	Gly	Ala	Ala	Ala	Xaa	Gly	Gly	Gly	Gly	Pro	Glu	Glu	Gly	Glu	Cys
65					70					75					80
Ala	Pro	Pro	Ala	Gly	Gly	Glu	Pro	Gly	Ala	Leu	Arg	Ala	Glu	Pro	Ala
				85					90					95	
Val	Gln	His	Leu	Glu	Arg	Gly	Asp	Val	Arg	His	Leu	Arg	Gln	Val	Arg
			100					105					110		
Arg	Asp	Pro	Ala	Asp	Pro	Ser	Gly	Gln	Arg	Gln	Gly	His	Ala	Arg	Asp
		115					120					125			
Arg	Leu	Arg	Cys	Leu	Xaa	Gly	His	Leu	Arg	Arg	Gln	Glu	Arg	Arg	Arg
	130					135					140				
Pro	Pro	Xaa	Arg	Leu	Gln	Arg	Arg	Gln	Pro	Leu	Pro	Tyr	Arg	Ala	Leu
145					150					155					160
Leu	Pro	Ala	Arg	Gln	Asp	Xaa	Gln	Glu	Xaa	Gly	Tyr	Xaa	Glu	Glu	Gly
				165					170					175	
Gly	Arg	Asp	Pro	Pro	Gly	Ser	Arg	Arg	Ser	Thr	Glu	Ser	Gly	Pro	Arg
			180					185					190		
Arg	Pro	Ala	Arg	Ala	Pro	Ala	Thr	Glu	Arg	Pro	Gly	Tyr	Cys	Leu	Cys
		195					200					205			
Ser	Leu	Leu	Tyr	Asp	Glu	Glu	Gln	Ser	Lys	Gly	Thr	Asn	Trp	Leu	Arg
	210					215					220				
Cys	Ala	Val	Leu	His	Pro	Ala	Ser	Leu	Ile	Thr	Leu	Leu	Leu	Phe	Arg
225					230					235					240
Leu	His	Asn	Asn												

(2) INFORMATION FOR SEQ ID NO:1926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1501724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926:

Met	Ser	Val	Gly	Thr	Leu	Pro	Glu	Ser	Ala	Thr	Asn	Arg	Pro	Arg	Ala
1				5					10					15	
Pro	Ala	Pro	Pro	Glu	Ala	Gln	Glu	Glu	Glu	Val	Ala	Ile	Arg	Asn	Lys
			20					25					30		
Gln	Ser	Ile	Xaa	Pro	Asn	Pro	Gln	Ser	Pro	Ile	Pro	Asn	Pro	Gln	Thr
		35					40					45			
Leu	Gly	Tyr	Leu	Gly	Ala	Ala	Ala	Xaa	Gly	Gly	Gly	Gly	Pro	Glu	Glu
	50					55					60				
Gly	Glu	Cys	Ala	Pro	Pro	Ala	Gly	Gly	Glu	Pro	Gly	Ala	Leu	Arg	Ala
65					70					75				80	
Glu	Pro	Ala	Val	Gln	His	Leu	Glu	Arg	Gly	Asp	Val	Arg	His	Leu	Arg
			85						90				95		
Gln	Val	Arg	Arg	Asp	Pro	Ala	Asp	Pro	Ser	Gly	Gln	Arg	Gln	Gly	His

(2) INFORMATION FOR SEQ ID NO:1927:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

(ix) FEATURE:

(A) NAM

(B) LOCATION: 1..129

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEO ID NO:1927:

Tyr Asp Ile Phe Gly Lys Tyr Gly Ala Ile Ar

(2) INFORMATION FOR SEQ ID NO:1928:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 916 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..916

(D) OTHER INFORMATION: / Ceres Seq. ID 1501730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928:

```
atccatgtca  tgacgatact  gcaggctcca  attgtcagct  gaactgtgtt  tgcattctgt      60
ccagctatag  ctcattttgt  tctacttgtc  gacatagact  caagcttgct  tattagtacg     120
```

tccaagaacg	acgtacatgg	cttcagctgc	tgcggctagc	gctgttaagg	aggccttggt	180
cgctcgtcgc	gtgtgcatcg	tgtctgtgct	ccactcttcg	gcgggacatc	agccgcccac	240
gtcgcgcgct	ccaccgcatt	gccattacac	ggggcagcag	ccaccgccct	cgccggtgsc	300
agcgtcgttg	tactcgccgc	cgccaccacc	accagtacca	gcgcccattg	cgtcgccgtc	360
gccgcgcgca	ccgccagtag	aagcgcccat	gccgcgcgcg	ccgccggcac	caacgccgac	420
acctgcgcca	acgcccammc	egtcgcgcgc	gccggmacc	gtcaataact	gcagctacat	480
gtactgcgcc	atgcaatgta	gcccgggtctg	ccaagccaaa	ccamgacgcc	ggcatcgcca	540
agtgcgaaag	cgacctcgcc	accaaactac	aacgggtgct	acgacagctg	caccagccat	600
gtctgccccg	gcgactcctg	cgccggcagt	ggctgcggct	tcggccactg	cccctgcgac	660
aacgccaacg	cgaccagctg	ctgccaatcc	tgcggcaacg	ttctgtaccg	cgaggagcag	720
cgctgccgga	attactacga	cagggctgtg	gagtactgca	tgatcgactg	ccaggacacc	780
tgctacaaga	actgcactca	ggcgcgtag	agagctcttg	attgggtctg	tcatctcagt	840
tagtctgaat	gtttctgtat	gttcatgacg	tttctacgat	tgatcaaata	aaacaaggtg	900
atgagcattg	agctcc					

(2) INFORMATION FOR SEQ ID NO:1929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..208
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929:

Met	Ala	Ser	Ala	Ala	Ala	Ser	Ala	Val	Lys	Glu	Ala	Leu	Val	Val
1			5				10					15		
Val	Ala	Val	Cys	Ile	Val	Leu	Leu	Leu	His	Ser	Ser	Ala	Gly	His
			20				25					30		Gln
Pro	Pro	Lys	Ser	Pro	Pro	Pro	Pro	His	Cys	His	Tyr	Thr	Gly	Gln
		35					40					45		Gln
Pro	Pro	Pro	Ser	Pro	Val	Pro	Ala	Ser	Leu	Tyr	Ser	Pro	Pro	Pro
		50					55				60			Pro
Pro	Pro	Val	Pro	Ala	Pro	Met	Pro	Ser	Pro	Ser	Pro	Pro	Pro	Pro
65					70				75					80
Val	Gln	Ala	Pro	Met	Pro	Pro	Pro	Pro	Ala	Pro	Thr	Pro	Thr	Pro
			85					90					95	
Ala	Pro	Thr	Pro	Xaa	Pro	Ser	Pro	Ser	Pro	Xaa	Pro	Val	Asn	Asn
			100					105					110	Cys
Ser	Tyr	Met	Tyr	Cys	Ala	Met	Gln	Cys	Ser	Pro	Val	Cys	Gln	Ala
		115					120					125		Lys
Pro	Xaa	Arg	Arg	His	Arg	Gln	Val	Arg	Lys	Arg	Pro	Arg	His	Gln
		130					135				140			Thr
Thr	Thr	Gly	Ala	Thr	Thr	Ala	Ala	Pro	Ala	Met	Ser	Ala	Pro	Ala
145						150				155				160
Pro	Ala	Pro	Ala	Val	Ala	Ala	Ala	Ser	Ala	Thr	Ala	Pro	Ala	Thr
			165					170					175	Thr
Pro	Thr	Arg	Pro	Ala	Ala	Ala	Asn	Pro	Ala	Ala	Thr	Phe	Cys	Thr
			180					185					190	Ala
Arg	Ser	Ser	Ala	Ala	Gly	Ile	Thr	Thr	Thr	Gly	Leu	Trp	Ser	Thr
			195				200					205		Ala

(2) INFORMATION FOR SEQ ID NO:1930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1501732

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930:

Met Pro Ser Pro Ser Pro Pro Pro Pro Val Gln Ala Pro Met Pro
1 5 10 15
Pro Pro Pro Pro Ala Pro Thr Pro Thr Pro Ala Pro Thr Pro Xaa Pro
20 25 30
Ser Pro Ser Pro Xaa Pro Val Asn Asn Cys Ser Tyr Met Tyr Cys Ala
35 40 45
Met Gln Cys Ser Pro Val Cys Gln Ala Lys Pro Xaa Arg Arg His Arg
50 55 60
Gln Val Arg Lys Arg Pro Arg His Gln Thr Thr Thr Gly Ala Thr Thr
65 70 75 80
Ala Ala Pro Ala Met Ser Ala Pro Ala Thr Pro Ala Pro Ala Val Ala
85 90 95
Ala Ala Ser Ala Thr Ala Pro Ala Thr Thr Pro Thr Arg Pro Ala Ala
100 105 110
Ala Asn Pro Ala Ala Thr Phe Cys Thr Ala Arg Ser Ser Ala Ala Gly
115 120 125
Ile Thr Thr Thr Gly Leu Trp Ser Thr Ala
130 135

(2) INFORMATION FOR SEQ ID NO:1931:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1501733

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1931:

Met Pro Pro Pro Pro Pro Ala Pro Thr Pro Thr Pro Ala Pro Thr Pro
1 5 10 15
Xaa Pro Ser Pro Ser Pro Xaa Pro Val Asn Asn Cys Ser Tyr Met Tyr
20 25 30
Cys Ala Met Gln Cys Ser Pro Val Cys Gln Ala Lys Pro Xaa Arg Arg
35 40 45
His Arg Gln Val Arg Lys Arg Pro Arg His Gln Thr Thr Thr Gly Ala
50 55 60
Thr Thr Ala Ala Pro Ala Met Ser Ala Pro Ala Thr Pro Ala Pro Ala
65 70 75 80
Val Ala Ala Ala Ser Ala Thr Ala Pro Ala Thr Thr Pro Thr Arg Pro
85 90 95
Ala Ala Ala Asn Pro Ala Ala Thr Phe Cys Thr Ala Arg Ser Ser Ala
100 105 110
Ala Gly Ile Thr Thr Thr Gly Leu Trp Ser Thr Ala
115 120

(2) INFORMATION FOR SEQ ID NO:1932:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

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(D) OTHER INFORMATION: / Ceres Seq. ID 1501737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1932:

attctgttcg gttccttccg aaaacacaac aggaaaaacac acgcacaaaaa ctgccgtttc	60
cgaatggcca cggccgtgct ccgccgccca ttctcgcgcg cgctcctccc cgccgccgga	120
ggggcgctccg ggacctctc ttgggttccgt ccccgagac gtaggtctc tccttccgtg	180
cgcgcggtgt cttccgactc cccaagccc gtcgcctcca cctcctccc caccggcggt	240
gacagccccg acgaggaacc accggtccta ccgctcctcc aggagcttgc ggattgcttg	300
attcttccac ccaagctcct cgctcagctc ccgagcgacc ttcgtctcga cctcaatgac	360
gctgcgtttg atctctccaa cgggccagtt ctgcacgagt gtggccaaga agtgggtgat	420
ctgctcctga acctggcaaa agcatgggag ttagctgata cgtcaacatc aaatagcatt	480
gccaaagcagc tgc	

(2) INFORMATION FOR SEQ ID NO:1933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1501738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933:

Ile	Leu	Phe	Gly	Ser	Phe	Arg	Lys	His	Asn	Arg	Lys	Thr	His	Ala	Gln	
1				5					10					15		
Asn	Cys	Arg	Phe	Arg	Met	Ala	Thr	Ala	Val	Leu	Arg	Arg	Pro	Phe	Leu	
			20					25					30			
Ala	Ala	Leu	Leu	Pro	Ala	Ala	Gly	Gly	Ala	Ser	Gly	Thr	Ser	Ser	Trp	
			35				40					45				
Phe	Arg	Pro	Arg	Arg	Arg	Arg	Ser	Ser	Pro	Ser	Val	Arg	Ala	Val	Ser	
			50				55				60					
Ser	Asp	Ser	Pro	Lys	Pro	Val	Ala	Ser	Thr	Ser	Ser	Pro	Thr	Gly	Gly	
65				70						75				80		
Asp	Ser	Pro	Asp	Glu	Glu	Pro	Pro	Val	Leu	Pro	Leu	Leu	Gln	Glu	Leu	
				85					90					95		
Ala	Asp	Cys	Leu	Ile	Leu	Pro	Pro	Lys	Leu	Leu	Ala	Gln	Leu	Pro	Ser	
			100					105					110			
Asp	Leu	Arg	Leu	Asp	Leu	Asn	Asp	Ala	Ala	Phe	Asp	Leu	Ser	Asn	Gly	
			115					120				125				
Pro	Val	Leu	Asp	Glu	Cys	Gly	Gln	Glu	Val	Gly	Asp	Leu	Leu	Leu	Asn	
			130				135				140					
Leu	Ala	Lys	Ala	Trp	Glu	Leu	Ala	Asp	Thr	Ser	Thr	Ser	Asn	Ser	Ile	
145					150					155					160	
Ala	Lys	Gln	Leu													

(2) INFORMATION FOR SEQ ID NO:1934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1501739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1934:

Phe	Cys	Ser	Val	Pro	Ser	Glu	Asn	Thr	Thr	Gly	Lys	His	Thr	His	Lys	
1				5					10					15		
Thr	Ala	Val	Ser	Glu	Trp	Pro	Arg	Pro	Cys	Ser	Ala	Ala	His	Ser	Ser	
			20					25					30			

Pro Arg Ser Ser Pro Pro Pro Glu Gly Arg Pro Gly Pro Pro Leu Gly
35 40 45
Ser Val Pro Gly Asp Val Gly Pro Leu Leu Pro Cys Ala Arg Cys Leu
50 55 60
Pro Thr Pro Pro Ser Pro Ser Pro Pro Pro Pro Pro Pro Ala Val
65 70 75 80
Thr Ala Pro Thr Arg Asn His Arg Ser Tyr Arg Ser Ser Arg Ser Leu
85 90 95
Arg Ile Ala

(2) INFORMATION FOR SEQ ID NO:1935:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1501740

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935:

Met Ala Thr Ala Val Leu Arg Arg Pro Phe Leu Ala Ala Leu Leu Pro
1 5 10 15
Ala Ala Gly Gly Ala Ser Gly Thr Ser Ser Trp Phe Arg Pro Arg Arg
20 25 30
Arg Arg Ser Ser Pro Ser Val Arg Ala Val Ser Ser Asp Ser Pro Lys
35 40 45
Pro Val Ala Ser Thr Ser Ser Pro Thr Gly Gly Asp Ser Pro Asp Glu
50 55 60
Glu Pro Pro Val Leu Pro Leu Leu Gln Glu Leu Ala Asp Cys Leu Ile
65 70 75 80
Leu Pro Pro Lys Leu Leu Ala Gln Leu Pro Ser Asp Leu Arg Leu Asp
85 90 95
Leu Asn Asp Ala Ala Phe Asp Leu Ser Asn Gly Pro Val Leu Asp Glu
100 105 110
Cys Gly Gln Glu Val Gly Asp Leu Leu Leu Asn Leu Ala Lys Ala Trp
115 120 125
Glu Leu Ala Asp Thr Ser Thr Ser Asn Ser Ile Ala Lys Gln Leu
130 135 140

(2) INFORMATION FOR SEQ ID NO:1936:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..363

(D) OTHER INFORMATION: / Ceres Seq. ID 1501741

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936:

acaaacttcc cctgtcacga gagtacgaga ccacgccttc cgtgggatca atcggctagg 60
gtttcggaga tgttcggccg cgcgccgaag aagagcgaca acaccggta ctacgagatc 120
ctgggggttt ccaaggacgc gtcacaggat gacctcaaga aggcctaccg caaggccgcc 180
atcaagaacc accccgacaa gggcggcgac cccgagaagt tcaaggagct atgtatgctg 240
tatgcatgtg gtgaagcaag tgctcgtcgg tgtgtagtgt tcgctcttct gatccattgt 300
ctgtgctctg tactgtagt atcagcgtca aaataaagaa atgcctgtcc ttgtttagaa 360
ttg

(2) INFORMATION FOR SEQ ID NO:1937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..105
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1501742
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937:

Thr	Asn	Phe	Pro	Cys	His	Glu	Ser	Thr	Arg	Pro	Arg	Leu	Pro	Trp	Asp
1			5						10					15	
Gln	Ser	Ala	Arg	Val	Ser	Glu	Met	Phe	Gly	Arg	Ala	Pro	Lys	Lys	Ser
			20					25					30		
Asp	Asn	Thr	Arg	Tyr	Tyr	Glu	Ile	Leu	Gly	Val	Ser	Lys	Asp	Ala	Ser
		35				40						45			
Gln	Asp	Asp	Leu	Lys	Lys	Ala	Tyr	Arg	Lys	Ala	Ala	Ile	Lys	Asn	His
	50					55					60				
Pro	Asp	Lys	Gly	Gly	Asp	Pro	Glu	Lys	Phe	Lys	Glu	Leu	Cys	Met	Leu
	65				70				75						80
Tyr	Ala	Cys	Gly	Glu	Ala	Ser	Ala	Arg	Arg	Cys	Val	Val	Phe	Ala	Leu
			85					90						95	
Leu	Ile	His	Cys	Leu	Cys	Ser	Val	Leu							
			100					105							

(2) INFORMATION FOR SEQ ID NO:1938:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501743

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938:

Gln	Thr	Ser	Pro	Val	Thr	Arg	Val	Arg	Asp	His	Ala	Phe	Arg	Gly	Ile
1			5					10						15	
Asn	Arg	Leu	Gly	Phe	Arg	Arg	Cys	Ser	Ala	Ala	Arg	Arg	Arg	Arg	Ala
		20					25						30		
Thr	Thr	Pro	Gly	Thr	Thr	Arg	Ser	Trp	Gly	Phe	Pro	Arg	Thr	Arg	His
		35				40						45			
Arg	Met	Thr	Ser	Arg	Arg	Pro	Thr	Ala	Arg	Pro	Pro	Ser	Arg	Thr	Thr
	50					55					60				
Pro	Thr	Arg	Ala	Ala	Thr	Pro	Arg	Ser	Ser	Arg	Ser	Tyr	Val	Cys	Cys
	65			70				75						80	
Met	His	Val	Val	Lys	Gln	Val	Leu	Val	Gly	Val					
			85					90							

(2) INFORMATION FOR SEQ ID NO:1939:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939:

Met Phe Gly Arg Ala Pro Lys Lys Ser Asp Asn Thr Arg Tyr Tyr Glu

(2) INFORMATION FOR SEO ID NO:1940:

(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..483
(D) OTHER INFORMATION: / Ceres Seq. ID 1501755

ctcgttttac	ccgcacccgc	cgcagcccgc	aacgccgaga	agacgcgaga	kgaagggagg	60
aggtgagcca	ccgaagcgga	gacgtgagta	gtcgaaccaac	cccgtcggtc	cggcgactcc	120
ggctgcggcg	cggcgtgcta	gatcgctacc	gacctggtt	gtggaggaga	tcgccgaggg	180
ggtgaaaaac	ctcaccgta	ccggagatgc	ggcggcttca	ggcgagagg	ggcagaggag	240
gggcggcgcg	ggcagaccaa	cgcgattccag	gtgtccaaca	ccaagaagcc	ctctctcttc	300
tacgtcaacc	tcgccaagag	tatatgcaac	agcacgacga	tgtagagcta	tccgctcttg	360
ggatggccat	agcaacagtt	gtgaccgttg	cagaaattct	gaagaacaat	ggatttgccg	420
ttgaaaaagaa	aattaggacc	tctactgttg	aaataaacga	cgaatcaaga	gggcgtccat	480
tcc						

(2) INFORMATION FOR SEO ID NO:1941:

(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..60
(D) OTHER INFORMATION: / Ceres Seq. ID 1501756

Arg 1	Phe	Thr	Arg	Thr 5	Arg	Arg	Ser	Pro	Gln 10	Arg	Arg	Glu	Asp	Ala 15	Arg
Xaa	Arg	Glu	Glu 20	Val	Ser	His	Arg	Ser 25	Gly	Asp	Val	Ser	Ser 30	Arg	Pro
Thr	Pro	Ser 35	Val	Arg	Arg	Leu 40	Arg	Leu 45	Arg	Arg	Gly	Val 45	Leu	Asp	Arg
Tyr 50	Arg	Pro	Trp	Trp	Trp 55	Arg	Arg	Ser	Pro	Arg	Gly 60				

(2) INFORMATION FOR SEQ ID NO:1942:

(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1501757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1942:

```
Met Val Val Glu Glu Ile Ala Glu Gly Val Lys Asn Leu Thr Val Thr
1          5          10          15
Gly Asp Ala Ala Ser Gly Gly Glu Gly Gln Arg Arg Gly Gly Gly
20          25          30
Gly Thr Ala Thr Ala Ser Arg Cys Pro Thr Pro Arg Ser Pro Ser Ser
35          40          45
Ser Thr Ser Thr Ser Pro Arg Val Tyr Ala Thr Ala Arg Arg Cys Arg
50          55          60
Ala Ile Arg Ser Trp Asp Gly His Ser Asn Ser Cys Asp Arg Gly Arg
65          70          75          80
Asn Ser Glu Glu Gln Trp Ile Cys Arg
85
```

(2) INFORMATION FOR SEQ ID NO:1943:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1501758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943:

```
Met Arg Arg Leu Gln Ala Glu Arg Gly Arg Gly Gly Ala Ala Ala Ala
1          5          10          15
Gln Gln Pro His Pro Gly Val Gln His Gln Glu Ala Pro Leu Leu Leu
20          25          30
Arg Gln Pro Arg Gln Glu Tyr Met Gln Gln His Asp Asp Val Glu Leu
35          40          45
Ser Ala Leu Gly Met Ala Ile Ala Thr Val Val Thr Val Ala Glu Ile
50          55          60
Leu Lys Asn Asn Gly Phe Ala Val Glu Lys Lys Ile Arg Thr Ser Thr
65          70          75          80
Val Glu Ile Asn Asp Glu Ser Arg Gly Arg Pro Phe
85          90
```

(2) INFORMATION FOR SEQ ID NO:1944:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..576

(D) OTHER INFORMATION: / Ceres Seq. ID 1501763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944:

```
aagattgggt ccaacaccag ccgcccgcct gtcgaagcga ggcargggag gttcggcggg 60
gaacaagttc cgcatgtcgc tgggtctgcc agtggccgcg acggtgaact gcgcggacaa 120
caccggcgcc aagaacctct acatcatctc cgtaaggggc atcaagggcc gcctcaatcg 180
cctcccggtc gctgcgttg gcgacatggg catggccacc gtcaagaagg ggaagcccga 240
cctcaggaag aaggtgatgc ccgccgtcat cgtaaggccg cgcaagccgt ggcgccgcaa 300
ggacgggggtc tacatgtact tcgaagataa tgctggagtg attgtgaatc ccaagggtga 360
gatgaaaggt tccgctatca ctggacctat cggcaaggag tgtgctgatc tttggcctag 420
gattgctagc gcagcaaacg ccattgtttg agagcttggt ggaatatggt cagacttcta 480
tatgatcatc ttattatcag ttgctagact gcaattgggc ttatgtttgt tcactcaatt 540
ttgtagtaaa cagaatttgg tataccaagg ggatct
```

(2) INFORMATION FOR SEQ ID NO:1945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..149
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945:

Arg Leu Gly Pro Thr Pro Ala Ala Ala Met Ser Lys Arg Gly Xaa Gly
1 5 10 15
Gly Ser Ala Gly Asn Lys Phe Arg Met Ser Leu Gly Leu Pro Val Ala
20 25 30
Ala Thr Val Asn Cys Ala Asp Asn Thr Gly Ala Lys Asn Leu Tyr Ile
35 40 45
Ile Ser Val Lys Gly Ile Lys Gly Arg Leu Asn Arg Leu Pro Ser Ala
50 55 60
Cys Val Gly Asp Met Val Met Ala Thr Val Lys Lys Gly Lys Pro Asp
65 70 75 80
Leu Arg Lys Lys Val Met Pro Ala Val Ile Val Arg Gln Arg Lys Pro
85 90 95
Trp Arg Arg Lys Asp Gly Val Tyr Met Tyr Phe Glu Asp Asn Ala Gly
100 105 110
Val Ile Val Asn Pro Lys Gly Glu Met Lys Gly Ser Ala Ile Thr Gly
115 120 125
Pro Ile Gly Lys Glu Cys Ala Asp Leu Trp Pro Arg Ile Ala Ser Ala
130 135 140
Ala Asn Ala Ile Val
145

(2) INFORMATION FOR SEQ ID NO:1946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946:

Met Ser Lys Arg Gly Xaa Gly Gly Ser Ala Gly Asn Lys Phe Arg Met
1 5 10 15
Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn Thr
20 25 30
Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly Arg
35 40 45
Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala Thr
50 55 60
Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala Val
65 70 75 80
Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Tyr Met
85 90 95
Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu Met
100 105 110
Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp Leu
115 120 125
Trp Pro Arg Ile Ala Ser Ala Ala Asn Ala Ile Val

130 135 140
(2) INFORMATION FOR SEQ ID NO:1947:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..125
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501766
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947:
Met Ser Leu Gly Leu Pro Val Ala Ala Thr Val Asn Cys Ala Asp Asn
1 5 10 15
Thr Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Gly Ile Lys Gly
20 25 30
Arg Leu Asn Arg Leu Pro Ser Ala Cys Val Gly Asp Met Val Met Ala
35 40 45
Thr Val Lys Lys Gly Lys Pro Asp Leu Arg Lys Lys Val Met Pro Ala
50 55 60
Val Ile Val Arg Gln Arg Lys Pro Trp Arg Arg Lys Asp Gly Val Tyr
65 70 75 80
Met Tyr Phe Glu Asp Asn Ala Gly Val Ile Val Asn Pro Lys Gly Glu
85 90 95
Met Lys Gly Ser Ala Ile Thr Gly Pro Ile Gly Lys Glu Cys Ala Asp
100 105 110
Leu Trp Pro Arg Ile Ala Ser Ala Asn Ala Ile Val
115 120 125

(2) INFORMATION FOR SEQ ID NO:1948:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 554 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..554
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501771
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948:
attatttctat caagtgtgtg tgcttttatt ttatgtgctg gagctgcact agtgctttat 60
ttcaagcttc gaaaccacat ccatttaact gaagcgtcac ttgtgccaac aaaacctaca 120
ggtcctgttt ctgcaatggt tgggaacagg ctagaaagca gacctatttc ggcataccca 180
tccttcagct caagtttggg ggcataataa ggatctgccca aaacatttaa cctgggtgag 240
atggagagag ctacactagg atttgatgag tccagaatta ttggtgaggg tggttttggg 300
cgtgtctatg aagggtattct tgaggatgga gaacgggttg ctatcaaggt tttaaagcgg 360
gacgatcaac aagggtacccg ggagtttttg gctgargtcg agatgcttag ccgattgcat 420
cataggaact tggttaagct gataggtata tgcacagagg ggcatagccg atgtttggtt 480
tatgagcttg ttccgaatgg cagtgtggga atctcacttg catggatcag ataaaggagg 540
ctgctcagtt tgat

(2) INFORMATION FOR SEQ ID NO:1949:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..177

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(D) OTHER INFORMATION: / Ceres Seq. ID 1501772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949:

Ile Ile Leu Ser Ser Val Cys Ala Phe Ile Leu Cys Ala Gly Ala Ala
1 5 10 15
Leu Val Leu Tyr Phe Lys Leu Arg Asn His Ile His Leu Thr Glu Ala
20 25 30
Ser Leu Val Pro Thr Lys Pro Thr Gly Pro Val Ser Ala Met Val Gly
35 40 45
Asn Arg Leu Glu Ser Arg Pro Ile Ser Ala Ser Pro Ser Phe Ser Ser
50 55 60
Ser Leu Val Ala Tyr Lys Gly Ser Ala Lys Thr Phe Asn Leu Val Glu
65 70 75 80
Met Glu Arg Ala Thr Leu Gly Phe Asp Glu Ser Arg Ile Ile Gly Glu
85 90 95
Gly Gly Phe Gly Arg Val Tyr Glu Gly Ile Leu Glu Asp Gly Glu Arg
100 105 110
Val Ala Ile Lys Val Leu Lys Arg Asp Asp Gln Gln Gly Thr Arg Glu
115 120 125
Phe Leu Ala Xaa Val Glu Met Leu Ser Arg Leu His His Arg Asn Leu
130 135 140
Val Lys Leu Ile Gly Ile Cys Thr Glu Gly His Ser Arg Cys Leu Val
145 150 155 160
Tyr Glu Leu Val Pro Asn Gly Ser Val Gly Ile Ser Leu Ala Trp Ile
165 170 175
Arg

(2) INFORMATION FOR SEQ ID NO:1950:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1501773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950:

Met Val Gly Asn Arg Leu Glu Ser Arg Pro Ile Ser Ala Ser Pro Ser
1 5 10 15
Phe Ser Ser Ser Leu Val Ala Tyr Lys Gly Ser Ala Lys Thr Phe Asn
20 25 30
Leu Val Glu Met Glu Arg Ala Thr Leu Gly Phe Asp Glu Ser Arg Ile
35 40 45
Ile Gly Glu Gly Gly Phe Gly Arg Val Tyr Glu Gly Ile Leu Glu Asp
50 55 60
Gly Glu Arg Val Ala Ile Lys Val Leu Lys Arg Asp Asp Gln Gln Gly
65 70 75 80
Thr Arg Glu Phe Leu Ala Xaa Val Glu Met Leu Ser Arg Leu His His
85 90 95
Arg Asn Leu Val Lys Leu Ile Gly Ile Cys Thr Glu Gly His Ser Arg
100 105 110
Cys Leu Val Tyr Glu Leu Val Pro Asn Gly Ser Val Gly Ile Ser Leu
115 120 125
Ala Trp Ile Arg
130

(2) INFORMATION FOR SEQ ID NO:1951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..97
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501774
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951:
Met Glu Arg Ala Thr Leu Gly Phe Asp Glu Ser Arg Ile Ile Gly Glu
1 5 10 15
Gly Gly Phe Gly Arg Val Tyr Glu Gly Ile Leu Glu Asp Gly Glu Arg
 20 25 30
Val Ala Ile Lys Val Leu Lys Arg Asp Gln Gln Gly Thr Arg Glu
 35 40 45
Phe Leu Ala Xaa Val Glu Met Leu Ser Arg Leu His His Arg Asn Leu
50 55 60
Val Lys Leu Ile Gly Ile Cys Thr Glu Gly His Ser Arg Cys Leu Val
65 70 75 80
Tyr Glu Leu Val Pro Asn Gly Ser Val Gly Ile Ser Leu Ala Trp Ile
 85 90 95
Arg

(2) INFORMATION FOR SEQ ID NO:1952:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..420
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501786
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952:
aaaaacctcg caagcgaccc cagtaatggc gaccaaggcg ctatccgtct cctcgctcac 60
ctccacggcc ttgctctct tttccttgcc gcggccccgc aggccttcac cttcgctctc 120
cctcctccgc cttctcgcc ctgcgcccg cgctccact ctctccgccc ccgctcccg 180
cgacgaggac ggcgtcgaca ccgtggagca gtcctccac ccamgcccgc ctgagacctc 240
agcccccgcc ggatccccgc gccgatcga mcgctcatg aagctccagc gcmgcgccga 300
cgggamgccc tgccccgggg ccggaggagg tggttccctt acctggacgc gttccggccc 360
gcggccgngn ggcgcggast gtccagcggg gaggtcatag aggtgctgga gccgcacatc 420

(2) INFORMATION FOR SEQ ID NO:1953:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..77
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501787
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1953:
Lys Asn Leu Ala Ser Asp Pro Ser Asn Gly Asp Gln Gly Ala Ile Arg
1 5 10 15
Leu Leu Ala His Leu His Gly Leu Cys Leu Leu Phe Leu Ala Ala Ala
 20 25 30
Pro Gln Ala Phe Thr Phe Ala Ser Pro Pro Pro Ser Arg Pro Ser
 35 40 45
Pro Pro Arg Leu His Ser Leu Arg Arg Arg Ser Arg Arg Arg Gly Arg
50 55 60

Arg Arg His Arg Gly Ala Ala Pro Pro Pro Xaa Pro Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:1954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501788

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954:

Lys Thr Ser Gln Ala Thr Pro Val Met Ala Thr Lys Ala Leu Ser Val
1 5 10 15
Ser Ser Leu Thr Ser Thr Ala Phe Ala Ser Phe Ser Leu Pro Arg Pro
20 25 30
Arg Arg Pro Ser Pro Ser Pro Pro Leu Leu Arg Leu Leu Gly Pro Arg
35 40 45
Pro Arg Ala Ser Thr Leu Ser Ala Ala Ala Pro Gly Asp Glu Asp Gly
50 55 60
Val Asp Thr Val Glu Gln Leu Leu His Pro Xaa Pro Pro Glu Thr Ser
65 70 75 80
Ala Pro Ala Gly Ser Arg Gly Arg Ile Xaa Arg Leu Met Lys Leu Gln
85 90 95
Arg Xaa Ala Asp Gly Xaa Pro Cys Pro Gly Ala Gly Gly Gly Gly Ser
100 105 110
Leu Thr Trp Thr Arg Ser Gly Pro Arg Pro Xaa Gly Ala Xaa Cys Pro
115 120 125
Ala Gly Arg Ser
130

(2) INFORMATION FOR SEQ ID NO:1955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501789

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955:

Met Ala Thr Lys Ala Leu Ser Val Ser Ser Leu Thr Ser Thr Ala Phe
1 5 10 15
Ala Ser Phe Ser Leu Pro Arg Pro Arg Arg Pro Ser Pro Ser Pro Pro
20 25 30
Leu Leu Arg Leu Leu Gly Pro Arg Pro Arg Ala Ser Thr Leu Ser Ala
35 40 45
Ala Ala Pro Gly Asp Glu Asp Gly Val Asp Thr Val Glu Gln Leu Leu
50 55 60
His Pro Xaa Pro Pro Glu Thr Ser Ala Pro Ala Gly Ser Arg Gly Arg
65 70 75 80
Ile Xaa Arg Leu Met Lys Leu Gln Arg Xaa Ala Asp Gly Xaa Pro Cys
85 90 95
Pro Gly Ala Gly Gly Gly Gly Ser Leu Thr Trp Thr Arg Ser Gly Pro
100 105 110
Arg Pro Xaa Gly Ala Xaa Cys Pro Ala Gly Arg Ser
115 120

(2) INFORMATION FOR SEQ ID NO:1956:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..493
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501794
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956:

```
aacctaaacc tcgtctcgcc tcgcctccgc cagtcagccc cctcaacccc ggcggccaaa      60
agtcgacgca ccgaagcggc ggccatggcg gactaaagcg gctgtcagag agccgggacc      120
tgacgcggat cgagccatcg gcgcgcactc ccacatccgg gggctagggc tggactcctc      180
catggaggcg cgcgacgcct cggagggcat ggtcgggcag ctgcccgcgc gccgsscgcg      240
ggnctcata ctccagctca tccgccaggg caagatcgcc ggccgcgcgc ttctcctcgc      300
gggcccagccc ggtaccggca agaccgcgct cgccatgggc atcgccaagt cgctcggcgc      360
ggagacgccc ttgcctccg tcgcagcctc ggagctcttc tcgctcgamc tctccaagam      420
ggaggcgctc acgcaggcct tccgccgcgc catcggggtgc gcatcaagga ggagacggaa      480
atcatcgagg gcg
```

- (2) INFORMATION FOR SEQ ID NO:1957:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..54
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1957:
Pro Lys Pro Arg Leu Ala Ser Pro Pro Val Ser Pro Leu Asn Pro
1 5 10 15
Gly Gly Gln Lys Ser Thr His Arg Ser Gly Gly His Gly Gly Leu Lys
 20 25 30
Arg Leu Ser Glu Ser Arg Asp Leu Thr Arg Ile Glu Pro Ser Ala Arg
 35 40 45
Thr Pro Thr Ser Gly Gly
50

- (2) INFORMATION FOR SEQ ID NO:1958:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..104
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1958:
Met Glu Ala Arg Asp Ala Ser Glu Gly Met Val Gly Gln Leu Pro Ala
1 5 10 15
Arg Xaa Xaa Arg Xaa Leu Ile Leu Gln Leu Ile Arg Gln Gly Lys Ile
 20 25 30
Ala Gly Arg Ala Val Leu Leu Ala Gly Gln Pro Gly Thr Gly Lys Thr
 35 40 45
Ala Leu Ala Met Gly Ile Ala Lys Ser Leu Gly Ala Glu Thr Pro Phe
50 55 60
Ala Ser Val Ala Ala Ser Glu Leu Phe Ser Leu Xaa Leu Ser Lys Xaa

[illegible]

(2) INFORMATION FOR SEQ ID NO:1959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..95
(D) OTHER INFORMATION: / Ceres Seq. ID 1501797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1959:

Met	Val	Gly	Gln	Leu	Pro	Ala	Arg	Xaa	Xaa	Arg	Xaa	Leu	Ile	Leu	Gln
1				5					10					15	
Leu	Ile	Arg	Gln	Gly	Lys	Ile	Ala	Gly	Arg	Ala	Val	Leu	Leu	Ala	Gly
			20					25					30		
Gln	Pro	Gly	Thr	Gly	Lys	Thr	Ala	Leu	Ala	Met	Gly	Ile	Ala	Lys	Ser
			35				40					45			
Leu	Gly	Ala	Glu	Thr	Pro	Phe	Ala	Ser	Val	Ala	Ala	Ser	Glu	Leu	Phe
			50			55					60				
Ser	Leu	Xaa	Leu	Ser	Lys	Xaa	Glu	Ala	Leu	Thr	Gln	Ala	Phe	Arg	Arg
65					70					75				80	
Ala	Ile	Gly	Cys	Ala	Ser	Arg	Arg	Arg	Arg	Lys	Ser	Ser	Arg	Ala	
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:1960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..461
(D) OTHER INFORMATION: / Ceres Seq. ID 1501804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1960:

atcccaaaga	gcacgcagcg	casactgaag	caccacttcc	tgcactcaact	gctagctgct	60
cacaccgtgc	tagtaacagt	ccatcaccag	tcaccacca	tggctcccaa	ggttgcgctc	120
ttccttgccc	tcggccttct	cttcgctgcc	gccgcgaatg	gctgcgaacc	ctactgtccc	180
ggcccagtcg	tcccaacgcc	gccagtcgtg	ccgacgccgt	cgtcgcacag	ccacggggcg	240
tgcccgatcg	acgcgctcaa	aatcatgtgt	gcgccaacgt	gctaggcctc	gtcaaggtcg	300
gcctgcccc	gcacgagcaa	tgtgtccca	ttctggaggg	tcttggtggac	ctcgacgccg	360
cactgtgcct	ctgcaccgsc	atcaaggcca	acggcgctga	ttctacatc	aacgggcatg	420
accactgcct	qqaacacatc	aqaacgaag	acaqcccaat	c		

(2) INFORMATION FOR SEQ ID NO:1961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..94
(D) OTHER INFORMATION: / Ceres Seq. ID 1501805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1961:

Ile Pro Lys Ser Thr Gln Arg Xaa Leu Lys His His Phe Leu His Ser
1 5 10 15
Leu Leu Ala Ala His Thr Val Leu Val Thr Val His His Gln Ser Pro
20 25 30
Pro Met Ala Pro Lys Val Ala Leu Phe Leu Ala Leu Gly Leu Leu Phe
35 40 45
Ala Ala Ala Ala Asn Gly Cys Glu Pro Tyr Cys Pro Gly Pro Val Val
50 55 60
Pro Thr Pro Pro Val Val Pro Thr Pro Ser Ser His Ser His Gly Arg
65 70 75 80
Cys Pro Ile Asp Ala Leu Lys Ile Met Cys Ala Pro Thr Cys
85 90

(2) INFORMATION FOR SEQ ID NO:1962:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1501806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1962:

Pro Lys Glu His Ala Ala Xaa Thr Glu Ala Pro Leu Pro Ala Leu Thr
1 5 10 15
Ala Ser Cys Ser His Arg Ala Ser Asn Ser Pro Ser Pro Val Thr Thr
20 25 30
Asn Gly Ser Gln Gly Cys Ala Leu Pro Cys Pro Arg Pro Ser Leu Arg
35 40 45
Cys Arg Arg Glu Trp Leu Arg Thr Leu Leu Ser Arg Pro Ser Arg Pro
50 55 60
Asn Ala Ala Ser Arg Ala Asp Ala Val Val Ala Gln Pro Arg Ala Leu
65 70 75 80
Pro Asp Arg Arg Ala Gln Asn His Val Cys Ala Asn Val Leu Gly Leu
85 90 95
Val Lys Val Gly Leu Pro Gln His Glu Gln Cys Cys Pro Leu Leu Glu
100 105 110
Gly Leu Val Asp Leu Asp Ala Ala Leu Cys Leu Cys Thr Xaa Ile Lys
115 120 125
Ala Asn Gly Val Asp Phe Tyr Ile Asn Gly His Asp His Cys Leu Glu
130 135 140
His Ile Ser Ser Arg Asp Ser Pro Ile
145 150

(2) INFORMATION FOR SEQ ID NO:1963:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1501807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1963:

Met Ala Ala Asn Pro Thr Val Pro Ala Gln Ser Ser Gln Arg Arg Gln
1 5 10 15
Ser Cys Arg Arg Arg Arg Thr Ala Thr Gly Ala Ala Arg Ser Thr
20 25 30
Arg Ser Lys Ser Cys Val Arg Gln Arg Ala Arg Pro Arg Gln Gly Arg

35 40 45
Pro Ala Pro Ala Arg Ala Met Leu Pro Thr Ser Gly Gly Ala Gly Gly
50 55 60
Pro Arg Arg Arg Thr Val Pro Leu His Xaa His Gln Gly Gln Arg Arg
65 70 75 80
Arg Phe Leu His Gln Arg Ala

(2) INFORMATION FOR SEQ ID NO:1964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..446
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1964:

agacaacccat	agaccgacga	ggtgtgaact	gtaatttcag	atttcagagc	gcgcaagaac	60
cctcttgacc	accgccgccg	ccgccgcgaa	scaagccaaa	ctgagtaagc	agctatggag	120
ggatccgccg	ccgctccgct	ccgcacgcgc	atctgcatca	tcgggagcgg	tcccgcctgcg	180
cacacggcag	ccatctacgc	ggcccgcgcg	gagctcaagc	ctgtdctctt	cgagggctgg	240
atggccaacg	acatcgccgc	ggcgggcgag	ctcaccacca	ccaccgacgt	cgagaacttc	300
ccgggcttcc	ccaacggcat	catgggcgcc	gacctcatgg	acaactgccg	cgcgcagtcc	360
ctgcgctttg	gcaccaacat	cctctccgag	accgtcaccg	ccgtcgactt	ttcggcctgc	420
ccattccgag	ttagtgcaga	ctccac				

(2) INFORMATION FOR SEQ ID NO:1965:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1965:

Met	Glu	Gly	Ser	Ala	Ala	Ala	Pro	Leu	Arg	Thr	Arg	Ile	Cys	Ile	Ile
1				5				10					15		
Gly	Ser	Gly	Pro	Ala	Ala	His	Thr	Ala	Ala	Ile	Tyr	Ala	Ala	Arg	Ala
			20					25					30		
Glu	Leu	Lys	Pro	Xaa	Leu	Phe	Glu	Gly	Trp	Met	Ala	Asn	Asp	Ile	Ala
		35					40					45			
Ala	Gly	Gly	Gln	Leu	Thr	Thr	Thr	Thr	Asp	Val	Glu	Asn	Phe	Pro	Gly
	50				55				60						
Phe	Pro	Asn	Gly	Ile	Met	Gly	Ala	Asp	Leu	Met	Asp	Asn	Cys	Arg	Ala
65				70					75					80	
Gln	Ser	Leu	Arg	Phe	Gly	Thr	Asn	Ile	Leu	Ser	Glu	Thr	Val	Thr	Ala
			85					90					95		
Val	Asp	Phe	Ser	Ala	Cys	Pro	Phe	Arg	Val	Ser	Ala	Asp	Ser		
		100					105						110		

(2) INFORMATION FOR SEQ ID NO:1966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..68
(D) OTHER INFORMATION: / Ceres Seq. ID 1501812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1966:

```
Met Ala Asn Asp Ile Ala Ala Gly Gly Gln Leu Thr Thr Thr Asp
1          5          10          15
Val Glu Asn Phe Pro Gly Phe Pro Asn Gly Ile Met Gly Ala Asp Leu
          20          25          30
Met Asp Asn Cys Arg Ala Gln Ser Leu Arg Phe Gly Thr Asn Ile Leu
          35          40          45
Ser Glu Thr Val Thr Ala Val Asp Phe Ser Ala Cys Pro Phe Arg Val
          50          55          60
Ser Ala Asp Ser
65
```

(2) INFORMATION FOR SEQ ID NO:1967:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 758 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..758
(D) OTHER INFORMATION: / Ceres Seq. ID 1501813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1967:

```
aaattcccaa ccgccgcacg gcaacaccag cggtcggatc gggggagaaa cggaagggca      60
acagcagagc gcgaattcca ccgacaaatc caagatttcg agcacagaca caggcgaaac      120
tcgatggcgg aggggtccaa gccggacgtg ccgctgttcc agctcctcag cgatcttctc      180
cagcaggtgg agtcaatgag caatcaggaa gaagtagagc tgcgcgctaa gattgaagca      240
ttaggattag aagtcactaa ggtaccagag cagcccgtca atmatctcag cgagctagaa      300
matagctgca gagttggaca aagctgtcat cgcggcttga ataaatgtcg acaaagatga      360
tatcatctgc catggcctca gatccagagg tgaagtctct tctgagcagc acatctgata      420
tctggatgcc ggtcataaca gcgtctgcc aatgagaggcg ggggtttggt gggacgagca      480
gcgaaggcag ccagaaagag caggagaatt ccaagaaata gctggtatat gggctgttaa      540
tagtttcggt ttgtgggtct gtaccgacct tatctatggt cattcaaact agtgtttcca      600
tgccaaaaag tttgtggcgt aataaacaat aaaaacccat gtccttcatt cggattagta      660
atgagtgatg atagatctaa attactatct tggtcgcccg ttagttcatt tttgaactaa      720
aacgcgaata atagaaaaga acggagggag tatgattt
```

(2) INFORMATION FOR SEQ ID NO:1968:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..119
(D) OTHER INFORMATION: / Ceres Seq. ID 1501814

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1968:

```
Lys Phe Pro Thr Ala Ala Arg Gln His Gln Arg Ser Asp Arg Gly Arg
1          5          10          15
Asn Gly Arg Ala Thr Ala Glu Arg Glu Phe His Arg Gln Ile Gln Asp
          20          25          30
Phe Glu His Arg His Arg Arg Asn Ser Met Ala Glu Gly Ser Lys Pro
          35          40          45
Asp Val Pro Leu Phe Gln Leu Leu Ser Asp Leu Leu Gln Gln Val Glu
          50          55          60
Ser Met Ser Asn Gln Glu Glu Val Glu Leu Arg Ala Lys Ile Glu Ala
65          70          75          80
```

Leu Gly Leu Glu Val Thr Lys Val Pro Glu Gln Pro Ala Asn Xaa Leu
85 90 95
Ser Glu Leu Glu Xaa Ser Cys Arg Val Gly Gln Ser Cys His Arg Gly
100 105 110
Leu Asn Lys Lys Cys Arg Gln Arg
115

(2) INFORMATION FOR SEQ ID NO:1969:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501815

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1969:

Ile Pro Asn Arg Arg Thr Ala Thr Pro Ala Val Gly Ser Gly Glu Lys
1 5 10 15
Arg Lys Gly Asn Ser Arg Ala Arg Ile Pro Pro Thr Asn Pro Arg Phe
20 25 30
Arg Ala Gln Thr Gln Ala Lys Leu Asp Gly Gly Gly Val Gln Ala Gly
35 40 45
Arg Ala Ala Val Pro Ala Pro Gln Arg Ser Ser Pro Ala Gly Gly Val
50 55 60
Asn Glu Gln Ser Gly Arg Ser Arg Ala Ala Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:1970:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1970:

Met Ala Glu Gly Ser Lys Pro Asp Val Pro Leu Phe Gln Leu Leu Ser
1 5 10 15
Asp Leu Leu Gln Val Glu Ser Met Ser Asn Gln Glu Glu Val Glu
20 25 30
Leu Arg Ala Lys Ile Glu Ala Leu Gly Leu Glu Val Thr Lys Val Pro
35 40 45
Glu Gln Pro Ala Asn Xaa Leu Ser Glu Leu Glu Xaa Ser Cys Arg Val
50 55 60
Gly Gln Ser Cys His Arg Gly Leu Asn Lys Cys Arg Gln Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:1971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..607
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501824

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1971:

aaaacgcaca	ggagataact	agcgagcgag	agcgtngaga	tcgaggagaa	gaaggcaagc	60
aggcagagaa	agagagagag	agatggatga	ggagtacgac	gtgatcgtgt	tggggacggg	120
gctcaaggag	tgcatacatca	gcggcctcct	ctccgtcgat	ggcctcaagg	tccttcacat	180
ggacaggaat	gactactacg	gaggagaatc	ttcgtccctg	aatctaacca	agctctggaa	240
taggttcaag	ggcaacgaca	gccctcccga	gcacctgggc	gtcacaaaga	gtacaacgtc	300
gacatggtgc	ccaagtccat	gatggcaaac	ggcgcgctgg	tccgcgtcct	gatccgcacc	360
agcgtgacca	agtatctcaa	cttcaaggct	gttgacggga	gctttgtgta	caacaatggc	420
aagatccaca	aagtcccggc	aaccgacgtg	gaggccctca	agtcgaacct	gatgggcctg	480
ttcgagaagc	ggcgcgcccc	gaagttcttc	atatacgtdc	aggactacga	ggaggacgac	540
cccaagtccc	acgagggcct	ggacctcaac	aaggtcacca	ccagggaagt	catctccaaa	600
tacggat						

(2) INFORMATION FOR SEQ ID NO:1972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501825

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1972:

Met	Val	Pro	Lys	Phe	Met	Met	Ala	Asn	Gly	Ala	Leu	Val	Arg	Val	Leu	
1			5						10						15	
Ile	Arg	Thr	Ser	Val	Thr	Lys	Tyr	Leu	Asn	Phe	Lys	Ala	Val	Asp	Gly	
			20						25					30		
Ser	Phe	Val	Tyr	Asn	Asn	Gly	Lys	Ile	His	Lys	Val	Pro	Ala	Thr	Asp	
			35				40					45				
Val	Glu	Ala	Leu	Lys	Ser	Asn	Leu	Met	Gly	Leu	Phe	Glu	Lys	Arg	Arg	
	50					55					60					
Ala	Arg	Lys	Phe	Phe	Ile	Tyr	Xaa	Gln	Asp	Tyr	Glu	Glu	Asp	Asp	Pro	
65					70					75					80	
Lys	Ser	His	Glu	Gly	Leu	Asp	Leu	Asn	Lys	Val	Thr	Thr	Arg	Glu	Val	
			85					90						95		
Ile	Ser	Lys	Tyr	Gly												
			100													

(2) INFORMATION FOR SEQ ID NO:1973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1973:

Met	Met	Ala	Asn	Gly	Ala	Leu	Val	Arg	Val	Leu	Ile	Arg	Thr	Ser	Val	
1			5						10						15	
Thr	Lys	Tyr	Leu	Asn	Phe	Lys	Ala	Val	Asp	Gly	Ser	Phe	Val	Tyr	Asn	
			20						25					30		
Asn	Gly	Lys	Ile	His	Lys	Val	Pro	Ala	Thr	Asp	Val	Glu	Ala	Leu	Lys	
		35				40						45				
Ser	Asn	Leu	Met	Gly	Leu	Phe	Glu	Lys	Arg	Arg	Ala	Arg	Lys	Phe	Phe	
	50				55						60					
Ile	Tyr	Xaa	Gln	Asp	Tyr	Glu	Glu	Asp	Asp	Pro	Lys	Ser	His	Glu	Gly	
65					70					75					80	
Leu	Asp	Leu	Asn	Lys	Val	Thr	Thr	Arg	Glu	Val	Ile	Ser	Lys	Tyr	Gly	

85

90

95

(2) INFORMATION FOR SEQ ID NO:1974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1974:

Met	Ala	Asn	Gly	Ala	Leu	Val	Arg	Val	Leu	Ile	Arg	Thr	Ser	Val	Thr
1			5						10					15	
Lys	Tyr	Leu	Asn	Phe	Lys	Ala	Val	Asp	Gly	Ser	Phe	Val	Tyr	Asn	Asn
			20					25					30		
Gly	Lys	Ile	His	Lys	Val	Pro	Ala	Thr	Asp	Val	Glu	Ala	Leu	Lys	Ser
		35					40					45			
Asn	Leu	Met	Gly	Leu	Phe	Glu	Lys	Arg	Arg	Ala	Arg	Lys	Phe	Phe	Ile
	50					55				60					
Tyr	Xaa	Gln	Asp	Tyr	Glu	Glu	Asp	Asp	Pro	Lys	Ser	His	Glu	Gly	Leu
65					70				75					80	
Asp	Leu	Asn	Lys	Val	Thr	Thr	Arg	Glu	Val	Ile	Ser	Lys	Tyr	Gly	
			85					90						95	

(2) INFORMATION FOR SEQ ID NO:1975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..526
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1975:

tctgttcccc	tttccctcct	gcgacccccg	tcttctcctc	cccgcgtcaa	accccagcac	60
aaaaagcaac	cgcccgcgcg	ctcctcgctc	ctctcccgaa	tcagccgtcg	cggtgcctaa	120
tccggccgac	ccccctccg	atccgcgggt	gcccgcgcga	gaggcgcgcc	tccgggcctc	180
ccccgatgta	tagcaacttc	aaggagcagg	cgatcgagta	cgtaagcag	gcagtccagg	240
aggacaatgc	cggsaactac	gtcaaggcgt	tccctctcta	catgaacgcg	ctcgagtact	300
tcaaaaccca	cctcaagtac	gagaagaacc	ccaagatcaa	ggaggccatc	accgccaagt	360
tcaccgagta	cctccgcmgc	gccgaggaga	tccgggcggg	cctcgatgag	ggcggcgcar	420
ggcctggggc	caacgggtgg	gacgcagctg	tmgccacgcg	ccccaaagacc	caagggcaag	480
gatkgggacg	gargcaacgg	argggatgac	tccgagcagt	ccaagc		

(2) INFORMATION FOR SEQ ID NO:1976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..168
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1976:

Cys Ser Pro Phe Pro Pro Ala His Pro Val Phe Ser Ser Pro Arg Gln

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1 5 10 15
Thr Pro Ala Gln Lys Ala Thr Ala Arg Arg Leu Leu Ala Pro Leu Pro
20 25 30
Asn Gln Pro Ser Arg Cys Leu Ile Arg Pro Thr Pro Pro Ile Arg
35 40 45
Gly Cys Pro Pro Gln Arg Arg Ala Ser Gly Pro Pro Pro Met Tyr Ser
50 55 60
Asn Phe Lys Glu Gln Ala Ile Glu Tyr Val Lys Gln Ala Val Gln Glu
65 70 75 80
Asp Asn Ala Xaa Asn Tyr Val Lys Ala Phe Pro Leu Tyr Met Asn Ala
85 90 95
Leu Glu Tyr Phe Lys Thr His Leu Lys Tyr Glu Lys Asn Pro Lys Ile
100 105 110
Lys Glu Ala Ile Thr Ala Lys Phe Thr Glu Tyr Leu Arg Xaa Ala Glu
115 120 125
Glu Ile Arg Ala Val Leu Asp Glu Gly Gly Ala Xaa Pro Gly Ala Asn
130 135 140
Gly Gly Asp Ala Ala Xaa Ala Thr Arg Pro Lys Thr Gln Gly Gln Gly
145 150 155 160
Xaa Gly Arg Xaa Gln Arg Xaa Gly
165

(2) INFORMATION FOR SEQ ID NO:1977:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1501830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1977:

Met Tyr Ser Asn Phe Lys Glu Gln Ala Ile Glu Tyr Val Lys Gln Ala
1 5 10 15
Val Gln Glu Asp Asn Ala Xaa Asn Tyr Val Lys Ala Phe Pro Leu Tyr
20 25 30
Met Asn Ala Leu Glu Tyr Phe Lys Thr His Leu Lys Tyr Glu Lys Asn
35 40 45
Pro Lys Ile Lys Glu Ala Ile Thr Ala Lys Phe Thr Glu Tyr Leu Arg
50 55 60
Xaa Ala Glu Glu Ile Arg Ala Val Leu Asp Glu Gly Gly Ala Xaa Pro
65 70 75 80
Gly Ala Asn Gly Gly Asp Ala Ala Xaa Ala Thr Arg Pro Lys Thr Gln
85 90 95
Gly Gln Gly Xaa Gly Arg Xaa Gln Arg Xaa Gly
100 105

(2) INFORMATION FOR SEQ ID NO:1978:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 534 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..534

(D) OTHER INFORMATION: / Ceres Seq. ID 1501850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1978:

atttttttta tatggagatt atttctggwt tatataaaag gacacaagtg gggacgaata 60
gcagaagact tcccttcgtc tgcttcccag agaccagcc atggcgatct cccagatctc 120

acgcatattc ctggccatcc ttctcctggm cgccgccttc gccgcccgcc cagctgcgct 180
tgcggacggc gacgacgtgg tggcccttac cgaatccacg ttcgagaagg aggtcggaaa 240
ggaccgcgcc gccctcgtcg agttctacgc cccctgggtg ggtcactgca agaagcttgc 300
tcctgagtat gaaagacttg gtgcaagttt taagaaagct aaatctgtct tgattgcyaa 360
ggttgattgt ratgagcaca agartttgtg cagcaagtat ggagtttccg ggtatccaac 420
aatccaatgg ttcccgaag gatccttga gcccaaaaag tatgaaggac aacgcactgc 480
agaagccctt gctgaatttc tcaatactga aggaggcaca aatgtaaagc tggc

(2) INFORMATION FOR SEQ ID NO:1979:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..116
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1979:

Phe Phe Tyr Met Glu Ile Ile Ser Xaa Leu Tyr Lys Arg Thr Gln Val
1 5 10 15
Gly Thr Asn Ser Arg Arg Leu Pro Phe Val Cys Phe Pro Glu Thr Gln
20 25 30
Pro Trp Arg Ser Pro Arg Ser His Ala Tyr Ser Trp Pro Ser Phe Ser
35 40 45
Trp Xaa Pro Pro Ser Pro Pro Gln Leu Arg Leu Arg Thr Ala Thr
50 55 60
Thr Trp Trp Pro Leu Pro Asn Pro Arg Ser Arg Arg Ser Glu Arg
65 70 75 80
Thr Ala Ala Pro Ser Ser Ser Ser Thr Pro Pro Gly Val Val Thr Ala
85 90 95
Arg Ser Leu Leu Ser Met Lys Asp Leu Val Gln Val Leu Arg Lys
100 105 110
Leu Asn Leu Ser
115

(2) INFORMATION FOR SEQ ID NO:1980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1980:

Met Glu Ile Ile Ser Xaa Leu Tyr Lys Arg Thr Gln Val Gly Thr Asn
1 5 10 15
Ser Arg Arg Leu Pro Phe Val Cys Phe Pro Glu Thr Gln Pro Trp Arg
20 25 30
Ser Pro Arg Ser His Ala Tyr Ser Trp Pro Ser Phe Ser Trp Xaa Pro
35 40 45
Pro Ser Pro Pro Pro Gln Leu Arg Leu Arg Thr Ala Thr Thr Trp Trp
50 55 60
Pro Leu Pro Asn Pro Arg Ser Arg Arg Arg Ser Glu Arg Thr Ala Ala
65 70 75 80
Pro Ser Ser Ser Ser Thr Pro Pro Gly Val Val Thr Ala Arg Ser Leu
85 90 95
Leu Leu Ser Met Lys Asp Leu Val Gln Val Leu Arg Lys Leu Asn Leu
100 105 110

Ser

(2) INFORMATION FOR SEQ ID NO:1981:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1981:

```
Met Ala Ile Ser Gln Ile Ser Arg Ile Phe Leu Ala Ile Leu Leu Leu
1          5          10          15
Xaa Ala Ala Phe Ala Ala Ala Pro Ala Ala Leu Ala Asp Gly Asp Asp
          20          25          30
Val Val Ala Leu Thr Glu Ser Thr Phe Glu Lys Glu Val Gly Lys Asp
          35          40          45
Arg Gly Ala Leu Val Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys
          50          55          60
Lys Leu Ala Pro Glu Tyr Glu Arg Leu Gly Ala Ser Phe Lys Lys Ala
          65          70          75          80
Lys Ser Val Leu Ile Xaa Lys Val Asp Cys Xaa Glu His Lys Xaa Leu
          85          90          95
Cys Ser Lys Tyr Gly Val Ser Gly Tyr Pro Thr Ile Gln Trp Phe Pro
          100          105          110
Lys Gly Ser Leu Glu Pro Lys Lys Tyr Glu Gly Gln Arg Thr Ala Glu
          115          120          125
Ala Leu Ala Glu Phe Leu Asn Thr Glu Gly Gly Thr Asn Val Lys Leu
          130          135          140
```

(2) INFORMATION FOR SEQ ID NO:1982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..569
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1982:

```
acagcctctc cgctccgct cctcgcgccg ccgccgctc tcctcctgta caggtaagga      60
gaggaagagg gcgaaatggt gaagcacaac aacgtcatcc ccaacgggca cttcaagaag      120
cactggcaga actatgtcaa gacatggttc aaccagcccg cccgcaagca gaggcgccgc      180
atcgctcgtc aaaagaaggc tgtgaagata ttccccgcc cgactgctgg tcctctacgc      240
cccatgttgc aatgccagac tttaaagtac aacatgaagt caagggctgg gagaggcttt      300
acccttgagg agctgaaggc tgggctcacc ggcgagygga ggcgcgcgcg ggactacctg      360
tgcgcgctgc cgcacaagat aaagaggatg gaagagaagg cccacgatag arcggtcaaa      420
gcacaaaaga aacccacacc catccccatc aactggatct tcgataggac cattcctgtc      480
attctacctt agtgtttatc tttttcgatc tttgtttgtg tatctatgct gttattgtaa      540
gctaattcca tggaccttga tagcgctcgt
```

(2) INFORMATION FOR SEQ ID NO:1983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

```

      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
      (A) NAME/KEY: peptide
      (B) LOCATION: 1..101
      (D) OTHER INFORMATION: / Ceres Seq. ID 1501863

```

[illegible]

(2) INFORMATION FOR SEQ ID NO:1984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1501864

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1984:

Met	Val	Lys	His	Asn	Asn	Val	Ile	Pro	Asn	Gly	His	Phe	Lys	Lys	His
1				5					10					15	
Trp	Gln	Asn	Tyr	Val	Lys	Thr	Trp	Phe	Asn	Gln	Pro	Ala	Arg	Lys	Gln
			20					25					30		
Arg	Arg	Arg	Ile	Ala	Arg	Gln	Lys	Lys	Ala	Val	Lys	Ile	Phe	Pro	Arg
		35					40					45			
Pro	Thr	Ala	Gly	Pro	Leu	Arg	Pro	Ile	Val	Gln	Cys	Gln	Thr	Leu	Lys
	50					55					60				
Tyr	Asn	Met	Lys	Ser	Arg	Ala	Gly	Arg	Gly	Phe	Thr	Leu	Glu	Glu	Leu
65					70					75					80
Lys	Ala	Gly	Leu	Thr	Gly	Glu	Gly	Arg	Arg	Ala	Arg	Asp	Tyr	Leu	Cys
				85					90					95	
Ala	Leu	Pro	His	Lys	Ile	Lys	Arg	Met	Glu	Glu	Lys	Ala	His	Asp	Arg
			100					105					110		
Xaa	Val	Lys	Ala	Gln	Lys	Lys	Pro	Thr	Pro	Ile	Pro	Ile	Asn	Trp	Ile
		115					120					125			
Phe	Asp	Arg	Thr	Ile	Pro	Val	Ile	Leu	Pro						
	130					135									

(2) INFORMATION FOR SEQ ID NO:1985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1501865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1985:

```
Met Lys Ser Arg Ala Gly Arg Gly Phe Thr Leu Glu Glu Leu Lys Ala
1          5          10          15
Gly Leu Thr Gly Glu Gly Arg Arg Ala Arg Asp Tyr Leu Cys Ala Leu
20          25          30
Pro His Lys Ile Lys Arg Met Glu Glu Lys Ala His Asp Arg Xaa Val
35          40          45
Lys Ala Gln Lys Lys Pro Thr Pro Ile Pro Ile Asn Trp Ile Phe Asp
50          55          60
Arg Thr Ile Pro Val Ile Leu Pro
65          70
```

(2) INFORMATION FOR SEQ ID NO:1986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..514

(D) OTHER INFORMATION: / Ceres Seq. ID 1501872

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1986:

```
atcgcaactcg tagtcgtagc tcaagcatca rcvgcaggag ctctggggcag cgtgcgcacg      60
trgggtacct agctcgctct gctagcctac catggctgat caccaccggg gcgcgacggg      120
argtgscggg ggctacggcg acctccagcg cgggggcggc atgcacggcg aggcgcagca      180
gcagcagaag cagggcgcca tgatgacggc gctcaaggcc gcgacggccg cgacctcctt      240
gaaccactgc cggcgcgggcg gcatatggcc cttaaaggcg gtggctgctg ctacgtacgc      300
tgccgtagag tctcggtcgc cgcgatatgct ctagctagtc gtttatgtgt tgtgctttgt      360
gtgtgcatgc ttgtgtctgg gggcatgcag tgcagtgcag tactatatgc tgtatgcgtc      420
tctctttgat cggagaggcg gatgtacagc atgctcgata tgtctagttt ggatgtcatg      480
tttatgatga ggaataaaat gcagtgttca ggtg
```

(2) INFORMATION FOR SEQ ID NO:1987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1501873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1987:

```
Arg Thr Arg Ser Arg Ser Ser Ser Ile Xaa Xaa Arg Ser Ser Gly Gln
1          5          10          15
Arg Ala His Xaa Gly Tyr Leu Ala Arg Ser Ala Ser Leu Pro Trp Leu
20          25          30
Ile Thr Thr Gly Ala Arg Arg Xaa Val Xaa Gly Ala Thr Ala Thr Ser
35          40          45
Ser Ala Gly Ala Ala Cys Thr Ala Arg Arg Ser Ser Ser Arg Ser Arg
50          55          60
Ala Pro
65
```

(2) INFORMATION FOR SEQ ID NO:1988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..78
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1988:
Met Ala Asp His His Arg Gly Ala Thr Gly Xaa Xaa Gly Gly Tyr Gly
1 5 10 15
Asp Leu Gln Arg Gly Gly Gly Met His Gly Glu Ala Gln Gln Gln Gln
 20 25 30
Lys Gln Gly Ala Met Met Thr Ala Leu Lys Ala Ala Thr Ala Ala Thr
 35 40 45
Ser Leu Asn His Cys Arg Arg Gly Gly Ile Trp Pro Leu Lys Ala Val
50 55 60
Ala Ala Ala Thr Tyr Ala Ala Val Glu Ser Arg Ser Pro Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:1989:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..55
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1989:
Met His Gly Glu Ala Gln Gln Gln Gln Lys Gln Gly Ala Met Met Thr
1 5 10 15
Ala Leu Lys Ala Ala Thr Ala Ala Thr Ser Leu Asn His Cys Arg Arg
 20 25 30
Gly Gly Ile Trp Pro Leu Lys Ala Val Ala Ala Ala Thr Tyr Ala Ala
35 40 45
Val Glu Ser Arg Ser Pro Arg
50 55

(2) INFORMATION FOR SEQ ID NO:1990:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 556 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..556
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1990:
aagggtgctg cctgcgccc accaaacgta ggagacccat tcacccatct cctctctttt 60
ctttccaaga aaagtcttct cttctctgtc tcagcgccga cgcttcccaa ttccctccaa 120
tcgattcttc gtctcgtcct cgtgtaatcc ccagcttgcc ctctcgtctc ttccctccca 180
aaaccctacg cctccctgac caagctccgg ggacgaatgg acggaggagc cggttcct 240
ggcacgcmgg tcccgcgctc gccggaggac gttttccggg actaccgcgc gcgccaggcc 300
ggcctaatac gggcgctcac caccgatgtt gagaagtctt acgtgatgtg cgacccagag 360
aaggataatt tatgtttata tggacttccc aatgagacat gggaagtaaa cttgctgct 420
gaggagggtt ctctgaact ccagagacca gctctcgga ttaattttgc tcgtgatggg 480
atgaatgaaa aagattggct atcacttggt gcagtgcata gtgattcttg gctaattgtc 540
gttgcatatt attttg

(2) INFORMATION FOR SEQ ID NO:1991:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..109
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1501885
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1991:

Gly Leu Arg Leu Arg Pro Thr Lys Arg Arg Arg Pro Ile His Pro Ser
1 5 10 15
Pro Leu Phe Ser Phe Gln Glu Lys Ser Ser Leu Leu Cys Leu Ser Ala
20 25 30
Asp Ala Ser Gln Phe Leu Pro Ile Asp Ser Ser Ser Arg Pro Arg Val
35 40 45
Ile Pro Ser Leu Pro Ser Ser Leu Phe Pro Pro Lys Thr Leu Arg Leu
50 55 60
Pro Asp Gln Ala Pro Gly Thr Asn Gly Arg Arg Ser Arg Leu Pro Trp
65 70 75 80
His Xaa Gly Pro Ala Leu Ala Gly Gly Arg Phe Pro Gly Leu Pro Arg
85 90 95
Ala Pro Gly Arg Pro Asn Gln Gly Ala His His Arg Cys
100 105

(2) INFORMATION FOR SEQ ID NO:1992:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..113
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1501886
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1992:

Met Asp Gly Gly Ala Gly Phe Pro Gly Thr Xaa Val Pro Arg Ser Pro
1 5 10 15
Glu Asp Val Phe Arg Asp Tyr Arg Ala Arg Gln Ala Gly Leu Ile Arg
20 25 30
Ala Leu Thr Thr Asp Val Glu Lys Phe Tyr Val Met Cys Asp Pro Glu
35 40 45
Lys Asp Asn Leu Cys Leu Tyr Gly Leu Pro Asn Glu Thr Trp Glu Val
50 55 60
Asn Leu Pro Ala Glu Glu Val Pro Pro Glu Leu Pro Glu Pro Ala Leu
65 70 75 80
Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu Lys Asp Trp Leu Ser
85 90 95
Leu Val Ala Val His Ser Asp Ser Trp Leu Met Ser Val Ala Phe Tyr
100 105 110
Phe

(2) INFORMATION FOR SEQ ID NO:1993:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1501887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1993:

Met Cys Asp Pro Glu Lys Asp Asn Leu Cys Leu Tyr Gly Leu Pro Asn
1 5 10 15
Glu Thr Trp Glu Val Asn Leu Pro Ala Glu Glu Val Pro Pro Glu Leu
20 25 30
Pro Glu Pro Ala Leu Gly Ile Asn Phe Ala Arg Asp Gly Met Asn Glu
35 40 45
Lys Asp Trp Leu Ser Leu Val Ala Val His Ser Asp Ser Trp Leu Met
50 55 60
Ser Val Ala Phe Tyr Phe
65 70

(2) INFORMATION FOR SEQ ID NO:1994:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..532

(D) OTHER INFORMATION: / Ceres Seq. ID 1501888

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1994:

gagcctttcg	gtttttctct	gtcttcatgt	gtgtttgtta	tagagaccct	gccttgctcg	60
ggcagcacac	ttgggacgcg	aggaggagga	gttggtgagc	gaactcggga	tcagtgggtg	120
accgcagagt	tcttgcttct	tcctcttga	ggargagggc	tgcagcctgc	aggggccgga	180
gagagcagga	ggaggcggag	acatgggtag	cttcgctaag	ctggcgagga	ggcggtgga	240
gacggacgct	ccggtcatgg	tgaagataca	agaactgctc	cgargggcca	aggatgtrat	300
gtcgcttgcg	cagggagttg	tttactggca	acctcccag	tcagctatgg	ataagatcga	360
aaagatcatc	agggaaacaa	tagtcagtaa	atatggttct	ratgatgggc	ttcctgagct	420
tcgagaagca	cttctcgaaa	agctaagcag	agagaacaag	cttaccaa	catctgtcat	480
ggtcactgct	ggtgcaa	atcaggcttttgk	gaacttggtc	ctcactcttt	gt	

(2) INFORMATION FOR SEQ ID NO:1995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1501889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1995:

Met Gly Ser Phe Ala Lys Leu Ala Arg Arg Ala Val Glu Thr Asp Ala
1 5 10 15
Pro Val Met Val Lys Ile Gln Glu Leu Arg Xaa Ala Lys Asp Xaa
20 25 30
Met Ser Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Pro Glu Ser Ala
35 40 45
Met Asp Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr
50 55 60
Gly Ser Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Leu Glu Lys
65 70 75 80
Leu Ser Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala
85 90 95
Gly Ala Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys
100 105 110

(2) INFORMATION FOR SEQ ID NO:1996:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..92
(D) OTHER INFORMATION: / Ceres Seq. ID 1501890
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1996:
Met Val Lys Ile Gln Glu Leu Leu Arg Xaa Ala Lys Asp Xaa Met Ser
1 5 10 15
Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Pro Glu Ser Ala Met Asp
20 25 30
Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr Gly Ser
35 40 45
Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Leu Glu Lys Leu Ser
50 55 60
Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala Gly Ala
65 70 75 80
Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys
85 90
(2) INFORMATION FOR SEQ ID NO:1997:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..78
(D) OTHER INFORMATION: / Ceres Seq. ID 1501891
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1997:
Met Ser Leu Ala Gln Gly Val Val Tyr Trp Gln Pro Pro Glu Ser Ala
1 5 10 15
Met Asp Lys Ile Glu Lys Ile Ile Arg Glu Pro Ile Val Ser Lys Tyr
20 25 30
Gly Ser Xaa Asp Gly Leu Pro Glu Leu Arg Glu Ala Leu Leu Glu Lys
35 40 45
Leu Ser Arg Glu Asn Lys Leu Thr Lys Ser Ser Val Met Val Thr Ala
50 55 60
Gly Ala Asn Gln Ala Phe Xaa Asn Leu Val Leu Thr Leu Cys
65 70 75
(2) INFORMATION FOR SEQ ID NO:1998:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 569 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..569
(D) OTHER INFORMATION: / Ceres Seq. ID 1501895
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1998:
aggatcggag aacatccgcc gcgactccat gtcacaggag atcaagtctg cctaccagat 60
tcttgcccac aagtaccatc ctgatatgaa taagagtccc gaagcagaag aaaagttcaa 120
ggagatcagt gctgcatatg agccaagctt ggatctgacc gctgtacttt gtgtcgccgc 180
ttgaatctac ggttctcttc ttccttggtc atcccgtaga tctgtcccggt ggtgggtccaa 240
gcattcgatt tctgctatta taacatccaa cgttggcggt gaagagcaag gggacagata 300

agcccaaaagg cagcaagggg aacgtcgaca aggaccccaa caagcctgac tcccaacatt 360
ttttgtccgc cgggtgctgta gcggaagccc aaaggcagca aggggaacgt cgacaaggac 420
cccaacaagg ctgactccca acattttttg tccgccggtg ctgtarcggc ggcgctggtg 480
arctccccc tgctgggctc tgggatgctc ccaggcgccg ggggttcggcg agacggggac 540
tgawctggtg ctgggctctg ggatgctcc

(2) INFORMATION FOR SEQ ID NO:1999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1501896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1999:

Gly Ser Glu Asn Ile Arg Arg Asp Ser Met Leu Gln Glu Ile Lys Ser
1 5 10 15
Ala Tyr Gln Ile Leu Ala His Lys Tyr His Pro Asp Met Asn Lys Ser
20 25 30
Pro Glu Ala Glu Glu Lys Phe Lys Glu Ile Ser Ala Ala Tyr Glu Pro
35 40 45
Ser Leu Asp Leu Thr Ala Val Leu Cys Val Ala Ala
50 55 60

(2) INFORMATION FOR SEQ ID NO:2000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1501897

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2000:

Met Leu Gln Glu Ile Lys Ser Ala Tyr Gln Ile Leu Ala His Lys Tyr
1 5 10 15
His Pro Asp Met Asn Lys Ser Pro Glu Ala Glu Glu Lys Phe Lys Glu
20 25 30
Ile Ser Ala Ala Tyr Glu Pro Ser Leu Asp Leu Thr Ala Val Leu Cys
35 40 45
Val Ala Ala
50

(2) INFORMATION FOR SEQ ID NO:2001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..32

(D) OTHER INFORMATION: / Ceres Seq. ID 1501898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2001:

Met Asn Lys Ser Pro Glu Ala Glu Lys Phe Lys Glu Ile Ser Ala
1 5 10 15
Ala Tyr Glu Pro Ser Leu Asp Leu Thr Ala Val Leu Cys Val Ala Ala
20 25 30

(2) INFORMATION FOR SEQ ID NO:2002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..432
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501899

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2002:

ccatccagtc	ctggagcctg	cgcggctgcs	cttgcacgcg	atctccgctg	tcgtcctcgc	60
ccacggaatc	cgtccaattc	cccacgcgcg	ccgtcgtcct	tttctataaa	attcactccg	120
ccaccaaatc	tcgaatcccc	atcgcgctgc	ttttccaccg	accccgcgcg	cgacgcgcgc	180
gccaccgcgc	ctccctcccc	agtccccaact	ccccttcccc	ggccgcggac	agagatccgc	240
ggcgcgcgcg	gatggcgaac	atcgacatgg	cgaagatcct	ggcggacctg	gaccgcggcg	300
ccagcggcgc	ncgacgcgcg	ggtgcccaag	accaagctcg	tatgcacgct	cggcccggcc	360
tcccgccacc	tgcccatgct	cgagaagctg	ctccgcgcgm	gcatgaacgt	cgcgcgcttc	420
aacttctccc	ac					

(2) INFORMATION FOR SEQ ID NO:2003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501900

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2003:

Pro	Ser	Ser	Pro	Gly	Ala	Cys	Ala	Ala	Xaa	Leu	Ala	Ser	His	Leu	Arg	
1				5					10					15		
Arg	Arg	Pro	Arg	Pro	Arg	Asn	Pro	Ser	Asn	Ser	Pro	Arg	Arg	Pro	Ser	
		20					25					30				
Ser	Phe	Ser	Ile	Lys	Phe	Thr	Pro	Pro	Pro	Asn	Leu	Glu	Ser	Pro	Ser	
		35				40					45					
Arg	Cys	Phe	Ser	Thr	Asp	Pro	Asp	Ala	Asp	Ala	Asp	Ala	Thr	Ala	Ala	
	50				55				60							
Pro	Ser	Pro	Val	Pro	Thr	Pro	Leu	Pro	Gly	Pro	Arg	Thr	Glu	Ile	Arg	
65				70					75					80		
Gly	Ala	Ala	Arg	Trp	Arg	Thr	Ser	Thr	Trp	Arg	Arg	Ser	Trp	Arg	Thr	
			85					90						95		
Trp	Thr	Ala	Ala	Pro	Ala	Ala	Xaa	Asp	Ala	Arg	Val	Pro	Lys	Thr	Lys	
		100				105						110				
Leu	Val	Cys	Thr	Leu	Gly	Pro	Ala	Ser	Arg	Thr	Val	Pro	Met	Leu	Glu	
	115				120						125					
Lys	Leu	Leu	Arg	Xaa	Gly	Met	Asn	Val	Ala	Arg	Phe	Asn	Phe	Ser	His	
	130				135						140					

(2) INFORMATION FOR SEQ ID NO:2004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1501901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2004:

Ile Gln Ser Trp Ser Leu Arg Gly Cys Xaa Cys Ile Ala Ser Pro Ser
1 5 10 15
Ser Ser Ser Pro Thr Glu Ser Val Gln Phe Pro Thr Pro Pro Val Val
20 25 30
Leu Phe Tyr Lys Ile His Ser Ala Thr Lys Ser Arg Ile Pro Ile Ala
35 40 45
Leu Leu Phe His Arg Pro Arg Arg Arg Arg Arg His Arg Arg Ser
50 55 60
Leu Pro Ser Pro His Ser Pro Ser Arg Ala Ala Asp Arg Asp Pro Gly
65 70 75 80
Arg Arg Ala Met Ala Asn Ile Asp Met Ala Lys Ile Leu Ala Asp Leu
85 90 95
Asp Arg Gly Ala Ser Gly Xaa Arg Arg Ala Gly Ala Gln Asp Gln Ala
100 105 110
Arg Met His Ala Arg Pro Gly Leu Pro His Arg Ala His Ala Arg Glu
115 120 125
Ala Ala Pro Arg Xaa His Glu Arg Arg Ala Leu Gln Leu Leu Pro
130 135 140

(2) INFORMATION FOR SEQ ID NO:2005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 429 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..429

(D) OTHER INFORMATION: / Ceres Seq. ID 1501902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2005:

aagctcctgc ttttccactg ctctgcgtct gcgtctgcgt ctgcgtctgc actgcttcgc 60
gtctccctcc ccccgccctcc gccccgggaa aaaaaaaagc aaaacacggc catggaaggc 120
tacgaccgcg agttctacca gttcagcgac cagctgcgcc tgcagacggc cgccttctcg 180
ggcctctccc tcggcgactc catctgggcc ccgcccggcc ggcgcaacaa cagcaacgac 240
gtcctcttcg ccgcctcggc gtcgcccgcc gacgccgccg ccaagaccaa cgccgtcgtc 300
ggcctcaagc tcaacgacgg agggcccggc ctcatcggtt ccgggaagct ggccttcggc 360
ggcgggcgga ccaaggccga ccgctacaac aacaacaacc tctccaacac cgacaacaag 420
accgtgtac

(2) INFORMATION FOR SEQ ID NO:2006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1501903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2006:

Lys Leu Leu Leu Phe His Cys Ser Ala Ser Ala Ser Ala Ser
1 5 10 15
Ala Leu Leu Arg Val Ser Leu Pro Pro Pro Pro Arg Glu Lys Lys
20 25 30
Lys Gln Asn Thr Ala Met Glu Gly Tyr Asp Arg Glu Phe Tyr Gln Phe
35 40 45

Ser Asp Gln Leu Arg Leu Gln Thr Ala Ala Phe Ser Gly Leu Ser Leu
50 55 60
Gly Asp Ser Ile Trp Ser Pro Ala Gly Arg Arg Asn Asn Ser Asn Asp
65 70 75 80
Val Leu Phe Ala Ala Ser Ala Ser Pro Ala Asp Ala Ala Ala Lys Thr
85 90 95
Asn Ala Val Val Gly Leu Lys Leu Asn Asp Gly Gly Pro Gly Leu Ile
100 105 110
Gly Ser Gly Lys Leu Ala Phe Gly Gly Gly Gly Thr Lys Ala Asp Arg
115 120 125
Tyr Asn Asn Asn Asn Leu Ser Asn Thr Asp Asn Lys Thr Val Tyr
130 135 140

(2) INFORMATION FOR SEQ ID NO:2007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1501904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2007:

Ser Ser Cys Phe Ser Thr Ala Leu Arg Leu Arg Leu Arg Leu Arg Leu
1 5 10 15
His Cys Phe Ala Ser Pro Ser Pro Arg Leu Arg Pro Gly Lys Lys Lys
20 25 30
Ser Lys Thr Arg Pro Trp Lys Ala Thr Thr Ala Ser Ser Thr Ser Ser
35 40 45
Ala Thr Ser Cys Ala Cys Arg Arg Pro Pro Ser Arg Ala Ser Pro Ser
50 55 60
Ala Thr Pro Ser Gly Pro Pro Pro Ala Gly Ala Thr Thr Ala Thr Thr
65 70 75 80
Ser Ser Ser Pro Pro Arg Arg Arg Pro Pro Thr Pro Pro Pro Arg Pro
85 90 95
Thr Pro Ser Ser Ala Ser Ser Ser Thr Thr Glu Gly Pro Ala Ser Ser
100 105 110
Ala Pro Gly Ser Trp Pro Ser Ala Ala Ala Pro Arg Pro Thr Ala
115 120 125
Thr Thr Thr Thr Thr Ser Pro Thr Pro Thr Thr Arg Pro Cys
130 135 140

(2) INFORMATION FOR SEQ ID NO:2008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1501905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2008:

Ala Pro Ala Phe Pro Leu Leu Cys Val Cys Val Cys Val Cys Val Cys
1 5 10 15
Thr Ala Ser Arg Leu Pro Pro Pro Ala Ser Ala Pro Gly Lys Lys Lys
20 25 30
Ala Lys His Gly His Gly Arg Leu Arg Pro Arg Val Leu Pro Val Gln
35 40 45
Arg Pro Ala Ala Pro Ala Asp Gly Arg Leu Leu Gly Pro Leu Pro Arg

50 55 60
Arg Leu His Leu Val Pro Arg Arg Pro Ala Gln Gln Gln Arg Arg
65 70 75 80
Pro Leu Arg Arg Leu Gly Val Ala Arg Arg Arg Arg Arg Gln Asp Gln
85 90 95
Arg Arg Arg Arg Pro Gln Ala Gln Arg Arg Arg Ala Arg Pro His Arg
100 105 110
Leu Arg Glu Ala Gly Leu Arg Arg Arg Arg His Gln Gly Arg Pro Leu
115 120 125
Gln Gln Gln Gln Pro Leu Gln His Arg Gln Gln Asp Arg Val
130 135 140

(2) INFORMATION FOR SEQ ID NO:2009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2009:

aaatatctct	gcacactatg	acctgagtaa	tgatttcttt	gctctttttc	tggatccgac	60
gatgacttac	tcttgttgta	ttttcaakgm	rraagatgag	agtttagaag	cagcgcasta	120
cgtaaacttg	acaatctaata	taataaggct	aaggtggatc	cggggcatca	tgctcttgac	180
attggctgtg	ggtggggctc	attggcaata	cgtttggtga	agagaactgg	ctgcaagtgc	240
acaggaatta	cattatcgga	ggagcaactg	aaatatggaa	agagaaaggt	gaaagaattt	300
ggattagagg	accgcataac	tctcctgctt	tgtgattacc	gtcaaatacc	gaacggccag	360
aagtttgata	ggattathag	ttgtgggatg	cttgaacacg	ttggccatga	gttctacgaa	420
gatttctttg	cctcctgcga	gtatcatttg	gccgaacacg	gcctacttgt	cctccagtc	480
atcgcggtcc	cagaggaact	gtacgacaaa	atgag			

(2) INFORMATION FOR SEQ ID NO:2010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2010:

Asn Ile Ser Ala His Tyr Asp Leu Ser Asn Asp Phe Phe Ala Leu Phe
1 5 10 15
Leu Asp Pro Thr Met Thr Tyr Ser Cys Gly Ile Phe Xaa Xaa Xaa Asp
20 25 30
Glu Ser Leu Glu Ala Ala Xaa Tyr Val Asn Leu Thr Ile
35 40 45

(2) INFORMATION FOR SEQ ID NO:2011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..42
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2011:
Met Leu Glu His Val Gly His Glu Phe Tyr Glu Asp Phe Phe Ala Ser
1 5 10 15
Cys Glu Tyr His Leu Ala Glu His Gly Leu Leu Val Leu Gln Ser Ile
20 25 30
Ala Val Pro Glu Glu Leu Tyr Asp Lys Met
35 40

(2) INFORMATION FOR SEQ ID NO:2012:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..35
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2012:

Met Ser Ser Thr Lys Ile Ser Leu Pro Pro Ala Ser Ile Ile Trp Pro
1 5 10 15
Asn Thr Ala Tyr Leu Ser Ser Ser Pro Ser Arg Ser Gln Arg Asn Cys
20 25 30
Thr Thr Lys
35

(2) INFORMATION FOR SEQ ID NO:2013:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..549
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2013:

acaacaagca gaagcagaag cagaagctag cagctagtag acgagcgcacg agtagctagc	60
tagctagcta tctagagagc tcatcatatc gctgctcgct ctcattccacc attatagaga	120
agagcagatc gagctgcagc tggcagaggc cgagttgttg ctagctagct cctgcttgct	180
aaatttgcac cgtatccgat ccattccatg aagaagtcgt cgatgatggc gcccatgacg	240
atcatggcga gagttgccgc tgtgctcgtc ctctgctcgg ctgccatggc ttccgccgca	300
ggagcagctg ggctggacat gaattttctac ggcagcacgt gcccgcgcgt ggaggccatc	360
gtcaaggagg agatggtggc gatcctcaag gcggcgccga cgctggcccg cccgctgctc	420
cgctccatt tccacgactg cttcgtcagg ggctgcgacg cctccgtgct cctggactcg	480
actcccacca gcacggcgga gaaggacgcc accccgaacc tcaccctccg gggcttcggc	540
tccgtgcag	

(2) INFORMATION FOR SEQ ID NO:2014:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2014:

Met Lys Lys Ser Ser Met Met Ala Pro Met Thr Ile Met Ala Arg Val
1 5 10 15

Ala Ala Val Leu Val Leu Ser Ser Ala Ala Met Ala Ser Ala Ala Gly
20 25 30
Ala Ala Gly Leu Asp Met Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val
35 40 45
Glu Ala Ile Val Lys Glu Glu Met Val Ala Ile Leu Lys Ala Ala Pro
50 55 60
Thr Leu Ala Gly Pro Leu Leu Arg Leu His Phe His Asp Cys Phe Val
65 70 75 80
Arg Gly Cys Asp Ala Ser Val Leu Leu Asp Ser Thr Pro Thr Ser Thr
85 90 95
Ala Glu Lys Asp Ala Thr Pro Asn Leu Thr Leu Arg Gly Phe Gly Ser
100 105 110
Val Gln

(2) INFORMATION FOR SEQ ID NO:2015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..109
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2015:

Met Met Ala Pro Met Thr Ile Met Ala Arg Val Ala Ala Val Leu Val
1 5 10 15
Leu Ser Ser Ala Ala Met Ala Ser Ala Ala Gly Ala Ala Gly Leu Asp
20 25 30
Met Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val Glu Ala Ile Val Lys
35 40 45
Glu Glu Met Val Ala Ile Leu Lys Ala Ala Pro Thr Leu Ala Gly Pro
50 55 60
Leu Leu Arg Leu His Phe His Asp Cys Phe Val Arg Gly Cys Asp Ala
65 70 75 80
Ser Val Leu Leu Asp Ser Thr Pro Thr Ser Thr Ala Glu Lys Asp Ala
85 90 95
Thr Pro Asn Leu Thr Leu Arg Gly Phe Gly Ser Val Gln
100 105

(2) INFORMATION FOR SEQ ID NO:2016:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2016:

Met Ala Pro Met Thr Ile Met Ala Arg Val Ala Ala Val Leu Val Leu
1 5 10 15
Ser Ser Ala Ala Met Ala Ser Ala Ala Gly Ala Ala Gly Leu Asp Met
20 25 30
Asn Phe Tyr Gly Ser Thr Cys Pro Arg Val Glu Ala Ile Val Lys Glu
35 40 45
Glu Met Val Ala Ile Leu Lys Ala Ala Pro Thr Leu Ala Gly Pro Leu
50 55 60
Leu Arg Leu His Phe His Asp Cys Phe Val Arg Gly Cys Asp Ala Ser

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..117
 (D) OTHER INFORMATION: / Ceres Seq. ID 1501928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2019:

Met Ile Ala Arg Val Thr Asp Gly Leu Pro Leu Ser Glu Gly Leu Asp
1 5 10 15
Asp Ser Arg Asp Leu Lys Asp Ala Asp Phe Tyr Lys Gln Gln Ala Lys
 20 25 30
Leu Leu Phe Lys Asn Leu Ser Arg Gly Gln His Glu Ala Ser Arg Met
 35 40 45
Ser Ile Glu Thr Gly Pro Tyr Leu Phe His Tyr Ile Ile Glu Gly Arg
50 55 60
Val Cys Tyr Leu Thr Leu Cys Asp Arg Ser Tyr Pro Lys Lys Leu Ala
65 70 75 80
Phe Gln Tyr Leu Glu Asp Leu Lys Asn Glu Phe Glu Lys Val Asn Gly
 85 90 95
Ser Gln Ile Glu Thr Ala Ala Arg Pro Tyr Xaa Phe Ile Lys Phe Asp
 100 105 110
Ala Phe Ile Gln Lys
 115

(2) INFORMATION FOR SEQ ID NO:2020:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..70
(D) OTHER INFORMATION: / Ceres Seq. ID 1501929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2020:

Met Ser Ile Glu Thr Gly Pro Tyr Leu Phe His Tyr Ile Ile Glu Gly
1 5 10 15
Arg Val Cys Tyr Leu Thr Leu Cys Asp Arg Ser Tyr Pro Lys Lys Leu
 20 25 30
Ala Phe Gln Tyr Leu Glu Asp Leu Lys Asn Glu Phe Glu Lys Val Asn
35 40 45
Gly Ser Gln Ile Glu Thr Ala Ala Arg Pro Tyr Xaa Phe Ile Lys Phe
50 55 60
Asp Ala Phe Ile Gln Lys
65 70

(2) INFORMATION FOR SEQ ID NO:2021:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..493
(D) OTHER INFORMATION: / Ceres Seq. ID 1501930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2021:

aagtctctttt	gtgtttttta	taggcttgag	agcttggaat	agcgggggggt	ggaggaagcg	60
gaagaggagc	ttcgttttgt	gttctagagg	ggagtcatgt	tccatggcgg	caggcctctg	120
tccctccggg	ggtctctcaa	ggcgcttgaa	gctgatatcc	accatgccaa	caccctggcg	180
catgctatac	acagggcgta	trgggggtgc	tgcgcagatg	naggctgtcc	tacagctcca	240
tggctccaat	ctttctcaac	cttatccaat	ggatggactg	cagctgctcc	ctgtcataca	300

cgctccctag ctaccttggc ctgctcgagg ttctcgtcta caaggtttat gtcgatgaag 360
atgcctccat atccaccata gaaaggaggg cgagcctgaa ggaattctac actatcatat 420
accctttctt gcaacaactg gaggacaact tgatggacaa ggactgcaag gacaaagggt 480
ggctcgtgc tgc

(2) INFORMATION FOR SEQ ID NO:2022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1501931

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2022:

Ser Leu Phe Val Phe Ile Gly Leu Arg Ala Trp Asn Ser Gly Gly
1 5 10 15
Trp Arg Lys Arg Lys Arg Ser Phe Val Leu Cys Ser Arg Gly Glu Ser
20 25 30
Cys Ser Met Ala Ala Gly Leu Cys Pro Ser Gly Gly Leu Ser Arg Arg
35 40 45
Leu Lys Leu Ile Ser Thr Met Pro Thr Pro Trp Arg Met Leu Tyr Thr
50 55 60
Gly Arg Xaa Gly Val Pro Ala Gln Met Xaa Ala Val Leu Gln Leu His
65 70 75 80
Gly Ser Asn Leu Ser Gln Pro Tyr Pro Met Asp Gly Leu Gln Leu Leu
85 90 95
Pro Val Ile His Ala Pro
100

(2) INFORMATION FOR SEQ ID NO:2023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1501932

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2023:

Met Phe His Gly Gly Arg Pro Leu Ser Leu Arg Gly Ser Leu Lys Ala
1 5 10 15
Leu Glu Ala Asp Ile His His Ala Asn Thr Leu Ala His Ala Ile His
20 25 30
Arg Ala Tyr Xaa Gly Ala Cys Ala Asp Xaa Gly Cys Pro Thr Ala Pro
35 40 45
Trp Leu Gln Ser Phe Ser Thr Leu Ser Asn Gly Trp Thr Ala Ala Ala
50 55 60
Pro Cys His Thr Arg Ser Leu Ala Thr Leu Ala Cys Ser Arg Phe Ser
65 70 75 80
Ser Thr Arg Phe Met Ser Met Lys Met Pro Pro Tyr Pro Pro
85 90

(2) INFORMATION FOR SEQ ID NO:2024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 1501933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2024:

Met	Ala	Pro	Ile	Phe	Leu	Asn	Leu	Ile	Gln	Trp	Met	Asp	Cys	Ser	Cys	
1				5					10					15		
Ser	Leu	Ser	Tyr	Thr	Leu	Pro	Ser	Tyr	Leu	Gly	Leu	Leu	Glu	Val	Leu	
			20					25					30			
Val	Tyr	Lys	Val	Tyr	Val	Asp	Glu	Asp	Ala	Ser	Ile	Ser	Thr	Ile	Glu	
		35					40					45				
Arg	Arg	Ala	Ser	Leu	Lys	Glu	Phe	Tyr	Thr	Ile	Ile	Tyr	Pro	Phe	Leu	
	50					55				60						
Gln	Gln	Leu	Glu	Asp	Asn	Leu	Met	Asp	Lys	Asp	Cys	Lys	Asp	Lys	Gly	
65					70				75					80		
Trp	Ser	Ala	Ala													

(2) INFORMATION FOR SEQ ID NO:2025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 586 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..586

(D) OTHER INFORMATION: / Ceres Seq. ID 1501949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2025:

ccgccgtcaa	acgtcatccg	aatccgcgcc	gcgaccagcg	aagaaggtag	gaagcatccg	60
gaacggagac	gcgcctcctg	cctcgctttc	ctcccatggc	gccgcccctc	gccgccgtct	120
catcgctcgtc	gcccctattc	tctccttcat	cgccccgcc	catccgccgc	tgccacgcac	180
ctcctccttc	tatctccttc	cagacgcggg	gacgctcgcc	cacggcgggc	gcggcagctg	240
agtccctctgt	cagtagcgtt	ctcgagggtg	gcggactcac	cgcatccgtg	aaggagactg	300
ggcagcagat	cctgcgcggc	gtcgacctca	ccatccgcga	gggcgagatt	catgcgatta	360
tgggaaaaaa	cggctccggc	aagagcacc	tcacgaaagt	tctcgtaggc	catcctcatt	420
atgaggtaac	tggtggtacc	attctcttca	agggtgagga	cctgggttgac	atggagccag	480
aggacagatc	tctagcaggc	cttttcatga	gtttccaagc	acctattgag	attccctgga	540
gtcagcaatt	ttgattttct	gctcatggct	gtgaatgctc	gcagag		

(2) INFORMATION FOR SEQ ID NO:2026:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1501950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2026:

Pro	Pro	Ser	Asn	Val	Ile	Arg	Ile	Arg	Ala	Ala	Thr	Ser	Glu	Glu	Gly	
1				5					10					15		
Arg	Lys	His	Pro	Glu	Arg	Arg	Arg	Ala	Ser	Cys	Leu	Ala	Phe	Leu	Pro	
			20					25					30			
Trp	Arg	Arg	Pro	Ser	Pro	Pro	Ser	His	Arg	Arg	Arg	Pro	Tyr	Ser	Leu	
		35					40					45				
Leu	His	Arg	Pro	Ala	Pro	Ser	Ala	Ala	Ala	Thr	His	Leu	Leu	Leu	Leu	
	50					55				60						
Ser	Pro	Ser	Arg	Arg	Gly	Asp	Ala	Arg	Pro	Arg	Arg	Arg	Arg	Gln	Leu	
65					70				75					80		

Ser Pro Leu Ser Val Arg Phe Ser Arg Cys Ala Asp Ser Pro His Pro
85 90 95

(2) INFORMATION FOR SEQ ID NO:2027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1501951

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2027:

Arg Arg Gln Thr Ser Ser Glu Ser Ala Pro Arg Pro Ala Lys Lys Val
1 5 10 15
Gly Ser Ile Arg Asn Gly Asp Ala Pro Pro Ala Ser Leu Ser Ser His
20 25 30
Gly Ala Ala Pro Arg Arg Arg Leu Ile Val Val Ala Pro Ile Leu Ser
35 40 45
Phe Ile Val Pro Pro His Pro Pro Leu Pro Arg Thr Ser Ser Phe Tyr
50 55 60
Leu Leu Pro Asp Ala Gly Thr Leu Ala His Gly Gly Gly Gly Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:2028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1501952

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2028:

Met Ala Pro Pro Leu Ala Ala Val Ser Ser Ser Pro Leu Phe Ser
1 5 10 15
Pro Ser Ser Ser Arg Pro Ile Arg Arg Cys His Ala Pro Pro Pro Ser
20 25 30
Ile Ser Phe Gln Thr Arg Gly Arg Ser Pro Thr Ala Ala Ala Ala
35 40 45
Glu Ser Ser Val Ser Thr Leu Leu Glu Val Arg Gly Leu Thr Ala Ser
50 55 60
Val Lys Glu Thr Gly Gln Gln Ile Leu Ala Gly Val Asp Leu Thr Ile
65 70 75 80
Arg Glu Gly Glu Ile His Ala Ile Met Gly Lys Asn Gly Ser Gly Lys
85 90 95
Ser Thr Leu Thr Lys Val Leu Val Gly His Pro His Tyr Glu Val Thr
100 105 110
Gly Gly Thr Ile Leu Phe Lys Gly Glu Asp Leu Val Asp Met Glu Pro
115 120 125
Glu Asp Arg Ser Leu Ala Gly Leu Phe Met Ser Phe Gln Ala Pro Ile
130 135 140
Glu Ile Pro Trp Ser Gln Gln Phe
145 150

(2) INFORMATION FOR SEQ ID NO:2029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..657
(D) OTHER INFORMATION: / Ceres Seq. ID 1501976
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2029:

```
agtgccggca cgcgcgctgt tgcagaagtt gcctcttttt tacgtcttgt ttctcctcca      60
ccccggcgac gcgaatggag aagggcagtg gaggcagcaa tcctccgccg ccaccgctcc      120
acatggagga cttccaactg gaggggaaga agcccgtaa gaaccccttt gtgcccacg      180
gcgcactggg tactgctgga gttctgactg ctggtctgat cagtttccga tatgggaact      240
ctcagctggg tcagaaactg atgagggcac gtgtagttgc tcaaggcgct acagtcgctc      300
tgatgattgg cagtgcctac tactatggcg atcaaatcaa gctgttcaag aaagggtcga      360
gcccagatgc ttcccatgaa tattgctggt tttggtgtat ggaggaatgc cttgtatacg      420
cataaatttc acctggactc tgctgcccct ttttaacatc attttggcct gacacgtggt      480
agctaacaag aaatcgctgt tggccgacg ggcaggattg aaaataaata attttgtttg      540
ttgatttttg tcaggatttg ttgggttgat taattaggct atatgcatca attgttatat      600
ctttgtacaa acacgcgttc tggtgtctgc aatcagcggc tgaagtgacc attttgc
```

(2) INFORMATION FOR SEQ ID NO:2030:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..125
(D) OTHER INFORMATION: / Ceres Seq. ID 1501977
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2030:

```
Val Pro Ala Pro Leu Leu Gln Lys Leu Pro Leu Phe Tyr Val Leu
1      5      10      15
Phe Leu Leu His Pro Gly Asp Ala Asn Gly Glu Gly Gln Trp Arg Gln
20      25      30
Gln Ser Ser Ala Ala Thr Ala Pro His Gly Gly Leu Pro Thr Gly Gly
35      40      45
Glu Glu Ala Arg Gln Glu Pro Leu Cys Ala His Arg Arg Thr Gly Tyr
50      55      60
Cys Trp Ser Ser Asp Cys Trp Ser Asp Gln Phe Pro Ile Trp Glu Leu
65      70      75      80
Ser Ala Gly Ser Glu Thr Asp Glu Gly Thr Cys Ser Cys Ser Arg Arg
85      90      95
Tyr Ser Arg Ser Asp Asp Trp Gln Cys Leu Leu Leu Trp Arg Ser Asn
100     105     110
Gln Ala Val Gln Glu Arg Val Glu Pro Met Ile Phe Pro
115     120     125
```

(2) INFORMATION FOR SEQ ID NO:2031:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..121
(D) OTHER INFORMATION: / Ceres Seq. ID 1501978
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2031:

Cys Arg His Arg Arg Cys Cys Arg Ser Cys Leu Phe Phe Thr Ser Cys

1 5 10 15
Phe Ser Ser Thr Pro Ala Thr Arg Met Glu Lys Gly Ser Gly Ser
20 25 30
Asn Pro Pro Pro Pro Pro Leu His Met Glu Asp Phe Gln Leu Glu Gly
35 40 45
Lys Lys Pro Val Lys Asn Pro Phe Val Pro Ile Gly Ala Leu Val Thr
50 55 60
Ala Gly Val Leu Thr Ala Gly Leu Ile Ser Phe Arg Tyr Gly Asn Ser
65 70 75 80
Gln Leu Gly Gln Lys Leu Met Arg Ala Arg Val Val Ala Gln Gly Ala
85 90 95
Thr Val Ala Leu Met Ile Gly Ser Ala Tyr Tyr Tyr Gly Asp Gln Ile
100 105 110
Lys Leu Phe Lys Lys Gly Ser Ser Pro
115 120

(2) INFORMATION FOR SEQ ID NO:2032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..97
- (D) OTHER INFORMATION: / Ceres Seq. ID 1501979

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2032:

Met Glu Lys Gly Ser Gly Gly Ser Asn Pro Pro Pro Pro Pro Leu His
1 5 10 15
Met Glu Asp Phe Gln Leu Glu Gly Lys Lys Pro Val Lys Asn Pro Phe
20 25 30
Val Pro Ile Gly Ala Leu Val Thr Ala Gly Val Leu Thr Ala Gly Leu
35 40 45
Ile Ser Phe Arg Tyr Gly Asn Ser Gln Leu Gly Gln Lys Leu Met Arg
50 55 60
Ala Arg Val Val Ala Gln Gly Ala Thr Val Ala Leu Met Ile Gly Ser
65 70 75 80
Ala Tyr Tyr Tyr Gly Asp Gln Ile Lys Leu Phe Lys Lys Gly Ser Ser
85 90 95
Pro

(2) INFORMATION FOR SEQ ID NO:2033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2033:

atgcgcctcg cggcgcgttc gacagtcctt cgcgttccat ttgcttcggc tcatctcaga 60
tcaagctagc gcacctgaca cccaccacct cctcccaga tccaccacc cagccatggc 120
caccgccttt gactccccga cctcctcccc cgcgcgcgcg cccttccacg acgacccttt 180
cctccatttc gacggctcgg cccccgcgcg cgcgcacggc ttcccggcct ccccggaacg 240
ctacgcgccc tcccccttcg gcatgcccc a tccaacggc gacctccacg acgacccttt 300
cgccgcacct gctgactcca acggtggggc catccttcgc ccgcccaccg agatggggccg 360
cgaggagggg ttcctgctcc gcgagtgggt ccgacaaaat gctattcacc ttgaggaaaa 420
agagaagaag gagaaggagc tgaggagcca aatcatcggt gatgctgaag agtttaag

(2) INFORMATION FOR SEQ ID NO:2034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1502004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2034:

Cys	Ala	Ser	Arg	Pro	Leu	Arg	Gln	Ser	Leu	Ala	Phe	His	Leu	Leu	Arg
1				5					10					15	
Leu	Ile	Ser	Asp	Gln	Ala	Ser	Ala	Pro	Asp	Thr	His	His	Leu	Pro	Pro
			20					25					30		
Arg	Ser	Thr	Thr	Pro	Ala	Met	Ala	Thr	Ala	Phe	Asp	Ser	Pro	Thr	Ser
		35					40					45			
Ser	Pro	Ala	Ala	Ala	Pro	Phe	His	Asp	Asp	Pro	Phe	Leu	His	Phe	Asp
		50				55				60					
Gly	Ser	Ala	Pro	Ala	Ala	Ala	Asp	Gly	Phe	Pro	Ala	Ser	Pro	Asp	Ala
65				70					75					80	
Tyr	Ala	Pro	Ser	Pro	Phe	Gly	Met	Pro	His	Ser	Asn	Gly	Asp	Leu	His
			85						90				95		
Asp	Asp	Pro	Phe	Ala	Ala	Pro	Ala	Asp	Ser	Asn	Gly	Gly	Pro	Ile	Leu
			100					105					110		
Pro	Pro	Pro	Thr	Glu	Met	Gly	Arg	Glu	Glu	Gly	Phe	Leu	Leu	Arg	Glu
		115					120					125			
Trp	Cys	Arg	Gln	Asn	Ala	Ile	His	Leu	Glu	Glu	Lys	Glu	Lys	Lys	Glu
	130					135					140				
Lys	Glu	Leu	Arg	Ser	Gln	Ile	Ile	Val	Asp	Ala	Glu	Glu	Phe	Lys	
145					150				155						

(2) INFORMATION FOR SEQ ID NO:2035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1502005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2035:

Ala	Pro	Arg	Gly	Arg	Phe	Asp	Ser	Pro	Ser	Arg	Ser	Ile	Cys	Phe	Gly
1				5					10					15	
Ser	Ser	Gln	Ile	Lys	Leu	Ala	His	Leu	Thr	Pro	Thr	Thr	Ser	Leu	Pro
		20						25					30		
Asp	Pro	Pro	Pro	Gln	Pro	Trp	Pro	Pro	Pro	Leu	Thr	Pro	Arg	Pro	Pro
		35				40						45			
Pro	Pro	Pro	Pro	Arg	Pro	Ser	Thr	Thr	Thr	Leu	Ser	Ser	Ile	Ser	Thr
		50				55				60					
Ala	Arg	Pro	Pro	Pro	Pro	Thr	Ala	Ser	Arg	Pro	Pro	Arg	Thr	Pro	
65				70					75					80	
Thr	Arg	Pro	Pro	Pro	Ser	Ala	Cys	Pro	Thr	Pro	Thr	Ala	Thr	Ser	Thr
			85						90					95	
Thr	Thr	Leu	Ser	Pro	His	Leu	Leu	Thr	Pro	Thr	Val	Gly	Pro	Ser	Phe
		100						105					110		
Arg	Arg	Pro	Pro	Arg	Trp	Ala	Ala	Arg	Arg	Asp	Ser	Cys	Ser	Ala	Ser
		115				120						125			
Gly	Ala	Asp	Lys	Met	Leu	Phe	Thr	Leu	Arg	Lys	Lys	Arg	Arg	Arg	Arg

130
Arg Ser
145

135

140

(2) INFORMATION FOR SEQ ID NO:2036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502006

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2036:

Met Ala Thr Ala Phe Asp Ser Pro Thr Ser Ser Pro Ala Ala Ala Pro
1 5 10 15
Phe His Asp Asp Pro Phe Leu His Phe Asp Gly Ser Ala Pro Ala Ala
20 25 30
Ala Asp Gly Phe Pro Ala Ser Pro Asp Ala Tyr Ala Pro Ser Pro Phe
35 40 45
Gly Met Pro His Ser Asn Gly Asp Leu His Asp Asp Pro Phe Ala Ala
50 55 60
Pro Ala Asp Ser Asn Gly Gly Pro Ile Leu Pro Pro Pro Thr Glu Met
65 70 75 80
Gly Arg Glu Glu Gly Phe Leu Leu Arg Glu Trp Cys Arg Gln Asn Ala
85 90 95
Ile His Leu Glu Glu Lys Glu Lys Lys Glu Lys Glu Leu Arg Ser Gln
100 105 110
Ile Ile Val Asp Ala Glu Glu Phe Lys
115 120

(2) INFORMATION FOR SEQ ID NO:2037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..713
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2037:

accaaaggta ccttgcaatc acaacgaaca gaagctctcg atctcaccga caccgaggaa 60
gaagagatca atggcgctccg agcagggagt cgtgatcgcg tgccacagca aggctgagtt 120
cgacgcccac atgaccaagg cccaggaagc cggcaagctg gtgggtcatcg acttcactgc 180
cgcttgagca gtactgcagg gacaccgtca tgaccatctg gcattaccac ggcgggtgcc 240
aggtcggcgc cgtcgtggac gacgattacc gggtgttcgg cgtgcagcga ctgatggtga 300
tcgacagctc cacgttcaag tactcccccg gcaccaacc gcaggccacc gtcgatgatgc 360
tcggaaggta tatgggtgtg aaaattcagg ccgagagatg gaggaaatga tcgagatttc 420
aagtatcagc atggtctagg gactaagcct ctagctgtga taatgaacat caatcaacac 480
atctgtaact gggttaactgc tctagcctct agagtaggtt ttatttttct ctagatatatt 540
tttaatctcc tctagacata ctctagctt ccgcatgttg ttggttccat tccaccacac 600
ccctagatgc attgttcagc atttcgcggg aataatgaga attatgctga aaaggcatga 660
tcgctcctcc tgcctattct acagaaaatt aaataaagaa ccgccatttc atc

(2) INFORMATION FOR SEQ ID NO:2038:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1502012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2038:

Pro Lys Val Pro Cys Asn His Asn Glu Gln Lys Leu Ser Ile Ser Pro
1 5 10 15
Thr Pro Arg Lys Lys Arg Ser Met Ala Ser Glu Gln Gly Val Val Ile
20 25 30
Ala Cys His Ser Lys Ala Glu Phe Asp Ala His Met Thr Lys Ala Gln
35 40 45
Glu Ala Gly Lys Leu Val Val Ile Asp Phe Thr Ala Ala
50 55 60

(2) INFORMATION FOR SEQ ID NO:2039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1502013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2039:

Met Thr Ile Trp His Tyr His Gly Gly Cys Gln Val Gly Ala Val Val
1 5 10 15
Asp Asp Asp Tyr Arg Val Phe Gly Val Gln Arg Leu Met Val Ile Asp
20 25 30
Ser Ser Thr Phe Lys Tyr Ser Pro Gly Thr Asn Pro Gln Ala Thr Val
35 40 45
Met Met Leu Gly Arg Tyr Met Gly Val Lys Ile Gln Ala Glu Arg Trp
50 55 60
Arg Lys
65

(2) INFORMATION FOR SEQ ID NO:2040:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..46

(D) OTHER INFORMATION: / Ceres Seq. ID 1502014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2040:

Met Leu Leu Val Pro Phe His His Thr Pro Arg Cys Ile Val Gln His
1 5 10 15
Phe Ala Gly Ile Met Arg Ile Met Leu Lys Arg His Asp Arg Ser Ser
20 25 30
Cys Leu Phe Tyr Arg Lys Leu Asn Lys Glu Pro Pro Phe His
35 40 45

(2) INFORMATION FOR SEQ ID NO:2041:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 567 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..567

(D) OTHER INFORMATION: / Ceres Seq. ID 1502015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2041:

ctcgcaaac	cacgtttcaa	aaaaaagaga	ggaaagcaaa	gttccttctt	ccctcgaaaa	60
aaaaaatcag	tctcgccatg	gagagcagcg	ttggcataga	gaaggccgca	gcggtggcgg	120
ttggtgcagg	tgtgggagg	ggaggtggag	ggtacggcts	cggcgggtgg	gagacgccga	180
agcgcgagga	gtscgcgcatc	ccggcgacgc	tgccgtgccc	cgcggcgccg	aggaaggccg	240
tgccggactt	cggaagcgg	cgcagcccyg	cccaagaacg	gctacttcca	gccgccggac	300
ctggaggcgc	tcttcgcgct	cgcgcgcgcg	cgccaggcct	tctgcgcgtg	acttggcrog	360
gacttgattt	tttggggagg	gagttgtaga	tagcttgccg	gtctcgctct	gttgactctt	420
ttctagtggg	ggtgtttagt	ggccscgggt	gtattagggg	ggcagtaggg	tggttttagg	480
gagtagtagg	taggtagggt	gtggactctt	aatcataag	catactgttt	ggttaagctg	540
atgaaatcct	tatatatgtt	tcctggc				

(2) INFORMATION FOR SEQ ID NO:2042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1502016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2042:

Ser	Gln	Thr	His	Val	Ser	Lys	Lys	Arg	Glu	Ser	Lys	Val	Pro	Ser	
1				5				10					15		
Ser	Leu	Glu	Lys	Lys	Asn	Gln	Ser	Arg	His	Gly	Glu	Gln	Arg	Trp	His
			20					25				30			
Arg	Glu	Gly	Arg	Ser	Gly	Gly	Gly	Trp	Cys	Arg	Cys	Gly	Arg	Gly	Arg
		35					40					45			
Trp	Arg	Val	Arg	Xaa	Arg	Arg	Val	Gly	Asp	Ala	Glu	Ala	Arg	Gly	Xaa
		50				55					60				
Pro	His	Pro	Gly	Asp	Ala	Ala	Val	Pro	Arg	Gly	Ala	Glu	Glu	Gly	Arg
65					70					75				80	
Ala	Gly	Leu	Arg	Glu	Ala	Ala	Gln	Pro	Xaa	Pro	Arg	Thr	Ala	Thr	Ser
			85					90						95	
Ser	Arg	Arg	Thr	Trp	Arg	Arg	Ser	Ser	Arg	Ser	Arg	Arg	Ala	Ala	Arg
			100					105					110		
Pro	Ser	Ala	Arg	Asp	Leu	Xaa	Arg	Thr							
			115					120							

(2) INFORMATION FOR SEQ ID NO:2043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1502017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2043:

Arg	Lys	Pro	Thr	Phe	Gln	Lys	Lys	Glu	Arg	Lys	Ala	Lys	Phe	Leu	Leu
1				5				10					15		
Pro	Ser	Lys	Lys	Lys	Ile	Ser	Leu	Ala	Met	Glu	Ser	Ser	Val	Gly	Ile
			20					25					30		
Glu	Lys	Ala	Ala	Ala	Val	Ala	Val	Gly	Ala	Gly	Val	Gly	Gly	Gly	Gly
			35				40						45		

Gly Gly Tyr Gly Xaa Gly Gly Trp Glu Thr Pro Lys Arg Glu Glu Xaa
50 55 60
Arg Ile Pro Ala Thr Leu Pro Cys Pro Ala Ala Pro Arg Lys Ala Val
65 70 75 80
Pro Asp Phe Gly Lys Arg Arg Ser Xaa Ala Gln Glu Arg Leu Leu Pro
85 90 95
Ala Ala Gly Pro Gly Gly Ala Leu Arg Ala Arg Ala Ala Pro Pro Gly
100 105 110
Leu Leu Arg Val Thr Trp Xaa Gly Leu Asp Phe Leu Gly Arg Glu Leu
115 120 125

(2) INFORMATION FOR SEQ ID NO:2044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2044:

Met Glu Ser Ser Val Gly Ile Glu Lys Ala Ala Val Ala Val Gly
1 5 10 15
Ala Gly Val Gly Gly Gly Gly Gly Gly Tyr Gly Xaa Gly Gly Trp Glu
20 25 30
Thr Pro Lys Arg Glu Glu Xaa Arg Ile Pro Ala Thr Leu Pro Cys Pro
35 40 45
Ala Ala Pro Arg Lys Ala Val Pro Asp Phe Gly Lys Arg Arg Ser Xaa
50 55 60
Ala Gln Glu Arg Leu Leu Pro Ala Ala Gly Pro Gly Gly Ala Leu Arg
65 70 75 80
Ala Arg Ala Ala Pro Pro Gly Leu Leu Arg Val Thr Trp Xaa Gly Leu
85 90 95
Asp Phe Leu Gly Arg Glu Leu
100

(2) INFORMATION FOR SEQ ID NO:2045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..542
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502023

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2045:

ggggtagcga ttacaccttg acacctaagg ccagagattg gagagagaaa gaagcagctg 60
agtggagcaa gaaagaagag gtcattggcg ttagtcttat cagctgagtg ggaagagtg 120
gagcaatggt ggggggctgt gccagcgcg acggcgccgc cgaagggacg ctgcgaggt 180
ggcggagggc ggcggccaaag cggatcgccc tctcatgcgc ctctctcttc tctacgccg 240
cctctccctc ccgcctcctc tccaagatca tctccactc cgcactgaat gcgcctgatg 300
gagagcagca aaagatggag gaaccaccca gcaccagagt ggctgacaag aatctatgtg 360
caatatgttt ggaactcctc agcagcagca tcagcagcga tgttgacagt ggtgaggcgg 420
cagcaatcta cacagcgag tgctccact cattccactt yctatgcac gcctccaaca 480
tccggcatgg caacgtcagc tgccctatct gccgtgcaca atggtctgag ctaccacgtg 540
ac

(2) INFORMATION FOR SEQ ID NO:2046:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..139
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502024
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2046:

Met Val Gly Gly Cys Ala Ser Gly Asp Gly Ala Ala Glu Gly Thr Leu
1 5 10 15
Ala Arg Trp Arg Arg Ala Ala Ala Lys Arg Ile Gly Leu Ser Cys Ala
 20 25 30
Ser Phe Phe Ser Tyr Ala Ala Ser Pro Ser Pro Pro Ser Lys Ile
 35 40 45
Ile Ser His Ser Ala Leu Asn Ala Pro Asp Gly Glu Gln Gln Lys Met
50 55 60
Glu Glu Pro Thr Ser Thr Arg Val Ala Asp Lys Asn Leu Cys Ala Ile
65 70 75 80
Cys Leu Glu Leu Leu Ser Thr Ser Ile Ser Ser Asp Val Asp Ser Gly
 85 90 95
Glu Ala Ala Ala Ile Tyr Thr Ala Gln Cys Ser His Ser Phe His Xaa
 100 105 110
Leu Cys Ile Ala Ser Asn Ile Arg His Gly Asn Val Ser Cys Pro Ile
115 120 125
Cys Arg Ala Gln Trp Ser Glu Leu Pro Arg Asp
130 135

(2) INFORMATION FOR SEQ ID NO:2047:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..84
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502025
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2047:

Met Arg Leu Met Glu Ser Ser Lys Arg Trp Arg Asn Pro Pro Ala Pro
1 5 10 15
Glu Trp Leu Thr Arg Ile Tyr Val Gln Tyr Val Trp Asn Ser Ser Ala
20 25 30
Arg Ala Ser Ala Ala Met Leu Thr Val Val Arg Arg Gln Gln Ser Thr
35 40 45
Gln Arg Ser Ala Pro Thr His Ser Thr Xaa Tyr Ala Ser Pro Pro Thr
50 55 60
Ser Gly Met Ala Thr Ser Ala Ala Leu Ser Ala Val His Asn Gly Leu
65 70 75 80
Ser Tyr His Val

(2) INFORMATION FOR SEQ ID NO:2048:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..81
(D) OTHER INFORMATION: / Ceres Seq. ID 1502026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2048:

Met	Glu	Ser	Ser	Lys	Arg	Trp	Arg	Asn	Pro	Pro	Ala	Pro	Glu	Trp	Leu
1				5				10					15		
Thr	Arg	Ile	Tyr	Val	Gln	Tyr	Val	Trp	Asn	Ser	Ser	Ala	Arg	Ala	Ser
			20				25					30			
Ala	Ala	Met	Leu	Thr	Val	Val	Arg	Arg	Gln	Gln	Ser	Thr	Gln	Arg	Ser
		35				40					45				
Ala	Pro	Thr	His	Ser	Thr	Xaa	Tyr	Ala	Ser	Pro	Pro	Thr	Ser	Gly	Met
	50					55				60					
Ala	Thr	Ser	Ala	Ala	Leu	Ser	Ala	Val	His	Asn	Gly	Leu	Ser	Tyr	His
65				70				75					80		
Val															

(2) INFORMATION FOR SEQ ID NO:2049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..502
(D) OTHER INFORMATION: / Ceres Seq. ID 1502027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2049:

acagcacagc	agagaacgca	ggcagaggca	ccataccagt	caaccaccac	cgcttcggtc	60
tcctcccaca	cgctcgccct	tcgcctcctt	ctgggtccca	tcttctatca	tccccgagct	120
ccagttctcc	acacctcacg	tctataaata	ataaataagg	cgcccgcggt	gccccatcaat	180
tcgtgtcacc	gcgtcccagag	agcgcaaatc	attccgcgcg	acgcaaaaac	cctagcccag	240
ccaccgatcc	ctctcatggc	aaccaccacc	acccaggcga	gcctcctcct	ccagaagcag	300
ctaagagatc	tcgcgaagca	cccgggtggat	gggttctctg	ctgggctggt	cgacgacagc	360
aatgtcttcg	agtggcaggt	caccatcatc	ggaccgcctg	acactctata	tgatggaggt	420
tacttcaatg	caataatgag	cttcccacaa	aattacccaa	acagcccgcc	atcagtcaga	480
tttacctctg	aaatgkggca	tc				

(2) INFORMATION FOR SEQ ID NO:2050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..49
(D) OTHER INFORMATION: / Ceres Seq. ID 1502028

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2050:

Gln	His	Ser	Arg	Glu	Arg	Arg	Gln	Arg	His	His	Thr	Ser	Gln	Pro	Pro
1				5				10					15		
Pro	Leu	Arg	Ser	Pro	Pro	Thr	Pro	Leu	Ala	Phe	Ala	Ser	Phe	Trp	Phe
			20				25					30			
Pro	Ser	Ser	Ile	Ile	Pro	Glu	Leu	Gln	Phe	Ser	Thr	Pro	His	Val	Tyr
		35				40						45			
Lys															

(2) INFORMATION FOR SEQ ID NO:2051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..51
(D) OTHER INFORMATION: / Ceres Seq. ID 1502029
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2051:

Ser Thr Ala Glu Asn Ala Gly Arg Gly Thr Ile Pro Val Asn His His
1 5 10 15
Arg Phe Val Leu Leu Pro His Arg Ser Pro Ser Pro Pro Ser Gly Ser
20 25 30
His Leu Leu Ser Ser Pro Ser Ser Ser Ser Pro His Leu Thr Ser Ile
35 40 45
Asn Asn Lys
50

(2) INFORMATION FOR SEQ ID NO:2052:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1502030
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2052:

Met Ala Thr Thr Thr Thr Gln Ala Ser Leu Leu Leu Gln Lys Gln Leu
1 5 10 15
Arg Asp Leu Ala Lys His Pro Val Asp Gly Phe Ser Ala Gly Leu Val
20 25 30
Asp Asp Ser Asn Val Phe Glu Trp Gln Val Thr Ile Ile Gly Pro Pro
35 40 45
Asp Thr Leu Tyr Asp Gly Gly Tyr Phe Asn Ala Ile Met Ser Phe Pro
50 55 60
Gln Asn Tyr Pro Asn Ser Pro Pro Ser Val Arg Phe Thr Ser Glu Met
65 70 75 80
Xaa His

(2) INFORMATION FOR SEQ ID NO:2053:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 526 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..526
(D) OTHER INFORMATION: / Ceres Seq. ID 1502031
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2053:

aattttctta tccccctca tctgctccac ctccgacctc gcgcgagacg agcaagccca 60
agtatggccg gagcagcagc agccgcgcgtg gcgtccgggg tctcggcccg gccggccgcg 120
ccgatgaggg cttctgcggg acgccgcgct cggctgtcgg ttgtgcgggc cgcgatatcc 180
ctcgagaagg gcgagaaggc gtacacggtg cagaagtccg aggagatctt caacgccgcc 240
aaggagctga tgcctggagg tgtaactcg ccagtcgcgt ccttcaaata tgttggtggg 300
cagccagtag tgttcgactc tgtaaagggt tctcgtatgt gggatgttga tgggaatgag 360
tacattgatt acgttggttc ctggggtcct gcaatcatcg gccatgcaga tgataagggt 420
aatgctgcat tgattgaac tctgaagaa ggaactagct ttggtgctcc atgtttgctg 480
gagaacgtat tggctgagat ggtcatctct gccgtgccaa gtatcg

(2) INFORMATION FOR SEQ ID NO:2054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502032

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2054:

Asn Phe Leu Ile Pro Pro His Leu Leu His Leu Arg Pro Arg Ala Arg
1 5 10 15
Arg Ala Ser Pro Ser Met Ala Gly Ala Ala Ala Ala Val Ala Ser
20 25 30
Gly Val Ser Ala Arg Pro Ala Ala Pro Met Arg Ala Ser Ala Gly Arg
35 40 45
Arg Ala Arg Leu Ser Val Val Arg Ala Ala Ile Ser Leu Glu Lys Gly
50 55 60
Glu Lys Ala Tyr Thr Val Gln Lys Ser Glu Glu Ile Phe Asn Ala Ala
65 70 75 80
Lys Glu Leu Met Pro Gly Gly Val Asn Ser Pro Val Arg Ala Phe Lys
85 90 95
Ser Val Gly Gly Gln Pro Val Val Phe Asp Ser Val Lys Gly Ser Arg
100 105 110
Met Trp Asp Val Asp Gly Asn Glu Tyr Ile Asp Tyr Val Gly Ser Trp
115 120 125
Gly Pro Ala Ile Ile Gly His Ala Asp Asp Lys Val Asn Ala Ala Leu
130 135 140
Ile Glu Thr Leu Lys Lys Gly Thr Ser Phe Gly Ala Pro Cys Leu Leu
145 150 155 160
Glu Asn Val Leu Ala Glu Met Val Ile Ser Ala Val Pro Ser Ile
165 170 175

(2) INFORMATION FOR SEQ ID NO:2055:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2055:

Met Ala Gly Ala Ala Ala Ala Val Ala Ser Gly Val Ser Ala Arg
1 5 10 15
Pro Ala Ala Pro Met Arg Ala Ser Ala Gly Arg Arg Ala Arg Leu Ser
20 25 30
Val Val Arg Ala Ala Ile Ser Leu Glu Lys Gly Glu Lys Ala Tyr Thr
35 40 45
Val Gln Lys Ser Glu Glu Ile Phe Asn Ala Ala Lys Glu Leu Met Pro
50 55 60
Gly Gly Val Asn Ser Pro Val Arg Ala Phe Lys Ser Val Gly Gly Gln
65 70 75 80
Pro Val Val Phe Asp Ser Val Lys Gly Ser Arg Met Trp Asp Val Asp
85 90 95
Gly Asn Glu Tyr Ile Asp Tyr Val Gly Ser Trp Gly Pro Ala Ile Ile
100 105 110
Gly His Ala Asp Asp Lys Val Asn Ala Ala Leu Ile Glu Thr Leu Lys

115 120 125
Lys Gly Thr Ser Phe Gly Ala Pro Cys Leu Leu Glu Asn Val Leu Ala
130 135 140
Glu Met Val Ile Ser Ala Val Pro Ser Ile
145 150

(2) INFORMATION FOR SEQ ID NO:2056:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1502034

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2056:

Met Arg Ala Ser Ala Gly Arg Arg Ala Arg Leu Ser Val Val Arg Ala
1 5 10 15
Ala Ile Ser Leu Glu Lys Gly Glu Lys Ala Tyr Thr Val Gln Lys Ser
20 25 30
Glu Glu Ile Phe Asn Ala Ala Lys Glu Leu Met Pro Gly Gly Val Asn
35 40 45
Ser Pro Val Arg Ala Phe Lys Ser Val Gly Gly Gln Pro Val Val Phe
50 55 60
Asp Ser Val Lys Gly Ser Arg Met Trp Asp Val Asp Gly Asn Glu Tyr
65 70 75 80
Ile Asp Tyr Val Gly Ser Trp Gly Pro Ala Ile Ile Gly His Ala Asp
85 90 95
Asp Lys Val Asn Ala Ala Leu Ile Glu Thr Leu Lys Lys Gly Thr Ser
100 105 110
Phe Gly Ala Pro Cys Leu Leu Glu Asn Val Leu Ala Glu Met Val Ile
115 120 125
Ser Ala Val Pro Ser Ile
130

(2) INFORMATION FOR SEQ ID NO:2057:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..474

(D) OTHER INFORMATION: / Ceres Seq. ID 1502035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2057:

aaggcagggc actgcactgc acgcatgcac tgacctgacg acgcgcgccca cagtccactc 60
cacactcagg catggcgatg ggcgcgcgtt ccatacctact gatgatgggtt tcgctggagg 120
ccctgcttct cgcgcgcgcc gccgcgcggcg ggaccatccg tctgcccagc gatgtcggag 180
gcgtttgctgc agaccttgct acggcgatgg cgagggcgag ggcaagggca aagcatcagc 240
ttcgcgacga ggagaggccg tgggggggaat gctgcgactt ggccgtatgc gtcaagacgt 300
acccgctaac ttgctcgtgc ttcgatcggg ttgagcgctg ctccgacgcc tgtaaggagt 360
gcgtggaaac ggaggactcg cgccacgtct gcgtcgacag gtaccgtggc gacccggggc 420
ccaggtgccca cgacgaggac gggaggagcg gcggacccgc tgacgacgac gctg

(2) INFORMATION FOR SEQ ID NO:2058:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..134
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502036
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2058:

Met Ala Met Gly Ala Ala Ser Ile Leu Leu Met Met Val Ser Leu Glu
1 5 10 15
Ala Leu Leu Leu Ala Ala Ala Ala Gly Gly Thr Ile Arg Leu Pro
 20 25 30
Ser Asp Val Gly Gly Val Ala Ala Asp Leu Val Thr Ala Met Ala Arg
 35 40 45
Ala Arg Ala Arg Ala Lys His Gln Leu Arg Asp Glu Glu Arg Pro Trp
50 55 60
Gly Glu Cys Cys Asp Leu Ala Val Cys Val Lys Thr Tyr Pro Leu Thr
65 70 75 80
Cys Ser Cys Phe Asp Arg Val Glu Arg Cys Ser Asp Ala Cys Lys Glu
 85 90 95
Cys Val Glu Thr Glu Asp Ser Arg His Val Cys Val Asp Arg Tyr Arg
 100 105 110
Gly Asp Pro Gly Pro Arg Cys His Asp Glu Asp Gly Arg Ser Gly Gly
115 120 125
Pro Ala Asp Asp Asp Ala
130

(2) INFORMATION FOR SEQ ID NO:2059:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..132
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502037
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2059:

Met Gly Ala Ala Ser Ile Leu Leu Met Met Val Ser Leu Glu Ala Leu
1 5 10 15
Leu Leu Ala Ala Ala Ala Ala Gly Gly Thr Ile Arg Leu Pro Ser Asp
 20 25 30
Val Gly Gly Val Ala Ala Asp Leu Val Thr Ala Met Ala Arg Ala Arg
35 40 45
Ala Arg Ala Lys His Gln Leu Arg Asp Glu Glu Arg Pro Trp Gly Glu
50 55 60
Cys Cys Asp Leu Ala Val Cys Val Lys Thr Tyr Pro Leu Thr Cys Ser
65 70 75 80
Cys Phe Asp Arg Val Glu Arg Cys Ser Asp Ala Cys Lys Glu Cys Val
 85 90 95
Glu Thr Glu Asp Ser Arg His Val Cys Val Asp Arg Tyr Arg Gly Asp
100 105 110
Pro Gly Pro Arg Cys His Asp Glu Asp Gly Arg Ser Gly Gly Pro Ala
115 120 125
Asp Asp Asp Ala
130

(2) INFORMATION FOR SEQ ID NO:2060:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1502038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2060:

Met	Met	Val	Ser	Leu	Glu	Ala	Leu	Leu	Ala	Ala	Ala	Ala	Gly
1				5				10				15	
Gly	Thr	Ile	Arg	Leu	Pro	Ser	Asp	Val	Gly	Gly	Val	Ala	Ala
			20				25					30	Asp
Val	Thr	Ala	Met	Ala	Arg	Ala	Arg	Ala	Arg	Ala	Lys	His	Gln
		35					40				45		Leu
Asp	Glu	Glu	Arg	Pro	Trp	Gly	Glu	Cys	Cys	Asp	Leu	Ala	Val
	50					55				60			Cys
Lys	Thr	Tyr	Pro	Leu	Thr	Cys	Ser	Cys	Phe	Asp	Arg	Val	Glu
65				70					75				80
Ser	Asp	Ala	Cys	Lys	Glu	Cys	Val	Glu	Thr	Glu	Asp	Ser	Arg
			85					90					95
Cys	Val	Asp	Arg	Tyr	Arg	Gly	Asp	Pro	Gly	Pro	Arg	Cys	His
			100					105					110
Asp	Gly	Arg	Ser	Gly	Gly	Pro	Ala	Asp	Asp	Asp	Ala		
			115				120						

(2) INFORMATION FOR SEQ ID NO:2061:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 895 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..895

(D) OTHER INFORMATION: / Ceres Seq. ID 1502048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2061:

atcgaaaaaa	aaaactcctc	tccccgagtc	ctctcctctc	cggggtattg	aattcgaacc	60
aaaaaatcaa	aacaactcag	cgattcgatt	cgcggcgagt	caagcgggat	gccgccgcgc	120
acggctccgg	cggcgacctc	aacccccgcc	cggaaaggtgc	ccctccggaa	gctgctgcgt	180
gcggcgctcg	tcgcctgcgg	ggtgcagttc	ggctggggcgc	tgcagctgtc	gttgctgacc	240
ccgtacgtgc	aggagctggg	catcccgcac	gcctttgcca	gtctcgtctg	gctgtgcggt	300
ccgctgtccg	gcctcctcgt	ccagccccctc	gtcggccacc	tctccgaccg	catcggcccc	360
gccgcttcgc	cgctcggggc	ccgcaggccc	ttcatcgccg	ccggcgccgc	gtgcatcgcc	420
gcagccgtgc	tcaccgtcgg	cttctccgct	gacctcggcc	gactcttcgg	cgacgacgtc	480
acccccgggt	caacgcgcct	cggcgccatc	tgcgtctacc	ttgtaggatt	ctggctgctc	540
gacgtgggca	acaacggcac	gcaggggccc	tgcagggcgt	tcctcgccga	cctcacagag	600
aatgacccaa	ggaggagagg	cgggacacac	cgataagtct	gctcatttac	cattacaggc	660
atcatcaagt	ctggaaactc	tttgtggggt	ggagaagagc	acgctgggag	ctcttgaatg	720
ctgtgtgctc	tttggtgggt	tgccccgttg	agctattttt	tgcttgtctc	ccaaatcttt	780
tggtgttcaa	ttcaactcga	atgtatgtac	gcacgtatgc	atgtatgtat	ttgtatgtat	840
gtggatcatt	tgtagagagc	ttaagcaatg	aataaaaagt	acaggagtta	cgttc	

(2) INFORMATION FOR SEQ ID NO:2062:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1502049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2062:

Arg Lys Lys Lys Leu Leu Ser Pro Ser Pro Leu Leu Ser Gly Val Leu

1 5 10 15
Asn Ser Asn Gln Lys Ile Lys Thr Thr Gln Arg Phe Asp Ser Arg Arg
20 25 30
Val Lys Arg Asp Ala Ala Ala His Gly Ser Gly Gly Asp Leu Asn Pro
35 40 45
Ala Ala Glu Gly Ala Pro Pro Glu Ala Ala Ala Cys Gly Val Gly Arg
50 55 60
Leu Arg Gly Ala Val Arg Leu Gly Ala Ala Ala Val Val Ala Asp Pro
65 70 75 80
Val Arg Ala Gly Ala Gly His Pro Ala Arg Leu Cys Gln Ser Arg Leu
85 90 95
Ala Val Arg Ser Ala Val Arg Pro Pro Arg Pro Ala Pro Arg Arg Pro
100 105 110
Pro Leu Arg Pro His Arg Pro Arg Arg Phe Ala Ala Arg Ala Pro Gln
115 120 125
Ala Leu His Arg Arg Arg Arg Arg Val His Arg Arg Ser Arg Ala His
130 135 140
Arg Arg Leu Leu Arg
145

(2) INFORMATION FOR SEQ ID NO:2063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..175
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2063:

Met Pro Pro Arg Thr Ala Pro Ala Ala Thr Ser Thr Pro Pro Arg Lys
1 5 10 15
Val Pro Leu Arg Lys Leu Leu Arg Ala Ala Ser Val Ala Cys Gly Val
20 25 30
Gln Phe Gly Trp Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln
35 40 45
Glu Leu Gly Ile Pro His Ala Phe Ala Ser Leu Val Trp Leu Cys Gly
50 55 60
Pro Leu Ser Gly Leu Leu Val Gln Pro Leu Val Gly His Leu Ser Asp
65 70 75 80
Arg Ile Gly Pro Ala Ala Ser Pro Leu Gly Arg Arg Arg Pro Phe Ile
85 90 95
Ala Ala Gly Ala Ala Cys Ile Ala Ala Ala Val Leu Thr Val Gly Phe
100 105 110
Ser Ala Asp Leu Gly Arg Leu Phe Gly Asp Asp Val Thr Pro Gly Ser
115 120 125
Thr Arg Leu Gly Ala Ile Cys Val Tyr Leu Val Gly Phe Trp Leu Leu
130 135 140
Asp Val Gly Asn Asn Gly Thr Gln Gly Pro Cys Arg Ala Phe Leu Ala
145 150 155 160
Asp Leu Thr Glu Asn Asp Pro Arg Arg Arg Gly Gly Thr His Arg
165 170 175

(2) INFORMATION FOR SEQ ID NO:2064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

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(A) NAME/KEY: -

(B) LOCATION: 1..490

(D) OTHER INFORMATION: / Ceres Seq. ID 1502056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2064:

atcttcgtct	ctctccgact	ctccctcgcc	cgcgcacctt	tccgcgcgcg	ctccttcctt	60
tcctcgcgtg	ctctggcgcg	cgcaaggatc	aaaaggcgcc	ggccactaga	ggcgagttag	120
tcgcatgtaa	acgaccacca	gctgctgtga	tctcaaaagg	gagcgagaga	caaaggagag	180
gcgagcaggt	cgtggcgggca	gcaatcgttg	cgaatccgcg	cgggattctg	tcctctgcac	240
cactgcttcc	cgcttttcctg	cccggcgggaa	gtggtataat	tctccaacgc	ggttgactgt	300
attgcctctc	gctctcggtg	ggtggggggca	tggacgaggc	agaggagatg	caggtggaga	360
ggctgcacga	ggaggccgat	gcggggggag	ccgacacgga	caagctcagc	tacgagatat	420
tctccatcct	cgagagcaag	ttcctgtttc	gctataccga	cccgcaccag	ctctggctgc	480
ccaagccagc						

(2) INFORMATION FOR SEQ ID NO:2065:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1502057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2065:

Ile	Phe	Val	Ser	Leu	Arg	Leu	Ser	Leu	Ala	Arg	Ala	Pro	Phe	Arg	Ala
1			5					10						15	
Ala	Ser	Phe	Leu	Ser	Ser	Arg	Ala	Leu	Ala	Arg	Ala	Arg	Ile	Lys	Arg
			20					25						30	
Arg	Arg	Pro	Leu	Glu	Ala	Ser	Glu	Ser	His	Val	Asn	Asp	His	Gln	Leu
			35				40							45	
Leu															

(2) INFORMATION FOR SEQ ID NO:2066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..53

(D) OTHER INFORMATION: / Ceres Seq. ID 1502058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2066:

Met	Asp	Glu	Ala	Glu	Glu	Met	Gln	Val	Glu	Arg	Leu	His	Glu	Glu	Ala
1			5						10					15	
Asp	Ala	Gly	Gly	Ala	Asp	Thr	Asp	Lys	Leu	Ser	Tyr	Glu	Ile	Phe	Ser
			20					25						30	
Ile	Leu	Glu	Ser	Lys	Phe	Leu	Phe	Gly	Tyr	Thr	Asp	Pro	His	Gln	Leu
			35				40							45	
Trp	Leu	Pro	Lys	Pro											

(2) INFORMATION FOR SEQ ID NO:2067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1502059

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2067:

Met	Gln	Val	Glu	Arg	Leu	His	Glu	Glu	Ala	Asp	Ala	Gly	Gly	Ala	Asp
1			5				10							15	
Thr	Asp	Lys	Leu	Ser	Tyr	Glu	Ile	Phe	Ser	Ile	Leu	Glu	Ser	Lys	Phe
			20				25							30	
Leu	Phe	Gly	Tyr	Thr	Asp	Pro	His	Gln	Leu	Trp	Leu	Pro	Lys	Pro	
		35					40							45	

(2) INFORMATION FOR SEQ ID NO:2068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 566 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..566

(D) OTHER INFORMATION: / Ceres Seq. ID 1502066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2068:

aaaaatcaaa	gtagcgctcgt	gctgccccaa	ctcggcaact	cccatcagc	tcaccccgat	60
ctaggggtttg	ggcaccctcc	gcttacgcgc	ctccccacca	agcaaagttg	agggcccgcg	120
gcatctccct	tcgggcgtca	tggcggctac	agggcaggag	ggggatgacg	tcgaccacta	180
cgaggtactc	tgcctcccgt	cgggggagga	agggcgggcg	ctgaccatcg	agcatatcga	240
gaaggcctac	cggacgcagt	cgcggctcgc	ccaccccgat	aagcgccccg	acgaccccaa	300
cgccaccgcc	gacttcagc	tcctctcgag	ttcctacaaa	ctcctccgcg	acgagtcctt	360
tcgccgccag	ttcgacgcgc	gcctccgcgg	ccgccgcgag	gccgcagccc	gcgccgccgc	420
cacgggcgtt	aagcgccgga	aggccgtctc	cgacctcgag	gagcgcgagc	gcgccgycgy	480
cgngggccac	cccgscgatc	ccgaggagct	cgccmagcgc	gaggcccara	gatggccscc	540
gacattgagc	gcgagctcgc	agcggt				

(2) INFORMATION FOR SEQ ID NO:2069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1502067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2069:

Met	Ala	Ala	Thr	Gly	Gln	Glu	Gly	Asp	Asp	Val	Asp	His	Tyr	Glu	Val
1			5				10							15	
Leu	Cys	Leu	Pro	Ser	Gly	Glu	Glu	Gly	Ala	Ala	Leu	Thr	Ile	Glu	His
			20				25							30	
Ile	Glu	Lys	Ala	Tyr	Arg	Thr	Gln	Ser	Arg	Leu	Arg	His	Pro	Asp	Lys
		35					40							45	
Arg	Pro	Asp	Asp	Pro	Asn	Ala	Thr	Ala	Asp	Phe	Gln	Leu	Leu	Ser	Ser
		50				55				60					
Ser	Tyr	Lys	Leu	Leu	Arg	Asp	Glu	Ser	Leu	Arg	Gln	Phe	Asp	Ala	
65					70					75				80	
Arg	Leu	Arg	Gly	Arg	Arg	Glu	Ala	Ala	Ala	Arg	Ala	Ala	Ala	Thr	Gly
			85						90					95	
Val	Lys	Arg	Arg	Lys	Ala	Val	Ser	Asp	Leu	Glu	Glu	Arg	Glu	Arg	Ala
			100					105						110	
Xaa	Xaa	Xaa	Gly	His	Pro	Xaa	Asp	Pro	Glu	Glu	Leu	Ala	Xaa	Arg	Glu
			115				120							125	
Ala	Xaa	Arg	Trp	Xaa	Pro	Thr	Leu	Ser	Ala	Ser	Ser	Gln	Arg		

130 135 140

(2) INFORMATION FOR SEQ ID NO:2070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1502074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2070:

aagaccacca	ctgcgccatt	ggccagctag	agccaaccag	aagagcttgc	agttactgag	60
agtgtttgag	agagagagga	tgatgggtgg	cagcggcagg	gctgctctgc	tgctggccct	120
ggtggccgtg	agcctggccg	tggagatcca	ggccgacgcc	gggtacgggt	acaccccgac	180
gccgacgccg	gccaccccca	ccccgaagcc	ggagaagccc	cccaccaagg	ggcccaagcc	240
ggagaagccg	ccaaaggagc	acaagccgcc	caaggagcac	gggcccgaagc	cggagaagcc	300
gcccgaaggag	cacaagccga	cgccgcccac	gtacaccccg	agccccaaac	ccacgcccgc	360
gacgtacact	cccaccccca	cgccccccaa	gccgacgcca	cccacatata	ctcccgccttc	420
tacgccccac	aaacccaactc	ccactcctcc	gacgtacacc	ccttc		

(2) INFORMATION FOR SEQ ID NO:2071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1502075

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2071:

Arg	Pro	Pro	Leu	Arg	His	Trp	Pro	Ala	Arg	Ala	Asn	Gln	Lys	Ser	Leu	
1			5					10					15			
Gln	Leu	Leu	Arg	Val	Phe	Glu	Arg	Glu	Arg	Met	Met	Gly	Gly	Ser	Gly	
			20					25					30			
Arg	Ala	Ala	Leu	Leu	Leu	Ala	Leu	Val	Ala	Val	Ser	Leu	Ala	Val	Glu	
			35				40					45				
Ile	Gln	Ala	Asp	Ala	Gly	Tyr	Gly	Tyr	Thr	Pro	Thr	Pro	Thr	Pro	Ala	
	50				55						60					
Thr	Pro	Thr	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Thr	Lys	Gly	Pro	Lys	Pro	
65				70						75				80		
Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro	Pro	Lys	Glu	His	Gly	Pro	Lys	
				85						90				95		
Pro	Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	
			100					105					110			
Pro	Ser	Pro	Lys	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro	Thr	Pro	Thr	Pro	
			115					120				125				
Pro	Lys	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro	Ala	Pro	Thr	Pro	His	Lys	
	130					135					140					
Pro	Thr	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro							
145				150												

(2) INFORMATION FOR SEQ ID NO:2072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..128
(D) OTHER INFORMATION: / Ceres Seq. ID 1502076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2072:

Met	Met	Gly	Gly	Ser	Gly	Arg	Ala	Ala	Leu	Leu	Leu	Ala	Leu	Val	Ala
1				5					10					15	
Val	Ser	Leu	Ala	Val	Glu	Ile	Gln	Ala	Asp	Ala	Gly	Tyr	Gly	Tyr	Thr
			20					25					30		
Pro	Thr	Pro	Thr	Pro	Ala	Thr	Pro	Thr	Pro	Lys	Pro	Glu	Lys	Pro	Pro
			35				40					45			
Thr	Lys	Gly	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro	Pro
	50					55					60				
Lys	Glu	His	Gly	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro
65					70					75				80	
Thr	Pro	Pro	Thr	Tyr	Thr	Pro	Ser	Pro	Lys	Pro	Thr	Pro	Pro	Thr	Tyr
				85					90					95	
Thr	Pro	Thr	Pro	Thr	Pro	Pro	Lys	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro
			100					105					110		
Ala	Pro	Thr	Pro	His	Lys	Pro	Thr	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro
			115				120						125		

(2) INFORMATION FOR SEQ ID NO:2073:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..127
(D) OTHER INFORMATION: / Ceres Seq. ID 1502077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2073:

Met	Gly	Gly	Ser	Gly	Arg	Ala	Ala	Leu	Leu	Leu	Ala	Leu	Val	Ala	Val
1				5				10					15		
Ser	Leu	Ala	Val	Glu	Ile	Gln	Ala	Asp	Ala	Gly	Tyr	Gly	Tyr	Thr	Pro
			20					25					30		
Thr	Pro	Thr	Pro	Ala	Thr	Pro	Thr	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Thr
			35				40					45			
Lys	Gly	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro	Pro	Lys
	50					55					60				
Glu	His	Gly	Pro	Lys	Pro	Glu	Lys	Pro	Pro	Lys	Glu	His	Lys	Pro	Thr
65					70					75				80	
Pro	Pro	Thr	Tyr	Thr	Pro	Ser	Pro	Lys	Pro	Thr	Pro	Pro	Thr	Tyr	Thr
				85					90					95	
Pro	Thr	Pro	Thr	Pro	Pro	Lys	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro	Ala
			100				105						110		
Pro	Thr	Pro	His	Lys	Pro	Thr	Pro	Thr	Pro	Pro	Thr	Tyr	Thr	Pro	
			115				120						125		

(2) INFORMATION FOR SEQ ID NO:2074:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..591
(D) OTHER INFORMATION: / Ceres Seq. ID 1502086

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2074:

atccaggcat	ccagcaaata	cagcgggtcc	gtactcatct	gcttcacctc	cgggctccgg	60
ctacggcggc	actcttctct	ggcaaccgga	ccacagaaac	ctctaggcga	cgaatcgagc	120
aggtagagga	gtaatcaggc	atccatggct	gagcatcttg	cgtccatctt	tggcacggag	180
aaggaccgcg	tgaactgccc	cttctacttc	aagatcggcg	catgcscac	ggcgaccggt	240
gctccgcct	gcacaacaag	ccttccatct	ccccgacgct	gctgctctgc	aacatgtacc	300
agcggccgga	catgatcacc	cggggcgtgg	acgcgcaggg	caaccccatc	gacccggagc	360
ggatccagga	ggacttcgag	gacttctacg	aggacatctt	cgtggagctg	agcaagcacg	420
gcgagatcga	gagcctccac	gtctgcgaca	acctcgcgga	ccacatgata	gggaacgtgt	480
acgtggagtt	ccgcgaggag	gagcaggcgg	scgcgcctct	gcargcgctg	carggccgcg	540
tactactcgg	gccgccccat	catcgccgag	ttctgcgag	tgactgactt	c	

(2) INFORMATION FOR SEQ ID NO:2075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1502087

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2075:

Met	Xaa	His	Gly	Asp	Arg	Cys	Ser	Arg	Leu	His	Asn	Lys	Pro	Ser	Ile
1			5						10					15	
Ser	Pro	Thr	Leu	Leu	Cys	Asn	Met	Tyr	Gln	Arg	Pro	Asp	Met	Ile	
			20					25					30		
Thr	Pro	Gly	Val	Asp	Ala	Gln	Gly	Asn	Pro	Ile	Asp	Pro	Glu	Arg	Ile
			35				40					45			
Gln	Glu	Asp	Phe	Glu	Asp	Phe	Tyr	Glu	Asp	Ile	Phe	Val	Glu	Leu	Ser
			50			55					60				
Lys	His	Gly	Glu	Ile	Glu	Ser	Leu	His	Val	Cys	Asp	Asn	Leu	Ala	Asp
65				70					75					80	
His	Met	Ile	Gly	Asn	Val	Tyr	Val	Glu	Phe	Arg	Glu	Glu	Glu	Gln	Ala
				85					90					95	
Xaa	Arg	Ala	Leu	Xaa	Ala	Leu	Xaa	Gly	Arg	Leu	Leu	Leu	Gly	Pro	Pro
			100				105						110		
His	His	Arg	Arg	Val	Leu	Ala	Gly	Asp							
			115				120								

(2) INFORMATION FOR SEQ ID NO:2076:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1502088

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2076:

Met	Tyr	Gln	Arg	Pro	Asp	Met	Ile	Thr	Pro	Gly	Val	Asp	Ala	Gln	Gly
1				5					10					15	
Asn	Pro	Ile	Asp	Pro	Glu	Arg	Ile	Gln	Glu	Asp	Phe	Glu	Asp	Phe	Tyr
			20					25					30		
Glu	Asp	Ile	Phe	Val	Glu	Leu	Ser	Lys	His	Gly	Glu	Ile	Glu	Ser	Leu
			35				40					45			
His	Val	Cys	Asp	Asn	Leu	Ala	Asp	His	Met	Ile	Gly	Asn	Val	Tyr	Val
			50			55				60					
Glu	Phe	Arg	Glu	Glu	Glu	Gln	Ala	Xaa	Arg	Ala	Leu	Xaa	Ala	Leu	Xaa
65				70					75					80	

Gly Arg Leu Leu Leu Gly Pro Pro His His Arg Arg Val Leu Ala Gly
85 90 95
Asp

(2) INFORMATION FOR SEQ ID NO:2077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1502089

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2077:

Met Ile Thr Pro Gly Val Asp Ala Gln Gly Asn Pro Ile Asp Pro Glu
1 5 10 15
Arg Ile Gln Glu Asp Phe Glu Asp Phe Tyr Glu Asp Ile Phe Val Glu
20 25 30
Leu Ser Lys His Gly Glu Ile Glu Ser Leu His Val Cys Asp Asn Leu
35 40 45
Ala Asp His Met Ile Gly Asn Val Tyr Val Glu Phe Arg Glu Glu Glu
50 55 60
Gln Ala Xaa Arg Ala Leu Xaa Ala Leu Xaa Gly Arg Leu Leu Leu Gly
65 70 75 80
Pro Pro His His Arg Arg Val Leu Ala Gly Asp
85 90

(2) INFORMATION FOR SEQ ID NO:2078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..314

(D) OTHER INFORMATION: / Ceres Seq. ID 1502090

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2078:

aaccatttgg acaccgatcc atccatccat ccagccccgt acgtgtctcg ctggcccgctcc 60
gtatatatag agagaggcat cggagattrg ccgccacgtt gccatcgcgcg gcrgcgccccg 120
ccggccaagg ccaaccatgc tggcgagggc tcctccgcgc cggccgtgct ccagcggcgct 180
ttgcatcgcc cgcgcacatc caagarcmgc cgccgtcgcg gccaggcccg nggacgacga 240
ggacgacgac gacggtcgcg gcggcgccgg cagaggccgc tntctaacgg gtcarcggcg 300
gcggccgctcg cagg

(2) INFORMATION FOR SEQ ID NO:2079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1502091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2079:

Asn His Leu Asp Thr Asp Pro Ser Ile His Pro Ala Pro Tyr Val Ser
1 5 10 15
Arg Trp Pro Ser Val Tyr Ile Glu Arg Gly Ile Gly Asp Xaa Pro Pro

20 25 30
Arg Cys His Arg Ala Xaa Arg Pro Pro Ala Lys Ala Asn His Ala Gly
35 40 45
Glu Gly Ser Ser Ala Ala Ala Val Leu Gln Arg Arg Leu His Arg Pro
50 55 60
Arg Thr Ser Lys Xaa Xaa Arg Arg Arg Gly Gln Ala Xaa Gly Arg Arg
65 70 75 80
Gly Arg Arg Arg Arg Ser Arg Arg Arg Arg Gln Arg Pro Xaa Ser Asn
85 90 95
Gly Ser Xaa Ala Ala Val Ala
100

(2) INFORMATION FOR SEQ ID NO:2080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502092

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2080:

Pro Phe Gly His Arg Ser Ile His Pro Ser Ser Pro Val Arg Val Ser
1 5 10 15
Leu Ala Val Arg Ile Tyr Arg Glu Arg His Arg Arg Xaa Ala Ala Thr
20 25 30
Leu Pro Ser Arg Xaa Ala Pro Ala Gly Gln Gly Gln Pro Cys Trp Arg
35 40 45
Gly Leu Leu Arg Arg Gly Arg Ala Pro Ala Ala Phe Ala Ser Pro Ala
50 55 60
His Ile Gln Xaa Xaa Pro Pro Ser Arg Pro Gly Arg Xaa Thr Thr Arg
65 70 75 80
Thr Thr Thr Thr Val Ala Ala Ala Ala Ala Glu Ala Ala Xaa
85 90

(2) INFORMATION FOR SEQ ID NO:2081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..59
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2081:

Met Leu Ala Arg Ala Pro Pro Pro Arg Pro Cys Ser Ser Gly Val Cys
1 5 10 15
Ile Ala Arg Ala His Pro Arg Xaa Ala Ala Val Ala Ala Arg Pro Xaa
20 25 30
Asp Asp Glu Asp Asp Asp Asp Gly Arg Gly Gly Gly Arg Gly Arg
35 40 45
Xaa Leu Thr Gly Xaa Arg Arg Arg Pro Ser Gln
50 55

(2) INFORMATION FOR SEQ ID NO:2082:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1036

(D) OTHER INFORMATION: / Ceres Seq. ID 1502094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2082:

accctatggt	catgccacca	tggaaggggt	tcgtattgga	gcaccgatta	tgcaggttta	60
tcatgagaaa	tcttttatct	tacctgatgt	ttcaaggggtg	cttgcttgcc	tttatgagaa	120
ggatgtcaag	tttgagactc	acacagcctc	atacaggagc	ctactcggat	tgcaggcatc	180
atctcatgct	ccagttccat	tctatgaagg	ccctactttt	ctagaagaat	ccagagaaat	240
ctgccgttat	atagcagaaa	agtatgaaaa	tcaaggatat	cogttcctcc	ttggaaagga	300
tgcccttgag	agggcttcaa	ttgaacaatg	gctccacaac	gaggagcatg	ctttcaaccc	360
tccgagccgg	gccttggttct	ttcatttggtc	ctttcccctg	ggtgaaggag	aagatgatga	420
tattgatggt	catacaagga	agctagaaga	ggttctggaa	gtttatgagc	aaaggctcag	480
tgacagcgaa	ttccttggtg	gaaacaagtt	cactcttgcc	gaccttggtc	acctgccaaa	540
ttcccactat	atcaaaagcat	ctaacaagtt	tctttacctt	tatgattcga	ggaaaaatgt	600
aaggaggtgg	tgggatgcta	tttctgaccg	gagttcttgg	aagaaaagtgc	tgaggtatat	660
gaagagcgtg	gaggagaaga	acaaacaaga	agaactcaag	aagcagcagc	agcagcagga	720
agaggctcct	agaacctcca	ccgacccaac	tcgggtagac	tcgagaaagc	agagcagaac	780
agagcctcgg	acaatattgg	ttcctcctgc	tgataacgag	tcatcagctt	cgatagttcc	840
tcgaacaaa	aagcctcttc	ctggtgatca	cttagtgtct	actcaacaaa	ttgatggtgt	900
tggtatgcca	gccacaaatt	gatggtgatg	gtcgtcttag	tggtgtttgt	cttgtctttt	960
attgtttggt	tctttaacaa	gagttatat	tttaccttct	gaccaaagag	ttgtttaaca	1020
ggatagtc	atgtacg					

(2) INFORMATION FOR SEQ ID NO:2083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 306 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..306

(D) OTHER INFORMATION: / Ceres Seq. ID 1502095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2083:

Pro	Tyr	Val	His	Ala	Thr	Met	Glu	Gly	Leu	Arg	Ile	Gly	Ala	Pro	Ile
1			5					10					15		
Met	Gln	Val	Tyr	His	Glu	Lys	Ser	Phe	Ile	Leu	Pro	Asp	Val	Ser	Arg
		20						25				30			
Val	Leu	Ala	Cys	Leu	Tyr	Glu	Lys	Asp	Val	Lys	Phe	Glu	Thr	His	Thr
	35					40					45				
Ala	Ser	Tyr	Arg	Ser	Leu	Leu	Gly	Leu	Gln	Ala	Ser	Ser	His	Ala	Pro
	50					55				60					
Val	Pro	Phe	Tyr	Glu	Gly	Pro	Thr	Phe	Leu	Glu	Glu	Ser	Arg	Glu	Ile
65				70				75						80	
Cys	Arg	Tyr	Ile	Ala	Glu	Lys	Tyr	Glu	Asn	Gln	Gly	Tyr	Pro	Phe	Leu
			85					90						95	
Leu	Gly	Lys	Asp	Ala	Leu	Glu	Arg	Ala	Ser	Ile	Glu	Gln	Trp	Leu	His
		100						105					110		
Asn	Glu	Glu	His	Ala	Phe	Asn	Pro	Pro	Ser	Arg	Ala	Leu	Phe	Phe	His
	115						120					125			
Leu	Ala	Phe	Pro	Leu	Gly	Glu	Gly	Glu	Asp	Asp	Asp	Ile	Asp	Val	His
	130					135				140					
Thr	Arg	Lys	Leu	Glu	Glu	Val	Leu	Glu	Val	Tyr	Glu	Gln	Arg	Leu	Ser
145				150				155						160	
Asp	Ser	Glu	Phe	Leu	Val	Gly	Asn	Lys	Phe	Thr	Leu	Ala	Asp	Leu	Val
			165					170						175	
His	Leu	Pro	Asn	Ser	His	Tyr	Ile	Lys	Ala	Ser	Asn	Lys	Phe	Leu	Tyr
		180						185					190		
Leu	Tyr	Asp	Ser	Arg	Lys	Asn	Val	Arg	Arg	Trp	Trp	Asp	Ala	Ile	Ser

195	200	205
Asp Arg Ser Ser Trp Lys Lys Val Leu Arg Tyr Met Lys Ser Val Glu		
210	215	220
Glu Lys Asn Lys Gln Glu Glu Leu Lys Lys Gln Gln Gln Gln Glu		
225	230	235
Glu Ala Pro Arg Thr Ser Thr Asp Pro Thr Arg Val Asp Ser Arg Lys		
	245	250
Gln Ser Arg Thr Glu Pro Arg Thr Ile Leu Val Pro Pro Ala Asp Asn		
	260	265
Glu Ser Ser Ala Ser Ile Val Pro Arg Thr Lys Lys Pro Leu Pro Gly		
	275	280
Asp His Leu Val Ser Thr Gln Gln Ile Asp Gly Val Gly Met Pro Ala		
290	295	300
Thr Asn		
305		

(2) INFORMATION FOR SEQ ID NO:2084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..300
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2084:

Met	Glu	Gly	Leu	Arg	Ile	Gly	Ala	Pro	Ile	Met	Gln	Val	Tyr	His	Glu
1			5				10				15				
Lys	Ser	Phe	Ile	Leu	Pro	Asp	Val	Ser	Arg	Val	Leu	Ala	Cys	Leu	Tyr
		20				25					30				
Glu	Lys	Asp	Val	Lys	Phe	Glu	Thr	His	Thr	Ala	Ser	Tyr	Arg	Ser	Leu
		35				40					45				
Leu	Gly	Leu	Gln	Ala	Ser	Ser	His	Ala	Pro	Val	Pro	Phe	Tyr	Glu	Gly
		50				55					60				
Pro	Thr	Phe	Leu	Glu	Glu	Ser	Arg	Glu	Ile	Cys	Arg	Tyr	Ile	Ala	Glu
65				70				75						80	
Lys	Tyr	Glu	Asn	Gln	Gly	Tyr	Pro	Phe	Leu	Gly	Lys	Asp	Ala	Leu	
			85					90					95		
Glu	Arg	Ala	Ser	Ile	Glu	Gln	Trp	Leu	His	Asn	Glu	Glu	His	Ala	Phe
		100						105					110		
Asn	Pro	Pro	Ser	Arg	Ala	Leu	Phe	His	Leu	Ala	Phe	Pro	Leu	Gly	
		115						120				125			
Glu	Gly	Glu	Asp	Asp	Asp	Ile	Asp	Val	His	Thr	Arg	Lys	Leu	Glu	Glu
		130				135					140				
Val	Leu	Glu	Val	Tyr	Glu	Gln	Arg	Leu	Ser	Asp	Ser	Glu	Phe	Leu	Val
145					150					155				160	
Gly	Asn	Lys	Phe	Thr	Leu	Ala	Asp	Leu	Val	His	Leu	Pro	Asn	Ser	His
			165					170					175		
Tyr	Ile	Lys	Ala	Ser	Asn	Lys	Phe	Leu	Tyr	Leu	Tyr	Asp	Ser	Arg	Lys
		180						185					190		
Asn	Val	Arg	Arg	Trp	Trp	Asp	Ala	Ile	Ser	Asp	Arg	Ser	Ser	Trp	Lys
		195					200					205			
Lys	Val	Leu	Arg	Tyr	Met	Lys	Ser	Val	Glu	Glu	Lys	Asn	Lys	Gln	Glu
		210				215					220				
Glu	Leu	Lys	Lys	Gln	Gln	Gln	Gln	Gln	Glu	Glu	Ala	Pro	Arg	Thr	Ser
225				230						235				240	
Thr	Asp	Pro	Thr	Arg	Val	Asp	Ser	Arg	Lys	Gln	Ser	Arg	Thr	Glu	Pro
			245						250					255	
Arg	Thr	Ile	Leu	Val	Pro	Pro	Ala	Asp	Asn	Glu	Ser	Ser	Ala	Ser	Ile
		260						265					270		

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Val Pro Arg Thr Lys Lys Pro Leu Pro Gly Asp His Leu Val Ser Thr
275 280 285
Gln Gln Ile Asp Gly Val Gly Met Pro Ala Thr Asn
290 295 300

(2) INFORMATION FOR SEQ ID NO:2085:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..290

(D) OTHER INFORMATION: / Ceres Seq. ID 1502097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2085:

Met Gln Val Tyr His Glu Lys Ser Phe Ile Leu Pro Asp Val Ser Arg
1 5 10 15
Val Leu Ala Cys Leu Tyr Glu Lys Asp Val Lys Phe Glu Thr His Thr
20 25 30
Ala Ser Tyr Arg Ser Leu Leu Gly Leu Gln Ala Ser Ser His Ala Pro
35 40 45
Val Pro Phe Tyr Glu Gly Pro Thr Phe Leu Glu Glu Ser Arg Glu Ile
50 55 60
Cys Arg Tyr Ile Ala Glu Lys Tyr Glu Asn Gln Gly Tyr Pro Phe Leu
65 70 75 80
Leu Gly Lys Asp Ala Leu Glu Arg Ala Ser Ile Glu Gln Trp Leu His
85 90 95
Asn Glu Glu His Ala Phe Asn Pro Pro Ser Arg Ala Leu Phe Phe His
100 105 110
Leu Ala Phe Pro Leu Gly Glu Gly Glu Asp Asp Asp Ile Asp Val His
115 120 125
Thr Arg Lys Leu Glu Glu Val Leu Glu Val Tyr Glu Gln Arg Leu Ser
130 135 140
Asp Ser Glu Phe Leu Val Gly Asn Lys Phe Thr Leu Ala Asp Leu Val
145 150 155 160
His Leu Pro Asn Ser His Tyr Ile Lys Ala Ser Asn Lys Phe Leu Tyr
165 170 175
Leu Tyr Asp Ser Arg Lys Asn Val Arg Arg Trp Trp Asp Ala Ile Ser
180 185 190
Asp Arg Ser Ser Trp Lys Lys Val Leu Arg Tyr Met Lys Ser Val Glu
195 200 205
Glu Lys Asn Lys Gln Glu Glu Leu Lys Lys Gln Gln Gln Gln Glu
210 215 220
Glu Ala Pro Arg Thr Ser Thr Asp Pro Thr Arg Val Asp Ser Arg Lys
225 230 235 240
Gln Ser Arg Thr Glu Pro Arg Thr Ile Leu Val Pro Pro Ala Asp Asn
245 250 255
Glu Ser Ser Ala Ser Ile Val Pro Arg Thr Lys Lys Pro Leu Pro Gly
260 265 270
Asp His Leu Val Ser Thr Gln Gln Ile Asp Gly Val Gly Met Pro Ala
275 280 285
Thr Asn
290

(2) INFORMATION FOR SEQ ID NO:2086:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..833

(D) OTHER INFORMATION: / Ceres Seq. ID 1502100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2086:

atcctagaag	gaaacaggaa	caggcagctc	tgaaagactg	aaactcacgg	ccatggccat	60
cctgggcgcc	ctcaggctcg	cgccgtctcc	acccgccctc	gccggcgctg	cgccaccggc	120
tacgtcgccg	tctgcggctg	tacgtctctc	cgtgcacttc	cacctcgcca	atgccggcgc	180
cgccgcgctc	ngtcgccgcc	tcgctcctcg	ccgccgaccc	cgccgtgggt	ttcattggag	240
gaggaccgta	cggggaagcag	gtgacgcggg	ggcaggacct	caccggcaag	gacttcagcg	300
gccagacact	catcaagcag	gacttcaaga	cgtctatact	gaggcaggcg	aacttcaaag	360
gcgcgaacct	gctcggcgcg	agcttcttcg	atgcagacct	cacaagcgct	gatctctctg	420
acgctgatct	tagaggcgct	gatttgtcgc	tggcgaattt	aacgaaggca	aacttatcaa	480
atgccaactt	agaaggggca	cttgccactg	ggaacacttc	tttcaaaggt	gccgacataa	540
ctggggcgaga	ttttaccgat	gtgccgctgc	gagatgatca	acggggagtac	ctctgcaaaa	600
tcgctgacgg	agtaaaattca	accactggaa	acccaacaaa	ggagactctg	ttctgcagct	660
gatcgacgga	aggacctggg	acttgtgact	tattcaacgt	cttgataaac	ttgcatctgc	720
tgctgtaagc	acgtgaggaa	tgtaaaattga	gttatagagg	gttcctagaa	ataataactg	780
gtaattacgt	gtaaataaac	caacaataaa	agtgtgtgct	gccctttgaa	tgt	

(2) INFORMATION FOR SEQ ID NO:2087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1502101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2087:

Met	Ala	Ile	Leu	Gly	Ala	Leu	Arg	Leu	Ala	Pro	Ser	Pro	Pro	Ala	Leu
1			5					10						15	
Ala	Gly	Ala	Ala	Pro	Pro	Ala	Thr	Ser	Pro	Ser	Ala	Ala	Val	Arg	Ser
			20					25					30		
Ser	Val	His	Phe	His	Leu	Ala	Asn	Ala	Gly	Ala	Ala	Ala	Leu	Xaa	Arg
		35					40					45			
Arg	Leu	Ala	Pro	Arg	Arg	Arg	Pro	Arg	Arg	Gly	Phe	His	Trp	Arg	Arg
		50				55					60				
Thr	Val	Arg	Glu	Ala	Gly	Asp	Ala	Gly	Ala	Gly	Pro	His	Arg	Gln	Gly
65					70					75				80	
Leu	Gln	Arg	Pro	Asp	Thr	His	Gln	Ala	Gly	Leu	Gln	Asp	Val	Tyr	Thr
				85					90					95	
Glu	Ala	Gly	Glu	Leu	Gln	Arg	Arg	Glu	Pro	Ala	Arg	Arg	Glu	Leu	Leu
			100					105					110		
Arg	Cys	Arg	Pro	His	Lys	Arg									
															115

(2) INFORMATION FOR SEQ ID NO:2088:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1502102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2088:

Met	Pro	Ala	Pro	Pro	Arg	Xaa	Val	Ala	Ala	Ser	Leu	Ala	Ala	Asp
1				5						10				15

Pro Ala Val Ala Phe Ile Gly Gly Gly Pro Tyr Gly Lys Gln Val Thr
20 25 30
Arg Gly Gln Asp Leu Thr Gly Lys Asp Phe Ser Gly Gln Thr Leu Ile
35 40 45
Lys Gln Asp Phe Lys Thr Ser Ile Leu Arg Gln Ala Asn Phe Lys Gly
50 55 60
Ala Asn Leu Leu Gly Ala Ser Phe Phe Asp Ala Asp Leu Thr Ser Ala
65 70 75 80
Asp Leu Ser Asp Ala Asp Leu Arg Gly Ala Asp Leu Ser Leu Ala Asn
85 90 95
Leu Thr Lys Ala Asn Leu Ser Asn Ala Asn Leu Glu Gly Ala Leu Ala
100 105 110
Thr Gly Asn Thr Ser Phe Lys Gly Ala Asp Ile Thr Gly Ala Asp Phe
115 120 125
Thr Asp Val Pro Leu Arg Asp Asp Gln Arg Glu Tyr Leu Cys Lys Ile
130 135 140
Ala Asp Gly Val Asn Ser Thr Thr Gly Asn Pro Thr Lys Glu Thr Leu
145 150 155 160
Phe Cys Ser

(2) INFORMATION FOR SEQ ID NO:2089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..468
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2089:

atctctatct catcgtcatac attagaaagg ccgaagcctt ctccgttcct cctcgacgcg	60
tctctttccac agccgcaacc tctatccctc gtctgggtatc gtctctccca caccctctg	120
ccccaaccca gaaaaacctt cgaaaagcgg cggcggcgcg acatggcgga ggtcgaggct	180
ccagctgctg cggttgcggc ggcgaccctt gaggtggcga cggtgaccga gggcggagcc	240
gctacggagg cgaagggtcc gcataagctg caccgccagt ggaccttctg gtacgacatc	300
cagtccaagc ccaagcccg cgtgcgctgg ggcacctccc tcaaaaaggc gtacaccttc	360
gacaccgtcg aggagttttg gggcttgat gatcatgttt tccgtccaag caagttgcct	420
ggaactgctg attttcacct attcaaggct ggagtagagc caaaatgg	

(2) INFORMATION FOR SEQ ID NO:2090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..156
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2090:

Ile Ser Ile Ser Ser Ser Ser Leu Glu Arg Pro Lys Pro Ser Pro Phe
1 5 10 15
Leu Leu Asp Ala Ser Leu Pro Gln Pro Gln Pro Leu Ser Leu Val Trp
20 25 30
Tyr Arg Leu Ser His Thr Pro Leu Pro Gln Pro Arg Lys Thr Leu Glu
35 40 45
Lys Arg Arg Arg Arg Asp Met Ala Glu Val Glu Ala Pro Ala Ala Ala
50 55 60
Val Ala Ala Ala Thr Pro Glu Val Ala Thr Val Thr Glu Gly Gly Ala

65 70 75 80
Ala Thr Glu Ala Lys Gly Pro His Lys Leu His Arg Gln Trp Thr Phe
85 90 95
Trp Tyr Asp Ile Gln Ser Lys Pro Lys Pro Gly Ala Ala Trp Gly Thr
100 105 110
Ser Leu Lys Lys Ala Tyr Thr Phe Asp Thr Val Glu Glu Phe Trp Gly
115 120 125
Leu Tyr Asp His Val Phe Arg Pro Ser Lys Leu Pro Gly Thr Ala Asp
130 135 140
Phe His Leu Phe Lys Ala Gly Val Glu Pro Lys Trp
145 150 155

(2) INFORMATION FOR SEQ ID NO:2091:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1502132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2091:

Met Ala Glu Val Glu Ala Pro Ala Ala Ala Val Ala Ala Ala Thr Pro
1 5 10 15
Glu Val Ala Thr Val Thr Glu Gly Gly Ala Ala Thr Glu Ala Lys Gly
20 25 30
Pro His Lys Leu His Arg Gln Trp Thr Phe Trp Tyr Asp Ile Gln Ser
35 40 45
Lys Pro Lys Pro Gly Ala Ala Trp Gly Thr Ser Leu Lys Lys Ala Tyr
50 55 60
Thr Phe Asp Thr Val Glu Phe Trp Gly Leu Tyr Asp His Val Phe
65 70 75 80
Arg Pro Ser Lys Leu Pro Gly Thr Ala Asp Phe His Leu Phe Lys Ala
85 90 95
Gly Val Glu Pro Lys Trp
100

(2) INFORMATION FOR SEQ ID NO:2092:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..513

(D) OTHER INFORMATION: / Ceres Seq. ID 1502133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2092:

aaacccaaat catttcatcc ccggaaccgg acgccgaacg gcagtgtctgc aaaagtccgg	60
acaaagctcg cgccgcccac cgcacccgat ccgcctcgcc caggcgtgct gccgtccgct	120
cccttctccc gcgccgtcgc ctccgcctac gcccgggccg acccgctgga ccagcgtgc	180
gccgtccac tcggacgcgc cgccgccctc tcgggttgag gcggaggtgc ttggggaccc	240
gccccatgg cgagcgccgg caacagcggc agcggggacg acgatgcagg agggaagctc	300
ctggcggtac gctaccagaa gggcgaggtc ctccgcgagg gcacgtatgg agtcgtcttc	360
aaggccatcg acaccaagac tggaaataca gtcgcggtaa agcgaatccg gataggaaa	420
gacaagaagg aaggtgtcaa cttcactgcg ttgagggaaa ttaactact taaggagctg	480
aaagatccta atattataga gctgattgat tgt	

(2) INFORMATION FOR SEQ ID NO:2093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..132
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502134
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2093:

Asn Gln Asn His Phe Ile Pro Gly Thr Gly Arg Arg Thr Ala Val Leu
1 5 10 15
Gln Lys Ser Gly Gln Ser Ser Arg Arg Pro Pro His Pro Ile Arg Leu
20 25 30
Ala Gln Ala Cys Cys Arg Pro Leu Pro Ser Pro Ala Pro Ser Pro Pro
35 40 45
Pro Thr Pro Gly Pro Thr Arg Trp Thr Gln Arg Ala Pro Leu His Ser
50 55 60
Asp Ala Pro Pro Pro Ser Arg Val Glu Ala Glu Val Leu Gly Asp Pro
65 70 75 80
Pro Pro Trp Arg Ala Pro Ala Thr Ala Ala Ala Gly Thr Thr Met Gln
85 90 95
Glu Gly Ser Ser Trp Arg Ile Ala Thr Arg Arg Ala Arg Ser Ser Ala
100 105 110
Arg Ala Arg Met Glu Ser Ser Ser Arg Pro Ser Thr Pro Arg Leu Glu
115 120 125
Ile Gln Ser Arg
130

(2) INFORMATION FOR SEQ ID NO:2094:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..153
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502135
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2094:

Thr Lys Ile Ile Ser Ser Pro Glu Pro Asp Ala Glu Arg Gln Cys Cys
1 5 10 15
Lys Ser Pro Asp Lys Ala Arg Ala Ala His Arg Thr Arg Ser Ala Ser
20 25 30
Pro Arg Arg Ala Ala Val Arg Ser Leu Leu Pro Arg Arg Arg Leu Arg
35 40 45
Leu Arg Pro Gly Arg Pro Ala Gly Pro Ser Val Arg Arg Ser Thr Arg
50 55 60
Thr Arg Arg Arg Pro Leu Gly Leu Arg Arg Arg Cys Leu Gly Thr Arg
65 70 75 80
Pro His Gly Glu Arg Arg Gln Gln Arg Gln Arg Gly Arg Arg Cys Arg
85 90 95
Arg Glu Ala Pro Gly Gly Ser Leu Pro Glu Gly Arg Gly Pro Arg Arg
100 105 110
Gly His Val Trp Ser Arg Leu Gln Gly His Arg His Gln Asp Trp Lys
115 120 125
Tyr Ser Arg Gly Lys Ala Asn Pro Asp Arg Lys Gly Gln Glu Gly Arg
130 135 140
Cys Gln Leu His Cys Val Glu Gly Asn
145 150

(2) INFORMATION FOR SEQ ID NO:2095:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..89
(D) OTHER INFORMATION: / Ceres Seq. ID 1502136
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2095:
Met Ala Ser Ala Gly Asn Ser Gly Ser Gly Asp Asp Asp Ala Gly Gly
1 5 10 15
Lys Leu Leu Ala Asp Arg Tyr Gln Lys Gly Glu Val Leu Gly Glu Gly
20 25 30
Thr Tyr Gly Val Val Phe Lys Ala Ile Asp Thr Lys Thr Gly Asn Thr
35 40 45
Val Ala Val Lys Arg Ile Arg Ile Gly Lys Asp Lys Lys Glu Gly Val
50 55 60
Asn Phe Thr Ala Leu Arg Glu Ile Lys Leu Leu Lys Glu Leu Lys Asp
65 70 75 80
Pro Asn Ile Ile Glu Leu Ile Asp Cys
85

(2) INFORMATION FOR SEQ ID NO:2096:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..522
(D) OTHER INFORMATION: / Ceres Seq. ID 1502153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2096:

aatccctccc gatcagatcc ctgcacaatg gcactccagg cagcctacga gtacctgcag 60
caggccgtcg gccatggcgc gtggctgctc acgcagacgc tgacgctgct gctcatcgcc 120
gtaccacccg tactactgct gctagcgctc ctgcgcaaga gcacgtcgct gtcgggtagg 180
ggcaagccgc cgtccctcc ctgcgcgcg ggcacctcc ccatcgctgg gcacctacac 240
cacatcgggc cccagaccca catctcgctc caggagctgg tggccaagta cgggcacaac 300
gggttcctgt tcttcgcgc cggcgccgtg cccaccctga tcgtgctgct gccacgcgcc 360
gccgaggccg tgatgcgcac ccacgaccac atcttcgct cccggccgtg gtccatggcc 420
tcccacatcc tccgctacaa cacctgcgac gtggccttct cgccgctcgg cgaatactgg 480
cagcagacca ggaagctgat gaacacgcac ctgctcagca ac

(2) INFORMATION FOR SEQ ID NO:2097:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..174
(D) OTHER INFORMATION: / Ceres Seq. ID 1502154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2097:

Asn Pro Ser Arg Ser Asp Pro Ser Thr Met Ala Leu Gln Ala Ala Tyr
1 5 10 15
Glu Tyr Leu Gln Gln Ala Val Gly His Gly Ala Trp Ser Ser Thr Gln
20 25 30
Thr Leu Thr Leu Leu Leu Ile Ala Val Pro Thr Val Leu Leu Leu Leu
35 40 45

Ala Ser Leu Ala Lys Ser Thr Ser Ser Ser Gly Arg Gly Lys Pro Pro
50 55 60
Leu Pro Pro Ser Pro Pro Gly Thr Leu Pro Ile Val Gly His Leu His
65 70 75 80
His Ile Gly Pro Gln Thr His Ile Ser Leu Gln Glu Leu Val Ala Lys
85 90 95
Tyr Gly His Asn Gly Phe Leu Phe Leu Arg Ala Gly Ala Val Pro Thr
100 105 110
Leu Ile Val Ser Ser Pro Ser Ala Ala Glu Ala Val Met Arg Thr His
115 120 125
Asp His Ile Phe Ala Ser Arg Pro Trp Ser Met Ala Ser His Ile Leu
130 135 140
Arg Tyr Asn Thr Cys Asp Val Ala Phe Ser Pro Leu Gly Glu Tyr Trp
145 150 155 160
Gln Gln Thr Arg Lys Leu Met Asn Thr His Leu Leu Ser Asn
165 170

(2) INFORMATION FOR SEQ ID NO:2098:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1502155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2098:

Met Ala Leu Gln Ala Ala Tyr Glu Tyr Leu Gln Gln Ala Val Gly His
1 5 10 15
Gly Ala Trp Ser Ser Thr Gln Thr Leu Thr Leu Leu Ile Ala Val
20 25 30
Pro Thr Val Leu Leu Leu Ala Ser Leu Ala Lys Ser Thr Ser Ser
35 40 45
Ser Gly Arg Gly Lys Pro Pro Leu Pro Pro Ser Pro Pro Gly Thr Leu
50 55 60
Pro Ile Val Gly His Leu His His Ile Gly Pro Gln Thr His Ile Ser
65 70 75 80
Leu Gln Glu Leu Val Ala Lys Tyr Gly His Asn Gly Phe Leu Phe Leu
85 90 95
Arg Ala Gly Ala Val Pro Thr Leu Ile Val Ser Ser Pro Ser Ala Ala
100 105 110
Glu Ala Val Met Arg Thr His Asp His Ile Phe Ala Ser Arg Pro Trp
115 120 125
Ser Met Ala Ser His Ile Leu Arg Tyr Asn Thr Cys Asp Val Ala Phe
130 135 140
Ser Pro Leu Gly Glu Tyr Trp Gln Gln Thr Arg Lys Leu Met Asn Thr
145 150 155 160
His Leu Leu Ser Asn
165

(2) INFORMATION FOR SEQ ID NO:2099:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 626 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..626

(D) OTHER INFORMATION: / Ceres Seq. ID 1502165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2099:

aaagccgaaa	aggagaaagt	accccggttc	gtcggccgca	gtgccgcacc	tgcacccacc	60
gcacgccgag	tcacgcccc	cctggaccag	ccaacgtgac	actccaccgc	cgccggcgcc	120
gcggcagccc	gtagcaaccg	ccaccgcctg	cccatctcct	ctctatcccg	cgccgcatgg	180
ccgcgtactt	caaccactcc	tcgtcctacc	cgccgcccgc	tcccccgccg	ggcacttccc	240
cgtacggcgc	gtaccgccac	gcctaccgcg	cgcgcccgcc	acccccggcc	gcttacggcg	300
cctactacga	ccgcgcagag	caggccctcc	cggcgcggga	cgaggtccgc	accctcttca	360
tcgctggcct	ccccgccgac	gccaagccgc	gcgaagtcta	caacctcttc	cgcgatttcc	420
ccggatacgt	ctcctccac	ctccgcacgg	gcaaatacctc	tcaggcggtat	gcgtttgctg	480
tgtttgcaga	tcaacagtct	gcactagctg	ccttgagtg	cacaaatgga	atggtatttg	540
atcttgagaa	aaattgttct	cttcatgtag	atctcgcaaa	atccaattcc	agatcaaaagc	600
gcttgagatc	agatgatact	tcacct				

(2) INFORMATION FOR SEQ ID NO:2100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..179

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2100:

Lys	Pro	Lys	Arg	Arg	Lys	Tyr	Pro	Val	Pro	Ser	Ala	Ala	Val	Pro	His
1			5					10						15	
Leu	His	Pro	Pro	His	Ala	Glu	Ser	Arg	Pro	Pro	Trp	Thr	Ser	Gln	Arg
			20					25						30	
Asp	Thr	Pro	Pro	Pro	Pro	Ala	Pro	Arg	Gln	Pro	Val	Ala	Thr	Ala	Thr
			35					40						45	
Ala	Cys	Pro	Ser	Pro	Leu	Tyr	Pro	Ala	Pro	His	Gly	Arg	Val	Leu	Gln
			50					55						60	
Pro	Leu	Leu	Val	Leu	Pro	Ala	Ala	Ala	Ser	Pro	Ala	Gly	His	Phe	Pro
65								70						75	
Val	Arg	Arg	Val	Pro	Pro	Arg	Leu	Pro	Ala	Gly	Ala	Gly	Thr	Pro	Gly
								85						90	
Arg	Leu	Arg	Arg	Leu	Leu	Arg	Pro	Arg	Ala	Gly	Pro	Pro	Gly	Ala	
								100						105	
Gly	Arg	Gly	Pro	His	Pro	Leu	His	Arg	Trp	Pro	Pro	Arg	Arg	Arg	Gln
								115						120	
Ala	Ala	Arg	Ser	Leu	Gln	Pro	Leu	Pro	Arg	Phe	Pro	Arg	Ile	Arg	Leu
								130						135	
Leu	Pro	Pro	Pro	His	Gly	Gln	Ile	Leu	Ser	Gly	Val	Cys	Val	Cys	Cys
145								150						155	
Val	Cys	Arg	Ser	Thr	Val	Cys	Thr	Ser	Cys	Leu	Glu	Cys	His	Lys	Trp
								165						170	
Asn	Gly	Ile												175	

(2) INFORMATION FOR SEQ ID NO:2101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..150

- (D) OTHER INFORMATION: / Ceres Seq. ID 1502167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2101:

Met Ala Ala Tyr Phe Asn His Ser Ser Ser Tyr Pro Pro Pro Pro Pro

1 5 10 15
Pro Pro Gly Thr Ser Pro Tyr Gly Ala Tyr Arg His Ala Tyr Pro Pro
20 25 30
Ala Pro Ala Pro Pro Ala Ala Tyr Gly Ala Tyr Tyr Asp Arg Ala Glu
35 40 45
Gln Ala Leu Pro Ala Arg Asp Glu Val Arg Thr Leu Phe Ile Ala Gly
50 55 60
Leu Pro Ala Asp Ala Lys Pro Arg Glu Val Tyr Asn Leu Phe Arg Asp
65 70 75 80
Phe Pro Gly Tyr Val Ser Ser His Leu Arg Thr Gly Lys Ser Ser Gln
85 90 95
Ala Tyr Ala Phe Ala Val Phe Ala Asp Gln Gln Ser Ala Leu Ala Ala
100 105 110
Leu Ser Ala Thr Asn Gly Met Val Phe Asp Leu Glu Lys Asn Cys Ser
115 120 125
Leu His Val Asp Leu Ala Lys Ser Asn Ser Arg Ser Lys Arg Leu Arg
130 135 140
Ser Asp Asp Thr Ser Pro
145 150

(2) INFORMATION FOR SEQ ID NO:2102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502168

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2102:

acgggaaagg	agtacggagt	accggagaca	tcgtcaacgc	catggccgga	ggaggtgcaa	60
cggtgtgcgt	gaccggagcc	ggcgggttca	tcgcctcgtg	ggtagtgaag	ctcctgctct	120
cccgcggtta	caccgtgcac	ggcaccgtcc	gccacctcag	tgacgagaag	acaggccacc	180
tgaagcgctt	ggagaatgct	gccggaaacc	ttaggatctt	caaggctgac	ctgctggact	240
acgacgccat	ggcagctgcg	gtcgtcgggt	gccagggggt	tttccatgtg	gccactcctg	300
tgccttcgga	ggacctgact	gacccagagc	tacaaatgct	gggtcctgct	gttaccggca	360
ccacgaatgt	gctcaaagct	gcctccagcg	cgaacgtcca	gcgagtgggt	gtggtgtcgt	420
ccatggttgc	cgtcgagatc	agccccaag	attggcctga	aggt		

(2) INFORMATION FOR SEQ ID NO:2103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2103:

Gly Lys Gly Val Arg Ser Thr Gly Asp Ile Val Asn Ala Met Ala Gly
1 5 10 15
Gly Gly Ala Thr Val Cys Val Thr Gly Ala Gly Gly Phe Ile Ala Ser
20 25 30
Trp Val Val Lys Leu Leu Leu Ser Arg Gly Tyr Thr Val His Gly Thr
35 40 45
Val Arg His Leu Ser Asp Glu Lys Thr Gly His Leu Lys Arg Leu Glu
50 55 60
Asn Ala Ala Gly Asn Leu Arg Ile Phe Lys Ala Asp Leu Leu Asp Tyr
65 70 75 80

Asp Ala Met Ala Ala Ala Val Val Gly Cys Gln Gly Val Phe His Val
85 90 95
Ala Thr Pro Val Pro Ser Glu Asp Leu Thr Asp Pro Glu Leu Gln Met
100 105 110
Leu Gly Pro Ala Val Thr Gly Thr Thr Asn Val Leu Lys Ala Ala Ser
115 120 125
Ser Ala Asn Val Gln Arg Val Val Val Val Ser Ser Met Val Ala Val
130 135 140
Glu Ile Ser Pro Lys Asp Trp Pro Glu Gly
145 150

(2) INFORMATION FOR SEQ ID NO:2104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1502170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2104:

Met Ala Gly Gly Gly Ala Thr Val Cys Val Thr Gly Ala Gly Gly Phe
1 5 10 15
Ile Ala Ser Trp Val Val Lys Leu Leu Leu Ser Arg Gly Tyr Thr Val
20 25 30
His Gly Thr Val Arg His Leu Ser Asp Glu Lys Thr Gly His Leu Lys
35 40 45
Arg Leu Glu Asn Ala Ala Gly Asn Leu Arg Ile Phe Lys Ala Asp Leu
50 55 60
Leu Asp Tyr Asp Ala Met Ala Ala Ala Val Val Gly Cys Gln Gly Val
65 70 75 80
Phe His Val Ala Thr Pro Val Pro Ser Glu Asp Leu Thr Asp Pro Glu
85 90 95
Leu Gln Met Leu Gly Pro Ala Val Thr Gly Thr Thr Asn Val Leu Lys
100 105 110
Ala Ala Ser Ser Ala Asn Val Gln Arg Val Val Val Val Ser Ser Met
115 120 125
Val Ala Val Glu Ile Ser Pro Lys Asp Trp Pro Glu Gly
130 135 140

(2) INFORMATION FOR SEQ ID NO:2105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..843

(D) OTHER INFORMATION: / Ceres Seq. ID 1502189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2105:

tcttcaccca cattataaag atcctccact tcgcactttc gccgccgcct ctctccttcc	60
cgagcaggag gcggacaagg taagcagcaa tcgcaggaac cctagcgccg ccgcaccgcg	120
aggaatgggt atcgacctcg tcgccggtgg gaggrkaag aagaccaagc gcaactgcgc	180
caagtctgac gatgtctacc tcaagctcct cgtcaagctc taccgtttcn ttggtcagga	240
ggaccaagag caatttcaac gctgtcatte tcaagaggct tttcatgagt aaaaccaacc	300
gaccaccaat ctccatgcgc cgccttgatca agtttatgga aggaaaggag aagaacattg	360
ctgtcattgt tggcacagtc acagatgaca aaaggatcca ggaggttcca gcaatgaagg	420
ttactgccct gaggttcacg gagacagcaa gggccaggat tgtcaatgct ggtggcgagt	480
gcctcacatt tgaccagctt gctcttcgtg ctccacttgg cgagaacacg gtcctcttga	540

ggggcccaaa gaatgcccggt gaggcagtga ggcacttttg caaggctcct ggagtgccgc 600
acagccacac caagccgtat gtgcgctcca agggaaggaa gttcgagaag gctcgtggca 660
ggaggaacag ccgtggattc aaggttttaa acaaattgtg gccctccgtg ttscatcag 720
catmstgcaa ccgttggtgt tgatcagtcg acagtaatta gtcatcactc tgtaccgaga 780
ttmstgacac aatttggtgt cctggtytga attytsgaag atatttgatg tcgtctccyt 840
att

(2) INFORMATION FOR SEQ ID NO:2106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1502190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2106:

Met Ser Thr Ser Ser Ser Ser Ser Ser Ser Thr Val Xaa Leu Val Arg
1 5 10 15
Arg Thr Lys Ser Asn Phe Asn Ala Val Ile Leu Lys Arg Leu Phe Met
20 25 30
Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys Phe
35 40 45
Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val Thr
50 55 60
Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Val Thr Ala Leu
65 70 75 80
Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile Val Asn Ala Gly Gly Glu
85 90 95
Cys Leu Thr Phe Asp Gln Leu Ala Leu Arg Ala Pro Leu Gly Glu Asn
100 105 110
Thr Val Leu Leu Arg Gly Pro Lys Asn Ala Arg Glu Ala Val Arg His
115 120 125
Phe Gly Lys Ala Pro Gly Val Pro His Ser His Thr Lys Pro Tyr Val
130 135 140
Arg Ser Lys Gly Arg Lys Phe Glu Lys Ala Arg Gly Arg Arg Asn Ser
145 150 155 160
Arg Gly Phe Lys Val
165

(2) INFORMATION FOR SEQ ID NO:2107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134

(D) OTHER INFORMATION: / Ceres Seq. ID 1502191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2107:

Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys
1 5 10 15
Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val
20 25 30
Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Val Thr Ala
35 40 45
Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg Ile Val Asn Ala Gly Gly
50 55 60
Glu Cys Leu Thr Phe Asp Gln Leu Ala Leu Arg Ala Pro Leu Gly Glu

65 70 75 80
Asn Thr Val Leu Leu Arg Gly Pro Lys Asn Ala Arg Glu Ala Val Arg
85 90 95
His Phe Gly Lys Ala Pro Gly Val Pro His Ser His Thr Lys Pro Tyr
100 105 110
Val Arg Ser Lys Gly Arg Lys Phe Glu Lys Ala Arg Gly Arg Arg Asn
115 120 125
Ser Arg Gly Phe Lys Val
130

(2) INFORMATION FOR SEQ ID NO:2108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..124

(D) OTHER INFORMATION: / Ceres Seq. ID 1502192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2108:

Met Arg Arg Leu Val Lys Phe Met Glu Gly Lys Glu Lys Asn Ile Ala
1 5 10 15
Val Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Gln Glu Val Pro
20 25 30
Ala Met Lys Val Thr Ala Leu Arg Phe Thr Glu Thr Ala Arg Ala Arg
35 40 45
Ile Val Asn Ala Gly Gly Glu Cys Leu Thr Phe Asp Gln Leu Ala Leu
50 55 60
Arg Ala Pro Leu Gly Glu Asn Thr Val Leu Leu Arg Gly Pro Lys Asn
65 70 75 80
Ala Arg Glu Ala Val Arg His Phe Gly Lys Ala Pro Gly Val Pro His
85 90 95
Ser His Thr Lys Pro Tyr Val Arg Ser Lys Gly Arg Lys Phe Glu Lys
100 105 110
Ala Arg Gly Arg Arg Asn Ser Arg Gly Phe Lys Val
115 120

(2) INFORMATION FOR SEQ ID NO:2109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..819

(D) OTHER INFORMATION: / Ceres Seq. ID 1502193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2109:

aaatccccac	gaaaacccta	aaccctcgct	acccggcggc	ggctacaagc	tcttcgctcg	60
ttcagcacca	tgargccacc	ggctagagga	ggacgtggtg	ggaggggtgg	cagggttcgat	120
ggcggcgcc	tctgtcgccg	cggccgttgc	atcgccccct	gcctcaccgt	tctcttcctt	180
ctcgcgctcg	cgggcttccct	cctctggccc	gcggaccg	acatctccct	ggcccgccctc	240
cacctagcgc	acgtctccgt	cgtggcacgc	cctgccgtcg	ccgtcactat	atccgccacg	300
ctcaagggttc	gcgttcgcaa	tcctgacctc	ttcgcgctcg	actacaccgc	cctcgacgtc	360
gctatcggct	accgcggtgc	ggggcttggc	cgggtaacat	ccggcgggcg	acgggtccgg	420
gcgcgcgctg	tctcgtacgt	cgacgccaac	ctgcagctcg	acggcatacg	cgtcgctcag	480
gacgcgatgt	acctgctcga	ggacctcgcg	caaggatccg	tgcccttcga	caccatcgcc	540
gaggtcgagg	gccacctcca	cttccttttc	ctcagcatcc	cgggtcaagg	gagaatatct	600
tgcgtaatgc	atattaatcc	acacaaccaa	accatagtac	atcaggactg	ctatcctgag	660
tgaattgctt	atggcggtga	aatgtggaag	ggtgtaagct	atgttgctt	gcgaatggat	720

cgttttgattt gtttctaacc ttgtcttcca gtcgtggttg taaaagtaag aaccaactaa 780
ggggtgtttg aatgtaatta agctaatagt tagttcgct

(2) INFORMATION FOR SEQ ID NO:2110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..197
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2110:

Met	Xaa	Pro	Pro	Ala	Arg	Gly	Gly	Arg	Gly	Gly	Arg	Gly	Gly	Arg	Phe
1				5				10						15	
Asp	Gly	Gly	Gly	Leu	Cys	Arg	Gly	Gly	Arg	Cys	Ile	Val	Pro	Cys	Leu
			20					25					30		
Thr	Val	Leu	Phe	Leu	Leu	Ala	Leu	Ala	Gly	Phe	Leu	Leu	Trp	Pro	Ala
		35				40						45			
Asp	Pro	Asp	Ile	Ser	Leu	Ala	Arg	Leu	His	Leu	Ala	His	Val	Ser	Val
	50					55				60					
Val	Ala	Arg	Pro	Ala	Val	Ala	Val	Thr	Ile	Ser	Ala	Thr	Leu	Lys	Val
65					70				75					80	
Arg	Val	Arg	Asn	Pro	Asp	Leu	Phe	Ala	Leu	Asp	Tyr	Thr	Arg	Leu	Asp
			85					90					95		
Val	Ala	Ile	Gly	Tyr	Arg	Gly	Ala	Gly	Leu	Gly	Arg	Val	Thr	Ser	Gly
			100					105					110		
Gly	Gly	Arg	Val	Arg	Ala	Arg	Ala	Val	Ser	Tyr	Val	Asp	Ala	Asn	Leu
			115				120					125			
Gln	Leu	Asp	Gly	Ile	Arg	Val	Val	Glu	Asp	Ala	Met	Tyr	Leu	Leu	Glu
	130					135				140					
Asp	Leu	Ala	Gln	Gly	Ser	Val	Pro	Phe	Asp	Thr	Ile	Ala	Glu	Val	Glu
145					150				155					160	
Gly	His	Leu	His	Phe	Leu	Phe	Leu	Ser	Ile	Pro	Val	Lys	Gly	Arg	Ile
				165				170					175		
Ser	Cys	Val	Met	His	Ile	Asn	Pro	His	Asn	Gln	Thr	Ile	Val	His	Gln
			180				185						190		
Asp	Cys	Tyr	Pro	Glu											
			195												

(2) INFORMATION FOR SEQ ID NO:2111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..508
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2111:

ataaatcaac	cgccggtgaa	gtctagtcgt	ctcgtcgtc	ggtccaccac	ctcagctccg	60
ccgcttgccc	gcttttgctc	tctccctccc	ggctctcggc	ttctttctaca	cgctaccgtc	120
tcacagccgt	aaacgcccc	cccgatcccc	gctagttcgc	caccgcccgc	cgcccgcccc	180
cctttcgcc	catcatggcc	gcctcgtcga	ccgccacctc	cgtccacgac	ttcatcgtca	240
aggatgcgag	cggc aaagac	gttgacctca	gcacctacaa	ggggaagggt	cttctcattg	300
ttaacgtcgc	atcccagtg	ggcttaacca	actccaacta	cactgagctg	gcccagctct	360
atgagaagta	caaggaccaa	ggctttgaaa	tccctggctt	cccatgcaac	cagtttggtg	420
ggcaggagcc	ttgtaccaat	aaggagattg	tccagtttgc	ctgcacacgc	ttcaaggctg	480
agtacccatc	ttcgacaagg	ttgatgtc				

(2) INFORMATION FOR SEQ ID NO:2112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2112:

```
Met Ala Ala Ser Ser Thr Ala Thr Ser Val His Asp Phe Ile Val Lys
1           5           10           15
Asp Ala Ser Gly Lys Asp Val Asp Leu Ser Thr Tyr Lys Gly Lys Val
20          25          30
Leu Leu Ile Val Asn Val Ala Ser Gln Cys Gly Leu Thr Asn Ser Asn
35          40          45
Tyr Thr Glu Leu Ala Gln Leu Tyr Glu Lys Tyr Lys Asp Gln Gly Phe
50          55          60
Glu Ile Leu Ala Phe Pro Cys Asn Gln Phe Gly Gly Gln Glu Pro Gly
65          70          75          80
Thr Asn Lys Glu Ile Val Gln Phe Ala Cys Thr Arg Phe Lys Ala Glu
85          90          95
Tyr Pro Ser Ser Thr Arg Leu Met
100
```

(2) INFORMATION FOR SEQ ID NO:2113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..523
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2113:

```
attggcacgt atgaatgctc agccacatgc gtatgtatac atcacggcca cgttcacgct      60
tcccccttct gcaagcaaac ctaaccaagc ctctgctggc cttcttcgaa tccaactcct      120
ccccgatccc caaaatcgaa cccaagtcga aaccctaacc tcggccttct cgatgtcggc      180
cgccacaacc gccccaaccc ctgcggtggc caccctgatg gcgcgcctc cgctgtaccc      240
ggcctcctcc acgatctccg cctccgtggc cgcgtcggc gaggaagagg acgacctcta      300
tggcgcctc aagtcgtccc agcgccacat ggagttcgtc gagatccagg aggagtacgt      360
taaagacgaa cagaagaacc tcaagcgca actcctccgt gcgcaggagg aggtcaagcg      420
gatccagtcc gtaccgntcg tcatcggcc gtttatggag atggtcgacg gcaacaacgg      480
catcgtgggt tctactacgg gcagcaacta ctatgtgcgg atc
```

(2) INFORMATION FOR SEQ ID NO:2114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..174
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2114:

```
Leu Ala Arg Met Asn Ala Gln Pro His Ala Tyr Val Tyr Ile Thr Ala
1           5           10           15
```

Thr Phe Thr Leu Pro Pro Ser Ala Ser Lys Pro Asn Gln Ala Ser Ala
20 25 30
Ala Leu Leu Arg Ile Gln Leu Leu Pro Asp Pro Gln Asn Arg Thr Gln
35 40 45
Val Glu Thr Leu Thr Ser Ala Phe Ser Met Ser Ala Ala Thr Thr Ala
50 55 60
Pro Thr Pro Ala Val Ala Thr Pro Met Ala Pro Pro Pro Ser Tyr Pro
65 70 75 80
Ala Ser Ser Thr Ile Ser Ala Ser Val Ala Ala Ser Val Glu Glu Glu
85 90 95
Asp Asp Leu Tyr Gly Arg Leu Lys Ser Leu Gln Arg His Met Glu Phe
100 105 110
Val Glu Ile Gln Glu Glu Tyr Val Lys Asp Glu Gln Lys Asn Leu Lys
115 120 125
Arg Glu Leu Leu Arg Ala Gln Glu Glu Val Lys Arg Ile Gln Ser Val
130 135 140
Pro Xaa Val Ile Gly Gln Phe Met Glu Met Val Asp Gly Asn Asn Gly
145 150 155 160
Ile Val Gly Ser Thr Thr Gly Ser Asn Tyr Tyr Val Arg Ile
165 170

(2) INFORMATION FOR SEQ ID NO:2115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1502222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2115:

Met Asn Ala Gln Pro His Ala Tyr Val Tyr Ile Thr Ala Thr Phe Thr
1 5 10 15
Leu Pro Pro Ser Ala Ser Lys Pro Asn Gln Ala Ser Ala Ala Leu Leu
20 25 30
Arg Ile Gln Leu Leu Pro Asp Pro Gln Asn Arg Thr Gln Val Glu Thr
35 40 45
Leu Thr Ser Ala Phe Ser Met Ser Ala Ala Thr Thr Ala Pro Thr Pro
50 55 60
Ala Val Ala Thr Pro Met Ala Pro Pro Pro Ser Tyr Pro Ala Ser Ser
65 70 75 80
Thr Ile Ser Ala Ser Val Ala Ala Ser Val Glu Glu Glu Asp Asp Leu
85 90 95
Tyr Gly Arg Leu Lys Ser Leu Gln Arg His Met Glu Phe Val Glu Ile
100 105 110
Gln Glu Glu Tyr Val Lys Asp Glu Gln Lys Asn Leu Lys Arg Glu Leu
115 120 125
Leu Arg Ala Gln Glu Glu Val Lys Arg Ile Gln Ser Val Pro Xaa Val
130 135 140
Ile Gly Gln Phe Met Glu Met Val Asp Gly Asn Asn Gly Ile Val Gly
145 150 155 160
Ser Thr Thr Gly Ser Asn Tyr Tyr Val Arg Ile
165 170

(2) INFORMATION FOR SEQ ID NO:2116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1502223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2116:

```
Met Ser Ala Ala Thr Thr Ala Pro Thr Pro Ala Val Ala Thr Pro Met
1          5          10          15
Ala Pro Pro Pro Ser Tyr Pro Ala Ser Ser Thr Ile Ser Ala Ser Val
20          25          30
Ala Ala Ser Val Glu Glu Glu Asp Leu Tyr Gly Arg Leu Lys Ser
35          40          45
Leu Gln Arg His Met Glu Phe Val Glu Ile Gln Glu Glu Tyr Val Lys
50          55          60
Asp Glu Gln Lys Asn Leu Lys Arg Glu Leu Leu Arg Ala Gln Glu Glu
65          70          75          80
Val Lys Arg Ile Gln Ser Val Pro Xaa Val Ile Gly Gln Phe Met Glu
85          90          95
Met Val Asp Gly Asn Asn Gly Ile Val Gly Ser Thr Thr Gly Ser Asn
100          105          110
Tyr Tyr Val Arg Ile
115
```

(2) INFORMATION FOR SEQ ID NO:2117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1058 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1058

(D) OTHER INFORMATION: / Ceres Seq. ID 1502224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2117:

```
ctcacacgcc ggccgcgcgcg caagagccgt ggccccgtcg acgtccgccc gcacaggact      60
ctccgagtgt gggattgagc cgtagttttt tttttttggt ggctcgggcc gatatccggt      120
actgtatgag ggttgccaac tactagactt taagatcgct gattcaatgg aggcctccga      180
ggcagcacct gcagcggcgg ccaccgcat ggaagcagag gatgtgagcg gcgggaaggg      240
cgaatggtac gtgcttgggg agcgggcgct gatggtgccc tacacgcggg agcacgtgcc      300
gcggtaccac gactggatgc aggaccgcgc gctgctggag gccaccgcgt cggagcccct      360
ctccctctcg caggagttcg aggtccaccg ytcattggacc ctgcaccctc taaagcacac      420
cttcatagtg ttggataagg agtccataga gggagagttc gtgccgggca acccgcacat      480
tgaagctatg gktggkgatg tgaacatata tatgaatgac tctgatgatg tgcagatcgc      540
ggagatagag attatgatag ctgaacataa gasccgtggg aagggatttg gtcaagaagc      600
aatcttactg atgatggcat ttgcagtaga gaaatatgga attcacacgt tcagggcaaa      660
aattagcgaa tcaaatatgg catcgcttaa gctcttcagg aagttgggct tcaaggatgc      720
ttcatacagt gtggtgttca aggaggtgac tctggaggca cccgctgact cactcccgtt      780
gagatttcct ctgaccattg gagactggtg acgtttgaca tgccccaagt taattccatg      840
cagacgacac aagaagctaa tgctgtttgt ctgtactatc tgaccaaagt ttactcgggc      900
tgatattgta tgaaaaaaat gaataaaaca gttgcacagt tgtgattcaa ttgcattaga      960
ccagtcgggt ttttcatgtc actattttga agaccccata tcttataaac aaatgtagac     1020
aagttttatc tcataatttt tttatagtat ctcccgtc
```

(2) INFORMATION FOR SEQ ID NO:2118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..214

(D) OTHER INFORMATION: / Ceres Seq. ID 1502225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2118:

Met Glu Ala Ser Glu Ala Ala Pro Ala Ala Ala Thr Val Met Glu
1 5 10 15
Ala Glu Asp Val Ser Gly Gly Lys Gly Glu Trp Tyr Val Leu Gly Glu
20 25 30
Arg Ala Leu Met Val Pro Tyr Thr Arg Glu His Val Pro Arg Tyr His
35 40 45
Asp Trp Met Gln Asp Pro Ala Leu Leu Glu Ala Thr Ala Ser Glu Pro
50 55 60
Leu Ser Leu Ser Gln Glu Phe Glu Val His Xaa Ser Trp Thr Leu Asp
65 70 75 80
Pro Leu Lys His Thr Phe Ile Val Leu Asp Lys Glu Leu Ile Glu Gly
85 90 95
Glu Phe Val Pro Gly Asn Pro His Ile Glu Ala Met Xaa Xaa Asp Val
100 105 110
Asn Ile Tyr Met Asn Asp Ser Asp Asp Val Gln Ile Ala Glu Ile Glu
115 120 125
Ile Met Ile Ala Glu His Lys Xaa Arg Gly Lys Gly Ile Gly Gln Glu
130 135 140
Ala Ile Leu Leu Met Met Ala Phe Ala Val Glu Lys Tyr Gly Ile His
145 150 155 160
Thr Phe Arg Ala Lys Ile Ser Glu Ser Asn Met Ala Ser Leu Lys Leu
165 170 175
Phe Arg Lys Leu Gly Phe Lys Asp Ala Ser Tyr Ser Val Val Phe Lys
180 185 190
Glu Val Thr Leu Glu Ala Pro Ala Asp Ser Leu Pro Leu Arg Phe Pro
195 200 205
Leu Thr Ile Gly Asp Trp
210

(2) INFORMATION FOR SEQ ID NO:2119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..200

(D) OTHER INFORMATION: / Ceres Seq. ID 1502226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2119:

Met Glu Ala Glu Asp Val Ser Gly Gly Lys Gly Glu Trp Tyr Val Leu
1 5 10 15
Gly Glu Arg Ala Leu Met Val Pro Tyr Thr Arg Glu His Val Pro Arg
20 25 30
Tyr His Asp Trp Met Gln Asp Pro Ala Leu Leu Glu Ala Thr Ala Ser
35 40 45
Glu Pro Leu Ser Leu Ser Gln Glu Phe Glu Val His Xaa Ser Trp Thr
50 55 60
Leu Asp Pro Leu Lys His Thr Phe Ile Val Leu Asp Lys Glu Leu Ile
65 70 75 80
Glu Gly Glu Phe Val Pro Gly Asn Pro His Ile Glu Ala Met Xaa Xaa
85 90 95
Asp Val Asn Ile Tyr Met Asn Asp Ser Asp Asp Val Gln Ile Ala Glu
100 105 110
Ile Glu Ile Met Ile Ala Glu His Lys Xaa Arg Gly Lys Gly Ile Gly
115 120 125
Gln Glu Ala Ile Leu Leu Met Met Ala Phe Ala Val Glu Lys Tyr Gly
130 135 140
Ile His Thr Phe Arg Ala Lys Ile Ser Glu Ser Asn Met Ala Ser Leu

145 150 155 160
Lys Leu Phe Arg Lys Leu Gly Phe Lys Asp Ala Ser Tyr Ser Val Val
 165 170 175
Phe Lys Glu Val Thr Leu Glu Ala Pro Ala Asp Ser Leu Pro Leu Arg
 180 185 190
Phe Pro Leu Thr Ile Gly Asp Trp
 195 200

(2) INFORMATION FOR SEQ ID NO:2120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..179
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2120:

Met Val Pro Tyr Thr Arg Glu His Val Pro Arg Tyr His Asp Trp Met
1 5 10 15
Gln Asp Pro Ala Leu Leu Glu Ala Thr Ala Ser Glu Pro Leu Ser Leu
 20 25 30
Ser Gln Glu Phe Glu Val His Xaa Ser Trp Thr Leu Asp Pro Leu Lys
 35 40 45
His Thr Phe Ile Val Leu Asp Lys Glu Leu Ile Glu Gly Glu Phe Val
 50 55 60
Pro Gly Asn Pro His Ile Glu Ala Met Xaa Xaa Asp Val Asn Ile Tyr
65 70 75 80
Met Asn Asp Ser Asp Asp Val Gln Ile Ala Glu Ile Glu Ile Met Ile
 85 90 95
Ala Glu His Lys Xaa Arg Gly Lys Gly Ile Gly Gln Glu Ala Ile Leu
 100 105 110
Leu Met Met Ala Phe Ala Val Glu Lys Tyr Gly Ile His Thr Phe Arg
 115 120 125
Ala Lys Ile Ser Glu Ser Asn Met Ala Ser Leu Lys Leu Phe Arg Lys
130 135 140
Leu Gly Phe Lys Asp Ala Ser Tyr Ser Val Val Phe Lys Glu Val Thr
145 150 155 160
Leu Glu Ala Pro Ala Asp Ser Leu Pro Leu Arg Phe Pro Leu Thr Ile
 165 170 175
Gly Asp Trp

(2) INFORMATION FOR SEQ ID NO:2121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..640
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2121:

acatccatcc atccatccat ccatccatcc ctaaaaatca aggctacaca ccaacttact	60
ttctaggtct caaattaaat ggcctcctcg tcctcctcct tgctgctggc gtcgatggcg	120
gtggcggcac tctttgtcgt cggctcgtgt ggcggcgcgc tcaccttcac gatcggaag	180
gactccagct ccaccaaact atccctcgtc actaacgttg ccactccga ggtgtcggtc	240
aaggagaagg gcgccctgga ctggtcggat gatctcaagg agtcgccagc caaaccttc	300
accctcgata gcaaggagcc gattaagggc cccatctccg tccgcttcgc tgtgaaaggt	360

ggtggctacc gcgctgtcga tgacgtcatc cctgccgact tcaagcctgg ctctgtttac 420
cagacaggcg aacaaatctg agtaatggat tctgctgcgt gcagattata ttgatctcta 480
aaataaatgt ttgacagaga ctaattaagc acmcaaacia agcaaggcmc taattcattt 540
cctatgttta ctttgtggta ggcaactgca aaacaatgta ttgtatgcat gttctcctct 600
cacatatgtt gbtgggtgtgc tgtatatata attaatyycc

(2) INFORMATION FOR SEQ ID NO:2122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1502229

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2122:

Ile His Pro Ser Ile His Pro Ser Ile Pro Lys Asn Gln Gly Tyr Thr
1 5 10 15
Pro Thr Tyr Phe Leu Gly Leu Lys Leu Asn Gly Leu Leu Val Leu Leu
20 25 30
Leu Ala Ala Gly Val Asp Gly Gly Gly Thr Leu Cys Arg Arg Leu
35 40 45
Val Trp Arg Arg Ala His Leu His Asp Arg Gln Gly Leu Gln Leu His
50 55 60
Gln Thr Ile Pro Arg His
65 70

(2) INFORMATION FOR SEQ ID NO:2123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1502230

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2123:

Met Ala Ser Ser Ser Ser Ser Leu Leu Leu Ala Ser Met Ala Val Ala
1 5 10 15
Ala Leu Phe Val Val Gly Ser Cys Gly Gly Ala Leu Thr Phe Thr Ile
20 25 30
Gly Lys Asp Ser Ser Ser Thr Lys Leu Ser Leu Val Thr Asn Val Ala
35 40 45
Ile Ser Glu Val Ser Val Lys Glu Lys Gly Ala Leu Asp Trp Ser Asp
50 55 60
Asp Leu Lys Glu Ser Pro Ala Lys Thr Phe Thr Leu Asp Ser Lys Glu
65 70 75 80
Pro Ile Lys Gly Pro Ile Ser Val Arg Phe Ala Val Lys Gly Gly Gly
85 90 95
Tyr Arg Val Val Asp Asp Val Ile Pro Ala Asp Phe Lys Pro Gly Ser
100 105 110
Val Tyr Gln Thr Gly Glu Gln Ile
115 120

(2) INFORMATION FOR SEQ ID NO:2124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1502231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2124:

Met	Ala	Val	Ala	Ala	Leu	Phe	Val	Val	Gly	Ser	Cys	Gly	Gly	Ala	Leu
1			5						10					15	
Thr	Phe	Thr	Ile	Gly	Lys	Asp	Ser	Ser	Ser	Thr	Lys	Leu	Ser	Leu	Val
			20					25					30		
Thr	Asn	Val	Ala	Ile	Ser	Glu	Val	Ser	Val	Lys	Glu	Lys	Gly	Ala	Leu
		35				40					45				
Asp	Trp	Ser	Asp	Asp	Leu	Lys	Glu	Ser	Pro	Ala	Lys	Thr	Phe	Thr	Leu
	50				55						60				
Asp	Ser	Lys	Glu	Pro	Ile	Lys	Gly	Pro	Ile	Ser	Val	Arg	Phe	Ala	Val
65				70					75					80	
Lys	Gly	Gly	Gly	Tyr	Arg	Val	Val	Asp	Asp	Val	Ile	Pro	Ala	Asp	Phe
			85					90						95	
Lys	Pro	Gly	Ser	Val	Tyr	Gln	Thr	Gly	Glu	Gln	Ile				
		100						105							

(2) INFORMATION FOR SEQ ID NO:2125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..481

(D) OTHER INFORMATION: / Ceres Seq. ID 1502270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2125:

cggtgcttc	gcttcgcttt	gsscgcgatt	cgatccaggc	tttggttgga	ggcatggcct	60
cgctgcccgc	gagcagctac	gactgctcct	tcaaggtcct	gcttatcggg	gattcggccg	120
tcggcaagag	cagcctcctc	gtcagcttcg	tctccgccgc	tcacatcgac	gacgacatcg	180
cgccaacccat	aggggtggat	tttaaaatca	aatttctcag	tgtgggtggg	aagaaactaa	240
aactgacaat	atgggacact	gccgggtcaag	agagggttcag	gacaattacc	agctcttact	300
acaggggtgc	tcattgggatt	attttagttt	atgacgttac	aaagagggag	agtttcacaa	360
atttggtgta	tgtgtggacc	aaggaaatag	agttacactc	aacaaataag	gaatgcataa	420
aatgcttgt	tggaaataaa	gtggacaagg	atgaggacag	aatggtgaca	aaagaagaag	480

(2) INFORMATION FOR SEQ ID NO:2126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1502271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2126:

Gly	Ala	Ser	Leu	Arg	Phe	Xaa	Arg	Asp	Ser	Ile	Gln	Ala	Leu	Val	Gly
1			5					10						15	
Gly	Met	Ala	Ser	Ser	Pro	Ala	Ser	Ser	Tyr	Asp	Cys	Ser	Phe	Lys	Val
			20					25					30		
Leu	Leu	Ile	Gly	Asp	Ser	Ala	Val	Gly	Lys	Ser	Ser	Leu	Leu	Val	Ser
		35				40					45				
Phe	Val	Ser	Ala	Ala	His	Ile	Asp	Asp	Asp	Ile	Ala	Pro	Thr	Ile	Gly
	50					55					60				

Val Asp Phe Lys Ile Lys Phe Leu Ser Val Gly Gly Lys Lys Leu Lys
65 70 75 80
Leu Thr Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr
85 90 95
Ser Ser Tyr Tyr Arg Gly Ala His Gly Ile Ile Leu Val Tyr Asp Val
100 105 110
Thr Lys Arg Glu Ser Phe Thr Asn Leu Ala Asp Val Trp Thr Lys Glu
115 120 125
Ile Glu Leu His Ser Thr Asn Lys Glu Cys Ile Lys Met Leu Val Gly
130 135 140
Asn Lys Val Asp Lys Asp Glu Asp Arg Met Val Thr Lys Glu Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:2127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1502272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2127:

Met Ala Ser Ser Pro Ala Ser Ser Tyr Asp Cys Ser Phe Lys Val Leu
1 5 10 15
Leu Ile Gly Asp Ser Ala Val Gly Lys Ser Ser Leu Leu Val Ser Phe
20 25 30
Val Ser Ala Ala His Ile Asp Asp Asp Ile Ala Pro Thr Ile Gly Val
35 40 45
Asp Phe Lys Ile Lys Phe Leu Ser Val Gly Gly Lys Lys Leu Lys Leu
50 55 60
Thr Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser
65 70 75 80
Ser Tyr Tyr Arg Gly Ala His Gly Ile Ile Leu Val Tyr Asp Val Thr
85 90 95
Lys Arg Glu Ser Phe Thr Asn Leu Ala Asp Val Trp Thr Lys Glu Ile
100 105 110
Glu Leu His Ser Thr Asn Lys Glu Cys Ile Lys Met Leu Val Gly Asn
115 120 125
Lys Val Asp Lys Asp Glu Asp Arg Met Val Thr Lys Glu Glu
130 135 140

(2) INFORMATION FOR SEQ ID NO:2128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..344

(D) OTHER INFORMATION: / Ceres Seq. ID 1502285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2128:

gaccgcgcgg caggggaagc ttagcacgga cgggaccagc tgacgaccag gccatgggga 60
agtacatgcg caagggaagc atgtccgggg aggtggccgt catggagggtc cccggcgggc 120
cgctgctkkc tgtccgcacc gctccgcac gctcgcgctg cagagggcgc agaggccgct 180
cgacaagggg gacgcggatg acgcccggcg acagtacctc gagctcagga gccggangna 240
gaagcctcat aaggaccatc agccgctgcc gctgccggcg cccgcccccg cagccaagag 300
gggcgcggg aggaaggccg cctccgcgcg cgccgcgcgc cacg

(2) INFORMATION FOR SEQ ID NO:2129:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..114
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502286
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2129:
Pro Arg Gly Arg Gly Ser Leu Ala Arg Thr Gly Pro Ala Asp Asp Gln
1 5 10 15
Ala Met Gly Lys Tyr Met Arg Lys Gly Lys Met Ser Gly Glu Val Ala
 20 25 30
Val Met Glu Val Pro Gly Gly Ala Leu Xaa Xaa Val Arg Thr Ala Pro
 35 40 45
Ala Arg Ser Arg Cys Arg Gly Arg Arg Gly Arg Ser Thr Arg Gly Thr
50 55 60
Arg Met Thr Pro Pro Asp Ser Thr Ser Ser Ser Gly Ala Gly Xaa Arg
65 70 75 80
Ser Leu Ile Arg Thr Ile Ser Arg Cys Arg Cys Arg Arg Pro Pro Pro
 85 90 95
Gln Pro Arg Gly Ala Pro Gly Gly Arg Pro Pro Pro Pro Pro Pro Arg
 100 105 110
Arg Thr

(2) INFORMATION FOR SEQ ID NO:2130:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..97
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502287
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2130:
Met Gly Lys Tyr Met Arg Lys Gly Lys Met Ser Gly Glu Val Ala Val
1 5 10 15
Met Glu Val Pro Gly Gly Ala Leu Xaa Xaa Val Arg Thr Ala Pro Ala
 20 25 30
Arg Ser Arg Cys Arg Gly Arg Arg Gly Arg Ser Thr Arg Gly Thr Arg
35 40 45
Met Thr Pro Pro Asp Ser Thr Ser Ser Ser Gly Ala Gly Xaa Arg Ser
50 55 60
Leu Ile Arg Thr Ile Ser Arg Cys Arg Cys Arg Arg Pro Pro Pro Gln
65 70 75 80
Pro Arg Gly Ala Pro Gly Gly Arg Pro Pro Pro Pro Pro Pro Arg Arg
 85 90 95
Thr

(2) INFORMATION FOR SEQ ID NO:2131:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1502288

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2131:

Met Arg Lys Gly Lys Met Ser Gly Glu Val Ala Val Met Glu Val Pro
1 5 10 15
Gly Gly Ala Leu Xaa Xaa Val Arg Thr Ala Pro Ala Arg Ser Arg Cys
20 25 30
Arg Gly Arg Arg Gly Arg Ser Thr Arg Gly Thr Arg Met Thr Pro Pro
35 40 45
Asp Ser Thr Ser Ser Ser Gly Ala Gly Xaa Arg Ser Leu Ile Arg Thr
50 55 60
Ile Ser Arg Cys Arg Cys Arg Arg Pro Pro Pro Gln Pro Arg Gly Ala
65 70 75 80
Pro Gly Gly Arg Pro Pro Pro Pro Pro Arg Arg Thr
85 90

(2) INFORMATION FOR SEQ ID NO:2132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..381

(D) OTHER INFORMATION: / Ceres Seq. ID 1502297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2132:

ctcacgcaag kntntgcctc cggttaagcc acaaacacac agacaccatg gccttcccag 60
ggactccggc gaggaagatc gtaccaggcg gcttcaccgc agcacgaacc gccgtggcca 120
gcgssgcgct cttagcttcg acctggacgg cgccggcgac tttttctggg gcctgtggca 180
gctcatcaag gcgaaggccg ccgaggcagc ggcctacctc gctgccctct tcgcggcgct 240
ggcggagaag gcggacgaga tcttcccgcc ggagaccgc tcggagacgc tccggcagtg 300
gatgcgcgtc gccgtcaccg tgggtattcc cggccctagt ggtcgccctc gtgctttgct 360
gctgctggcg ctgctgctgc t

(2) INFORMATION FOR SEQ ID NO:2133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1502298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2133:

Ser Arg Lys Xaa Xaa Pro Pro Val Lys Pro Gln Thr His Arg His His
1 5 10 15
Gly Leu Pro Arg Asp Ser Gly Glu Glu Asp Arg Thr Arg Arg Leu His
20 25 30
Arg Ser Thr Asn Arg Arg Gly Gln Xaa Xaa Ala Leu Ser Phe Asp Leu
35 40 45
Asp Gly Ala Gly Asp Phe Phe Trp Gly Leu Trp Gln Leu Ile Lys Ala
50 55 60
Lys Ala Ala Glu Ala Ala Ala Tyr Leu Ala Ala Leu Phe Ala Ala Leu
65 70 75 80
Ala Glu Lys Ala Asp Glu Ile Phe Pro Pro Glu Thr Arg Ser Glu Thr
85 90 95
Leu Arg Gln Trp Met Arg Val Ala Val Thr Val Val Ile Pro Gly Pro
100 105 110

Ser Gly Arg Pro Arg Ala Leu Leu Leu Leu Ala Leu Leu Leu
115 120 125

(2) INFORMATION FOR SEQ ID NO:2134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2134:

His Ala Xaa Xaa Cys Leu Arg Leu Ser His Lys His Thr Asp Thr Met
1 5 10 15
Ala Phe Pro Gly Thr Pro Ala Arg Lys Ile Val Pro Gly Gly Phe Thr
20 25 30
Ala Ala Arg Thr Ala Val Ala Ser Xaa Ala Leu Leu Ala Ser Thr Trp
35 40 45
Thr Ala Pro Ala Thr Phe Ser Gly Ala Cys Gly Ser Ser Arg Arg
50 55 60
Arg Pro Pro Arg Gln Arg Pro Thr Ser Leu Pro Ser Ser Arg Arg Trp
65 70 75 80
Arg Arg Arg Arg Thr Arg Ser Ser Arg Arg Arg Pro Ala Arg Arg Arg
85 90 95
Ser Gly Ser Gly Cys Ala Ser Pro Ser Pro Trp
100 105

(2) INFORMATION FOR SEQ ID NO:2135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2135:

Met Ala Phe Pro Gly Thr Pro Ala Arg Lys Ile Val Pro Gly Gly Phe
1 5 10 15
Thr Ala Ala Arg Thr Ala Val Ala Ser Xaa Ala Leu Leu Ala Ser Thr
20 25 30
Trp Thr Ala Pro Ala Thr Phe Ser Gly Ala Cys Gly Ser Ser Ser Arg
35 40 45
Arg Arg Pro Pro Arg Gln Arg Pro Thr Ser Leu Pro Ser Ser Arg Arg
50 55 60
Trp Arg Arg Arg Arg Thr Arg Ser Ser Arg Arg Arg Pro Ala Arg Arg
65 70 75 80
Arg Ser Gly Ser Gly Cys Ala Ser Pro Ser Pro Trp
85 90

(2) INFORMATION FOR SEQ ID NO:2136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..456

(D) OTHER INFORMATION: / Ceres Seq. ID 1502315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2136:

cttgtttcaa	atcctgggtc	cgccattggg	ggcggtgagg	ccaccctagt	agaggctaga	60
ggatgatata	cacggcgatc	gacacgttct	acctgacaga	tgagcagctc	cgtgactcgc	120
catcacggaa	ggatggggtc	gacgaggcca	ccgagactgc	gcttcssstc	tatggctgtg	180
acctcatcca	ggagagcggc	atcctcctca	ggctaccaca	agcagtgatg	gccacggcac	240
aagtattgtt	ccatcgcttt	tactgcaaga	aatcatttgt	tcgatttagt	gcaaagagag	300
ttgctgctag	ctgtgttttg	ctggcaggga	agttggagga	gagtcccagg	aaatcaaggc	360
atattatatt	tgtcttccac	agaatggaat	gtaggagaga	aaacttgcca	attgaatttt	420
tagatgtttt	ttcaaagaaa	tattcggaac	tgaggc			

(2) INFORMATION FOR SEQ ID NO:2137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1502316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2137:

Met	Ile	Tyr	Thr	Ala	Ile	Asp	Thr	Phe	Tyr	Leu	Thr	Asp	Glu	Gln	Leu	
1				5					10					15		
Arg	Asp	Ser	Pro	Ser	Arg	Lys	Asp	Gly	Ile	Asp	Glu	Ala	Thr	Glu	Thr	
			20					25					30			
Ala	Leu	Xaa	Xaa	Tyr	Gly	Cys	Asp	Leu	Ile	Gln	Glu	Ser	Gly	Ile	Leu	
		35				40						45				
Leu	Arg	Leu	Pro	Gln	Ala	Val	Met	Ala	Thr	Ala	Gln	Val	Leu	Phe	His	
		50				55					60					
Arg	Phe	Tyr	Cys	Lys	Lys	Ser	Phe	Val	Arg	Phe	Ser	Ala	Lys	Arg	Val	
65				70						75				80		
Ala	Ala	Ser	Cys	Val	Trp	Leu	Ala	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Arg	
			85					90					95			
Lys	Ser	Arg	His	Ile	Ile	Phe	Val	Phe	His	Arg	Met	Glu	Cys	Arg	Arg	
			100					105					110			
Glu	Asn	Leu	Pro	Ile	Glu	Phe	Leu	Asp	Val	Phe	Ser	Lys	Lys	Tyr	Ser	
		115					120						125			
Glu	Leu	Arg														
		130														

(2) INFORMATION FOR SEQ ID NO:2138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1502317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2138:

Met	Ala	Thr	Ala	Gln	Val	Leu	Phe	His	Arg	Phe	Tyr	Cys	Lys	Lys	Ser	
1				5					10					15		
Phe	Val	Arg	Phe	Ser	Ala	Lys	Arg	Val	Ala	Ala	Ser	Cys	Val	Trp	Leu	
			20					25					30			
Ala	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Arg	Lys	Ser	Arg	His	Ile	Ile	Phe	
		35				40						45				
Val	Phe	His	Arg	Met	Glu	Cys	Arg	Arg	Glu	Asn	Leu	Pro	Ile	Glu	Phe	
		50				55						60				

Leu Asp Val Phe Ser Lys Lys Tyr Ser Glu Leu Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2139:

gatttggctc	ttgccatgga	ggtgccgctc	tccccaccgc	gtgcccacgc	cggcctcctc	60
tgctgcagct	ccactcccgt	cgctctcggc	ctccgctccc	gctccgccac	cgctccgagc	120
cgccgcgcaa	ggccactcct	tgcccgcaga	accgggacag	ccggagcgac	gaggagaccg	180
cggcggassc	aagatcatca	cggtcgggcg	gccgggggnak	agcgggcggc	ggcgcaacag	240
gaagcagcag	cagcagcagc	agcagacggc	ggcgaaggaa	gaagaagaag	aggaggagga	300
agatgaggac	gacgaggagg	agcgtgacgc	gacgatcccc	gagtgggtgac	gaaccggatg	360
atgcggcggg	gtgggcgcgt	cgggtggggc	tccgctggcg	ctgggcgtgg	ggtttcttcc	420
cgggtgttcta	ctacctgaag	gcgktggcga	aggtggacgt	gccgacgtgg	atccccctt	

(2) INFORMATION FOR SEQ ID NO:2140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..101
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2140:

Asp	Leu	Ala	Leu	Ala	Met	Glu	Val	Pro	Leu	Ser	Pro	Pro	Arg	Ala	His
1				5					10					15	
Ala	Gly	Leu	Leu	Cys	Cys	Ser	Ser	Thr	Pro	Val	Val	Leu	Gly	Leu	Arg
		20						25					30		
Ser	Arg	Ser	Ala	Thr	Ala	Pro	Ser	Arg	Arg	Ala	Arg	Pro	Leu	Leu	Ala
		35					40					45			
Arg	Arg	Thr	Gly	Thr	Ala	Gly	Ala	Thr	Arg	Arg	Pro	Arg	Arg	Xaa	Gln
		50				55					60				
Asp	His	His	Gly	Arg	Ala	Ala	Gly	Xaa	Xaa	Arg	Ala	Ala	Ala	Gln	Gln
65				70					75					80	
Glu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Asp	Gly	Gly	Glu	Gly	Arg	Arg	Arg
			85					90					95		
Arg	Gly	Gly	Gly	Arg											
			100												

(2) INFORMATION FOR SEQ ID NO:2141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2141:

Ile Trp Leu Leu Pro Trp Arg Cys Arg Ser Pro His Arg Val Pro Thr

1 5 10 15
Pro Ala Ser Ser Ala Ala Ala Pro Leu Pro Ser Ser Ser Ala Ser Ala
20 25 30
Pro Ala Pro Pro Pro Leu Arg Ala Ala Ala Gln Gly His Ser Leu Pro
35 40 45
Ala Glu Pro Gly Gln Pro Glu Arg Arg Gly Asp Arg Gly Gly Xaa Lys
50 55 60
Ile Ile Thr Val Gly Arg Pro Gly Xaa Ser Gly Arg Arg Arg Asn Arg
65 70 75 80
Lys Gln Gln Gln Gln Gln Gln Thr Ala Ala Lys Glu Glu Glu Glu
85 90 95
Glu Glu Glu Glu Asp Glu Asp Asp Glu Glu Glu Arg Asp Ala Thr Ile
100 105 110
Pro Glu Trp
115

(2) INFORMATION FOR SEQ ID NO:2142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..158
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2142:

Phe Gly Ser Cys His Gly Gly Ala Ala Leu Pro Thr Ala Cys Pro Arg
1 5 10 15
Arg Pro Pro Leu Leu Gln Leu His Ser Arg Arg Pro Arg Pro Pro Leu
20 25 30
Pro Leu Arg His Arg Ser Glu Pro Arg Lys Ala Thr Pro Cys Pro
35 40 45
Gln Asn Arg Asp Ser Arg Ser Asp Glu Glu Thr Ala Ala Xaa Xaa Arg
50 55 60
Ser Ser Arg Ser Gly Gly Arg Xaa Xaa Ala Gly Gly Gly Ala Thr Gly
65 70 75 80
Ser Ser Ser Ser Ser Ser Arg Arg Arg Arg Lys Lys Lys Lys
85 90 95
Arg Arg Arg Lys Met Arg Thr Thr Arg Arg Ser Val Thr Arg Arg Ser
100 105 110
Arg Ser Gly Asp Glu Pro Asp Asp Ala Ala Gly Trp Ala Arg Arg Trp
115 120 125
Gly Phe Arg Trp Arg Trp Ala Trp Gly Phe Phe Pro Val Phe Tyr Tyr
130 135 140
Leu Lys Ala Xaa Ala Lys Val Asp Val Pro Thr Trp Ile Pro
145 150 155

(2) INFORMATION FOR SEQ ID NO:2143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2143:

ttaacttgat tgatttagct gggagtgagc gtcttgctaa aagtggtctcc acaggtgatc 60
gcttgaagga aactcagtca atcaataaaa gcttgctggc tttgagcgat gtaatcttcg 120

cgatcgcaaa aggagatgac cacgttccgt tcagaaattc aaaacttaca tacctattgc 180
agccttgccct tggagggtgac tcgaaagctc tcatgtttgt caacatttca ccggagcatc 240
ctccgttggt gagacgatat ghtcgttgag gtttgcttca aggggtgaatg cttgtgagat 300
tggaatacca agacgtcaca cataagcccg tcccttcggt ctaggctgaa ttatgggtga 360
aggtagctgt agggatcatg ataattgtat atataatgtg ttggtttggt ccgcatttgg 420
ccacaaaggt gatgccaac aaaattcttg taacttgtac agtgtagggt atggtgg

(2) INFORMATION FOR SEQ ID NO:2144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2144:

Asn Leu Ile Asp Leu Ala Gly Ser Glu Arg Leu Ala Lys Ser Gly Ser
1 5 10 15
Thr Gly Asp Arg Leu Lys Glu Thr Gln Ser Ile Asn Lys Ser Leu Ser
20 25 30
Ala Leu Ser Asp Val Ile Phe Ala Ile Ala Lys Gly Asp Asp His Val
35 40 45
Pro Phe Arg Asn Ser Lys Leu Thr Tyr Leu Leu Gln Pro Cys Leu Gly
50 55 60
Gly Asp Ser Lys Ala Leu Met Phe Val Asn Ile Ser Pro Glu His Pro
65 70 75 80
Pro Leu Val Arg Arg Tyr Xaa Arg
85

(2) INFORMATION FOR SEQ ID NO:2145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..388
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2145:

attaacagcc aggaagctgg cgtcttgctt gtccttgctt ttttccacc cggctacccc 60
cgtcgtcgcc gccgctttcc ccgtggnttc agagctcgag tcggctagct aggcgcctg 120
gctaattctcc ctgccttcta taagtacaga gatcaggag gcggcacact ccatccactg 180
accgctcatg gcgaaggtcc acctctacgt cgccgcggcc tgcgcgctcg tctcgcgct 240
cgccgccccg gccctcgccg ggcaccccg catgctgcag gacgtctgcc cggctgacta 300
cgctccccg gtgaagctga acgggttcgc gtgcaaggcg aacttttcgg cggacgactt 360
cttcttcgac gggctgagga acnccggc

(2) INFORMATION FOR SEQ ID NO:2146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2146:

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Leu Thr Ala Arg Lys Leu Ala Ser Cys Leu Ser Leu Phe Phe Ser His
1 5 10 15
Pro Ala Thr Pro Val Val Ala Ala Ala Phe Pro Val Xaa Ser Glu Leu
20 25 30
Glu Ser Ala Ser
35

(2) INFORMATION FOR SEQ ID NO:2147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..67
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2147:

Met Ala Lys Val His Leu Tyr Val Ala Ala Ala Cys Ala Val Val Leu
1 5 10 15
Ala Leu Ala Ala Pro Ala Leu Ala Gly Asp Pro Asp Met Leu Gln Asp
20 25 30
Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu Asn Gly Phe Ala
35 40 45
Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe Asp Gly Leu Arg
50 55 60
Asn Xaa Gly
65

(2) INFORMATION FOR SEQ ID NO:2148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2148:

Met Leu Gln Asp Val Cys Pro Ala Asp Tyr Ala Ser Pro Val Lys Leu
1 5 10 15
Asn Gly Phe Ala Cys Lys Ala Asn Phe Ser Ala Asp Asp Phe Phe Phe
20 25 30
Asp Gly Leu Arg Asn Xaa Gly
35

(2) INFORMATION FOR SEQ ID NO:2149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..397
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2149:

ttaactgttg	ctgtcaagac	actcaacat	gatgggttg	aggggcataa	agagtgggtg	60
gcagaagttg	atctttcttg	aaaccttcag	catccacatc	tagtgaaatt	ggttggctac	120
tgcatgaag	atgaccagag	gttgcttg	tatgaattta	tgccccgtg	aagtttgag	180

aatcatcttt ttagaaagtc attgcctcta ccatgggcca ttagaatgaa aattgctctt 240
ggtgctgcga aaggcctcgc ttttcttcat gaagaagctg aaagaccagt aatctatcgg 300
gacttcaaaa cctccaatat tcttttagat gcggactata acgcaaaaact ctctgatttt 360
ggacttgcta aagatggccc tgagggtgat aaaacac

(2) INFORMATION FOR SEQ ID NO:2150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2150:

Leu Thr Val Ala Val Lys Thr Leu Asn His Asp Gly Leu Gln Gly His
1 5 10 15
Lys Glu Trp Val Ala Glu Val Asp Phe Leu Gly Asn Leu Gln His Pro
20 25 30
His Leu Val Lys Leu Val Gly Tyr Cys Ile Glu Asp Asp Gln Arg Leu
35 40 45
Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu Asn His Leu Phe
50 55 60
Arg Lys Ser Leu Pro Leu Pro Trp Ala Ile Arg Met Lys Ile Ala Leu
65 70 75 80
Gly Ala Ala Lys Gly Leu Ala Phe Leu His Glu Glu Ala Glu Arg Pro
85 90 95
Val Ile Tyr Arg Asp Phe Lys Thr Ser Asn Ile Leu Leu Asp Ala Asp
100 105 110
Tyr Asn Ala Lys Leu Ser Asp Phe Gly Leu Ala Lys Asp Gly Pro Glu
115 120 125
Gly Asp Lys Thr
130

(2) INFORMATION FOR SEQ ID NO:2151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2151:

Met Pro Arg Gly Ser Leu Glu Asn His Leu Phe Arg Lys Ser Leu Pro
1 5 10 15
Leu Pro Trp Ala Ile Arg Met Lys Ile Ala Leu Gly Ala Ala Lys Gly
20 25 30
Leu Ala Phe Leu His Glu Glu Ala Glu Arg Pro Val Ile Tyr Arg Asp
35 40 45
Phe Lys Thr Ser Asn Ile Leu Leu Asp Ala Asp Tyr Asn Ala Lys Leu
50 55 60
Ser Asp Phe Gly Leu Ala Lys Asp Gly Pro Glu Gly Asp Lys Thr
65 70 75

(2) INFORMATION FOR SEQ ID NO:2152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..480
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2152:

aagacctagg	gttgcttcct	tccttttaac	ctcgcgccgc	catccgacgc	ccatctcctc	60
caccagccg	cngccgccgc	ctaaggagaa	gagggtcg	ccgtctcctt	gccccgatgg	120
cgtccgagaa	gaagcagtc	aaccgcgatg	gggagatcaa	ggtgcagaag	ctggtcctca	180
acatatccgt	aggagagcgc	gcgaccgcct	caccgcgcgc	gccaagggtc	tggagcagct	240
cagcggccag	acccccgtct	tctccaaggc	gaggtacacg	gtgcgctcgt	tcggcatccg	300
gcgtaacgag	aagatcgcc	gctacgtcac	ggtcaggggc	gacaaggcca	tgcagctgct	360
tgagagcggc	ctcaagggtc	aggagtacga	gctgctcagg	aggaacttca	gcgacaccgg	420
ctgcttcggg	ttcggcatcc	aagagcacat	cgaccttggt	atcaagtatg	atccatcaac	480

(2) INFORMATION FOR SEQ ID NO:2153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..159
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2153:

Arg	Pro	Arg	Val	Ala	Ser	Phe	Leu	Leu	Thr	Ser	Arg	Arg	His	Pro	Thr
1			5						10					15	
Pro	Ile	Ser	Ser	Thr	Gln	Pro	Xaa	Pro	Pro	Pro	Lys	Glu	Lys	Arg	Val
			20					25					30		
Arg	Pro	Ser	Pro	Cys	Pro	Asp	Gly	Val	Arg	Glu	Glu	Ala	Val	Gln	Pro
		35					40					45			
Asp	Ala	Gly	Asp	Gln	Gly	Ala	Glu	Ala	Gly	Pro	Gln	His	Ile	Arg	Arg
	50					55					60				
Glu	Ser	Gly	Asp	Arg	Leu	Thr	Arg	Ala	Ala	Lys	Val	Leu	Glu	Gln	Leu
65					70					75				80	
Ser	Gly	Gln	Thr	Pro	Val	Phe	Ser	Lys	Ala	Arg	Tyr	Thr	Val	Arg	Ser
			85					90						95	
Phe	Gly	Ile	Arg	Arg	Asn	Glu	Lys	Ile	Ala	Cys	Tyr	Val	Thr	Val	Arg
		100						105					110		
Gly	Asp	Lys	Ala	Met	Gln	Leu	Leu	Glu	Ser	Gly	Leu	Lys	Val	Lys	Glu
		115					120					125			
Tyr	Glu	Leu	Leu	Arg	Arg	Asn	Phe	Ser	Asp	Thr	Gly	Cys	Phe	Gly	Phe
	130					135					140				
Gly	Ile	Gln	Glu	His	Ile	Asp	Leu	Gly	Ile	Lys	Tyr	Asp	Pro	Ser	
145					150					155					

(2) INFORMATION FOR SEQ ID NO:2154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..121
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2154:

Met	Ala	Ser	Glu	Lys	Lys	Gln	Ser	Asn	Pro	Met	Arg	Glu	Ile	Lys	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1		5		10		15									
Gln	Lys	Leu	Val	Leu	Asn	Ile	Ser	Val	Gly	Arg	Ala	Ala	Thr	Ala	Ser
		20						25					30		
Pro	Ala	Pro	Pro	Arg	Cys	Trp	Ser	Ser	Ser	Ala	Ala	Arg	Pro	Pro	Ser
		35					40					45			
Ser	Pro	Arg	Arg	Gly	Thr	Arg	Cys	Ala	Arg	Ser	Ala	Ser	Gly	Val	Thr
	50					55					60				
Arg	Arg	Ser	Pro	Ala	Thr	Ser	Arg	Ser	Gly	Ala	Thr	Arg	Pro	Cys	Ser
65					70					75				80	
Cys	Leu	Arg	Ala	Ala	Ser	Arg	Ser	Arg	Ser	Thr	Ser	Cys	Ser	Gly	Gly
			85						90					95	
Thr	Ser	Ala	Thr	Pro	Ala	Ala	Ser	Gly	Ser	Ala	Ser	Lys	Ser	Thr	Ser
		100						105						110	
Thr	Leu	Val	Ser	Ser	Met	Ile	His	Gln							
		115						120							

(2) INFORMATION FOR SEQ ID NO:2155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2155:

Met	Arg	Glu	Ile	Lys	Val	Gln	Lys	Leu	Val	Leu	Asn	Ile	Ser	Val	Gly
1				5				10					15		
Arg	Ala	Ala	Thr	Ala	Ser	Pro	Ala	Pro	Pro	Arg	Cys	Trp	Ser	Ser	Ser
		20						25					30		
Ala	Ala	Arg	Pro	Pro	Ser	Ser	Pro	Arg	Arg	Gly	Thr	Arg	Cys	Ala	Arg
		35				40					45				
Ser	Ala	Ser	Gly	Val	Thr	Arg	Arg	Ser	Pro	Ala	Thr	Ser	Arg	Ser	Gly
	50					55					60				
Ala	Thr	Arg	Pro	Cys	Ser	Cys	Leu	Arg	Ala	Ala	Ser	Arg	Ser	Arg	Ser
65					70					75				80	
Thr	Ser	Cys	Ser	Gly	Thr	Ser	Ala	Thr	Pro	Ala	Ala	Ser	Gly	Ser	
			85					90					95		
Ala	Ser	Lys	Ser	Thr	Ser	Thr	Leu	Val	Ser	Ser	Met	Ile	His	Gln	
		100						105						110	

(2) INFORMATION FOR SEQ ID NO:2156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2156:

attcagccca	tcgctagctc	tcgcgtctcg	cctgtctcct	ctagtagcac	aagaccacga	60
gggattaagc	gatgacaacc	tctaagctcg	ctgtcctcac	tctgtttgcc	ctgctcggct	120
ccgtgtcatg	ccagtccggg	ggctactact	tctacccaac	cccgcagcaa	ccatctccaa	180
cacccagccc	tccttctagt	ccgcaactca	tggtcggata	ctacaaggac	aagtgtgccg	240
cttacgtgga	tgttgaagct	attgtcaaga	agcacgtcaa	ggccaccgat	gctggcatgc	300
aggccggggt	tgtccgtctc	ttattccacg	actgcttcgt	ccgtggatgc	gacggctccg	360
tcctcctcga	cacgttcagc	aacgacacca	gcctgacccc	agagaagttc	ggcgtgccca	420
acttccccag	cctgcggggc	ttcgaggtga	tcgacgcggc	caaggccgag	atcgaggc	

(2) INFORMATION FOR SEQ ID NO:2157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..135
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502408

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2157:

Met	Thr	Thr	Ser	Lys	Leu	Ala	Val	Leu	Thr	Leu	Phe	Ala	Leu	Leu	Gly
1				5					10					15	
Ser	Val	Ser	Cys	Gln	Ser	Gly	Gly	Tyr	Tyr	Phe	Tyr	Pro	Thr	Pro	Gln
			20					25					30		
Gln	Pro	Ser	Pro	Thr	Pro	Ser	Pro	Pro	Ser	Ser	Pro	Gln	Leu	Met	Val
			35				40					45			
Gly	Tyr	Tyr	Lys	Asp	Lys	Cys	Ala	Ala	Tyr	Val	Asp	Val	Glu	Ala	Ile
			50				55				60				
Val	Lys	Lys	His	Val	Lys	Ala	Thr	Asp	Ala	Gly	Met	Gln	Ala	Gly	Leu
65					70					75					80
Val	Arg	Leu	Leu	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys	Asp	Gly	Ser
				85					90					95	
Val	Leu	Leu	Asp	Thr	Phe	Ser	Asn	Asp	Thr	Ser	Leu	Thr	Pro	Glu	Lys
			100					105					110		
Phe	Gly	Val	Pro	Asn	Phe	Pro	Ser	Leu	Arg	Gly	Phe	Glu	Val	Ile	Asp
			115				120						125		
Ala	Ala	Lys	Ala	Glu	Ile	Glu									
			130			135									

(2) INFORMATION FOR SEQ ID NO:2158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..89
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502409

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2158:

Met	Val	Gly	Tyr	Lys	Asp	Lys	Cys	Ala	Ala	Tyr	Val	Asp	Val	Glu
1				5				10					15	
Ala	Ile	Val	Lys	Lys	His	Val	Lys	Ala	Thr	Asp	Ala	Gly	Met	Gln
			20					25				30		
Gly	Leu	Val	Arg	Leu	Leu	Phe	His	Asp	Cys	Phe	Val	Arg	Gly	Cys
			35				40					45		
Gly	Ser	Val	Leu	Leu	Asp	Thr	Phe	Ser	Asn	Asp	Thr	Ser	Leu	Thr
			50				55			60				
Glu	Lys	Phe	Gly	Val	Pro	Asn	Phe	Pro	Ser	Leu	Arg	Gly	Phe	Glu
65					70					75				80
Ile	Asp	Ala	Ala	Lys	Ala	Glu	Ile	Glu						
				85										

(2) INFORMATION FOR SEQ ID NO:2159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..437
(D) OTHER INFORMATION: / Ceres Seq. ID 1502420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2159:

aacccttttcg cctccgccgc cgcctgatag ctccagcgcc ctccgccgtcg gctgcccgggc	60
tgccgctcctc ccgctacgag ctaggcattct ccttcgccga tccagcatgg gtaagacacg	120
tggtatggga gctggggcgca asstcaagac ccacaggagg aaccagaggt ggtgctgaca	180
aagcctacaa gaagagccat cttggcaacg agtgggaagaa accctttgct ggatcatctc	240
acgcaaaggg gatcgctcctc gaaaagatcg gcatcgaggc caagcagcct aactctgcta	300
ttcgtaagtg tgctcgtggt cagctgggtga agaacggtaa gaagattgcc gcctttgtgc	360
cgaacgacgg ctgcttgaac tacatcgagg aaaacgatga ggtgctgac gcgggggttcg	420
gctgtaaggg ccacgct	

(2) INFORMATION FOR SEQ ID NO:2160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..145
(D) OTHER INFORMATION: / Ceres Seq. ID 1502421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2160:

Pro Phe Arg Leu Arg Arg Arg Leu Ile Ala Pro Ala Pro Ser Pro Ser	
1 5 10 15	
Ala Ala Arg Leu Pro Ser Ser Arg Tyr Glu Leu Gly Ile Ser Phe Ala	
20 25 30	
Asp Pro Ala Trp Val Arg His Val Val Trp Glu Leu Gly Ala Xaa Ser	
35 40 45	
Arg Pro Thr Gly Gly Thr Arg Gly Gly Ala Asp Lys Ala Tyr Lys Lys	
50 55 60	
Ser His Leu Gly Asn Glu Trp Lys Lys Pro Phe Ala Gly Ser Ser His	
65 70 75 80	
Ala Lys Gly Ile Val Leu Glu Lys Ile Gly Ile Glu Ala Lys Gln Pro	
85 90 95	
Asn Ser Ala Ile Arg Lys Cys Ala Arg Val Gln Leu Val Lys Asn Gly	
100 105 110	
Lys Lys Ile Ala Ala Phe Val Pro Asn Asp Gly Cys Leu Asn Tyr Ile	
115 120 125	
Glu Glu Asn Asp Glu Val Leu Ile Ala Gly Phe Gly Arg Lys Gly His	
130 135 140	
Ala	
145	

(2) INFORMATION FOR SEQ ID NO:2161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..501
(D) OTHER INFORMATION: / Ceres Seq. ID 1502422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2161:

aaagtgaata cagaaacctc cagccccagg ccaattcctc gaccgcacgc ccacccaccc	60
catctccatg gctacctccg cgacctcacc gcggggaaga aggtgggtgct cttcgccgtg	120
cccggsscgt tcacgcccac ctgcacccag aagcacctcc cggggttcgt ggccaaggcc	180
ggggagctcc gcgccaaggg ctcgacaccg tggcctgcgt ctccgtcaac gacgccttcg	240

tgatgcgcgc gtggaaggag agtctgggga tcggggacga ggtgctgctc ctgtcggacg 300
gcaacggcga gctggcgcgc gcatgggctc gagctcgacc tctccgacaa gcccggtggg 360
tcggcggtccg gtcccgcgcg tacgsgctgc tcgcgaggga cggcgtgggtc aaggtgatca 420
acctcgagga gggcggcgcg ttcaccaaca gcagcgccga ggacatgctc aacgcgctct 480
gaactcgcga cgccatggtt g

(2) INFORMATION FOR SEQ ID NO:2162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1502423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2162:

Lys Val Asn Thr Glu Thr Ser Ser Pro Arg Pro Ile Pro Arg Pro His
1 5 10 15
Arg His Pro Pro His Leu His Gly Tyr Leu Arg Asp Leu Thr Ala Gly
20 25 30
Lys Lys Val Val Leu Phe Ala Val Pro Xaa Xaa Phe Thr Pro Thr Cys
35 40 45
Thr Gln Lys His Leu Pro Gly Phe Val Ala Lys Ala Gly Glu Leu Arg
50 55 60
Ala Lys Gly Ser Thr Pro Trp Pro Ala Ser Pro Ser Thr Thr Pro Ser
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:2163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1502424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2163:

Ser Glu Tyr Arg Asn Leu Gln Pro Gln Ala Asn Ser Ser Thr Ala Ser
1 5 10 15
Pro Pro Thr Pro Ser Pro Trp Leu Pro Pro Arg Pro His Arg Gly Glu
20 25 30
Glu Gly Gly Ala Leu Arg Arg Ala Arg Xaa Val His Ala His Leu His
35 40 45
Pro Glu Ala Pro Pro Gly Val Arg Gly Gln Gly Arg Gly Ala Pro Arg
50 55 60
Gln Gly Leu Asp Thr Val Ala Cys Val Ser Val Asn Asp Ala Phe Val
65 70 75 80
Met Arg Ala Trp Lys Glu Ser Leu Gly Ile Gly Asp Glu Val Leu Leu
85 90 95
Leu Ser Asp Gly Asn Gly Glu Leu Ala Arg Ala Trp Ala Arg Ala Arg
100 105 110
Pro Leu Arg Gln Ala Arg Gly Val Gly Val Arg Ser Arg Arg Tyr Xaa
115 120 125
Leu Leu Ala Glu Asp Gly Val Val Lys Val Ile Asn Leu Glu Glu Gly
130 135 140
Gly Ala Phe Thr Asn Ser Ser Ala Glu Asp Met Leu Asn Ala Leu
145 150 155

(2) INFORMATION FOR SEQ ID NO:2164:

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(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 144 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..144
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502425
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2164:
Met Ala Thr Ser Ala Thr Ser Pro Arg Gly Arg Arg Trp Cys Ser Ser
1      5      10      15
Pro Cys Pro Xaa Arg Ser Arg Pro Pro Ala Pro Arg Ser Thr Ser Arg
      20      25      30
Gly Ser Trp Pro Arg Pro Gly Ser Ala Pro Arg Ala Arg His Arg
      35      40      45
Gly Leu Arg Leu Arg Gln Arg Arg Leu Arg Asp Ala Arg Val Glu Gly
      50      55      60
Glu Ser Gly Asp Arg Gly Arg Gly Ala Ala Pro Val Gly Arg Gln Arg
65      70      75      80
Arg Ala Gly Ala Arg Met Gly Ser Ser Ser Thr Ser Pro Thr Ser Pro
      85      90      95
Trp Gly Arg Arg Pro Val Pro Pro Leu Xaa Ala Ala Arg Gly Gly Arg
      100     105     110
Arg Gly Gln Gly Asp Gln Pro Arg Gly Gly Arg Arg Val His Gln Gln
      115     120     125
Gln Arg Arg Gly His Ala Gln Arg Ala Leu Asn Ser Arg Arg His Gly
      130     135     140

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(2) INFORMATION FOR SEQ ID NO:2165:

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 398 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
    (A) NAME/KEY: -
    (B) LOCATION: 1..398
    (D) OTHER INFORMATION: / Ceres Seq. ID 1502429
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2165:
acgatcacac accactccac agcagtagca agagggatag agcaaggcca cacacacaca      60
caccactagg ctaggttagc cttttagtcg tcgtcgagga gcaagaaggg cgcgcacgca      120
agcaggcaag caagaagaga gccgatcgac cgagagctag cacgcgatgg cgaggtcttc      180
caagatgatg gttgcggcas stctgctggc cctggccctg gccgtgtcga ccgccgaggc      240
gaggaacatc aagacgacga cgacggagaa gaaggacgac gcggtggtgc agccgcagac      300
attccccccc ttgcaccgcc tcggcggcgc gcgtccccgg cgttcggcgg cctccccggc      360
ggcgacattc ctggcagcag cattccggg  ttcaqcat

```

(2) INFORMATION FOR SEQ ID NO:2166:

```
(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 77 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
    (A) NAME/KEY: peptide
    (B) LOCATION: 1..77
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1502430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2166:

Met Ala Arg Ser Ser Lys Met Met Val Ala Ala Xaa Leu Leu Ala Leu
1 5 10 15
Ala Leu Ala Val Ser Thr Ala Glu Ala Arg Asn Ile Lys Thr Thr Thr
20 25 30
Thr Glu Lys Lys Asp Asp Ala Val Val Gln Pro Gln Thr Phe Pro Pro
35 40 45
Phe Asp Arg Leu Gly Gly Ala Arg Pro Arg Arg Ser Ala Ala Ser Pro
50 55 60
Ala Ala Ala Phe Leu Ala Ala Ala Phe Pro Gly Ser Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:2167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1502431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2167:

Met Met Val Ala Ala Xaa Leu Leu Ala Leu Ala Leu Ala Val Ser Thr
1 5 10 15
Ala Glu Ala Arg Asn Ile Lys Thr Thr Thr Glu Lys Lys Asp Asp
20 25 30
Ala Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly
35 40 45
Ala Arg Pro Arg Arg Ser Ala Ala Ser Pro Ala Ala Ala Phe Leu Ala
50 55 60
Ala Ala Phe Pro Gly Ser Ala
65 70

(2) INFORMATION FOR SEQ ID NO:2168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1502432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2168:

Met Val Ala Ala Xaa Leu Leu Ala Leu Ala Leu Ala Val Ser Thr Ala
1 5 10 15
Glu Ala Arg Asn Ile Lys Thr Thr Thr Thr Glu Lys Lys Asp Asp Ala
20 25 30
Val Val Gln Pro Gln Thr Phe Pro Pro Phe Asp Arg Leu Gly Gly Ala
35 40 45
Arg Pro Arg Arg Ser Ala Ala Ser Pro Ala Ala Ala Phe Leu Ala Ala
50 55 60
Ala Phe Pro Gly Ser Ala
65 70

(2) INFORMATION FOR SEQ ID NO:2169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..362
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502441

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2169:

aggttcacgg	gaggcgagga	ccttgcccc	ctgcattcct	ccggtcgctg	gacctccggc	60
acaaccagct	gacggggccc	atcccggcgg	gctgggtgcag	gggcagttcc	ggtcgctggt	120
cctgtcctac	aaccagctca	cgggccccat	cccgcgcgac	gacgcgnanc	gagatcaaca	180
ccgtcgacct	ctcccacaac	aggctcaccg	gcgaccctc	ccacctgttt	cgcgcggcgc	240
cggcccatte	ggcaagggtg	acctgtcgtg	gaactacctc	aacttcgacc	tcagcaggct	300
ggtgttcccg	ccggagctca	cgtacctgga	cctgtcccac	aacctcatcc	gcggcaccgt	360
gc						

(2) INFORMATION FOR SEQ ID NO:2170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2170:

Gly	Ser	Arg	Glu	Ala	Arg	Thr	Leu	Pro	Pro	Cys	Ile	Pro	Pro	Val	Ala	
1			5				10				15					
Gly	Pro	Pro	Ala	Gln	Pro	Ala	Asp	Gly	Pro	His	Pro	Gly	Gly	Leu	Val	
			20				25				30					
Gln	Gly	Gln	Phe	Arg	Ser	Leu	Val	Leu	Ser	Tyr	Asn	Gln	Leu	Thr	Gly	
			35				40				45					
Pro	Ile	Pro	Arg	Asp	Asp	Ala	Xaa	Arg	Asp	Gln	His	Arg	Arg	Pro	Leu	
			50				55				60					
Pro	Gln	Gln	Ala	His	Arg	Arg	Pro	Leu	Pro	Pro	Val	Ser	Pro	Pro	Ala	
			65				70				75				80	
Gly	Pro	Phe	Gly	Lys	Val	Asp	Leu	Ser	Trp	Asn	Tyr	Leu	Asn	Phe	Asp	
			85				90				95					
Leu	Ser	Arg	Leu	Val	Phe	Pro	Pro	Glu	Leu	Thr	Tyr	Leu	Asp	Leu	Ser	
			100				105				110					
His	Asn	Leu	Ile	Arg	Gly	Thr	Val									
			115				120									

(2) INFORMATION FOR SEQ ID NO:2171:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2171:

Val	His	Gly	Arg	Arg	Gly	Pro	Cys	Pro	Pro	Ala	Phe	Leu	Arg	Ser	Leu	
1			5				10				15					
Asp	Leu	Arg	His	Asn	Gln	Leu	Thr	Gly	Pro	Ile	Pro	Ala	Gly	Trp	Cys	
			20				25				30					
Arg	Gly	Ser	Ser	Gly	Arg	Trp	Ser	Cys	Pro	Thr	Thr	Ser	Ser	Arg	Ala	
			35				40				45					
Pro	Ser	Arg	Ala	Thr	Thr	Xaa	Xaa	Glu	Ile	Asn	Thr	Val	Asp	Leu	Ser	

50 55 60
His Asn Arg Leu Thr Gly Asp Pro Ser His Leu Phe Arg Arg Arg Pro
65 70 75 80
Ala His Ser Ala Arg Trp Thr Cys Arg Gly Thr Thr Ser Thr Ser Thr
85 90 95
Ser Ala Gly Trp Cys Ser Arg Arg Ser Ser Arg Thr Trp Thr Cys Pro
100 105 110
Thr Thr Ser Ser Ala Ala Pro Cys
115 120

(2) INFORMATION FOR SEQ ID NO:2172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..396
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2172:

aaaaccctag ccaaccctag tccgccgans stntcgcgcg ccgcacctcc tcccgcgtgcc	60
ccctcctccg gcggcgcat ccacgcgggc cgtctccgcg cgcaaccacg gggggcgcac	120
ggcntgagct ctcgggcccg accccgcgcg tggtggnctg cacctccggc aaggkcggcg	180
tcggaaagas saccaccacc gccaacctcg ccgcctctct cgcgcgcttc ggctcccag	240
ccgtcgccgt cgacgcgat gctggcctcc gcaacctcga cctcctgctc ggctcgcaga	300
accgcgtcca cctcaccgcc gccgacdtcc tcgcgggaga ctgccgactc gaccaggcgc	360
tcgtccgcca ccgcgcgtt ccacgacctc cacctc	

(2) INFORMATION FOR SEQ ID NO:2173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..132
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2173:

Lys Thr Leu Ala Asn Pro Ser Pro Pro Xaa Xaa Ser Arg Ala Ala Pro
1 5 10 15
Pro Pro Ala Ala Pro Ser Ser Gly Gly Ile His Ala Gly Arg Leu
20 25 30
Arg Ala Gln Pro Arg Gly Ala His Gly Xaa Ser Ser Arg Ala Arg Pro
35 40 45
Arg Ala Trp Trp Xaa Ser Pro Pro Ala Arg Xaa Ala Ser Glu Arg Xaa
50 55 60
Pro Pro Pro Pro Thr Ser Pro Pro Leu Ser Arg Ala Ser Ala Ser Gln
65 70 75 80
Pro Ser Pro Ser Thr Pro Met Leu Ala Ser Ala Thr Ser Thr Ser Cys
85 90 95
Ser Ala Ser Arg Thr Ala Ser Thr Ser Pro Pro Pro Xaa Ser Ser Arg
100 105 110
Glu Thr Ala Asp Ser Thr Arg Arg Ser Ser Ala Thr Ala Arg Phe His
115 120 125
Asp Leu His Leu
130

(2) INFORMATION FOR SEQ ID NO:2174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..497
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2174:

caaaggatgt	caagaaggag	gctccaaagg	aggcccccaa	gccaaagggtg	gttgaggcac	60
cagcagaaga	ggaagcacca	aagccaaagc	caaagaatcc	tcttgacttg	ctgccaccaa	120
gcaagatggt	ccttgatgac	tggaagaggc	tatactcaaa	cacaaagact	aacttccggg	180
agggttgccat	caaaggtttc	tgggacatgt	acgaccacga	ggctactctt	tgtggttctg	240
tgactacaag	tacaatgatg	agaacaccgt	ctcctttgtg	accctgaaca	aggttgggtg	300
attcctgcag	cggatggacc	tgtgccgcaa	gtacgccttt	gggaagatgc	tcgtgatagg	360
ctctgagcca	cccttcaagc	tgaagggcct	ttggctcttc	cgtggccagg	atgttcccaa	420
gtttgtaatg	gacgaggtct	atgacatgga	gctctacgag	tgggaccaag	gtggacatct	480
ctgatgaggc	cagaagg					

(2) INFORMATION FOR SEQ ID NO:2175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2175:

Gln	Arg	Met	Ser	Arg	Arg	Arg	Leu	Gln	Arg	Arg	Pro	Pro	Ser	Gln	Arg
1			5					10					15		
Trp	Leu	Arg	His	Gln	Gln	Lys	Arg	Lys	His	Gln	Ser	Gln	Ser	Gln	Arg
			20					25					30		
Ile	Leu	Leu	Thr	Cys	Cys	His	Gln	Ala	Arg	Trp	Ser	Leu	Met	Thr	Gly
			35				40					45			
Arg	Gly	Tyr	Thr	Gln	Thr	Gln	Arg	Leu	Thr	Ser	Gly	Arg	Leu	Pro	Ser
			50			55					60				
Lys	Val	Ser	Gly	Thr	Cys	Thr	Thr	Gln	Arg	Leu	Leu	Phe	Val	Val	Leu
65					70				75						80

(2) INFORMATION FOR SEQ ID NO:2176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..92
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2176:

Lys	Asp	Val	Lys	Lys	Glu	Ala	Pro	Lys	Glu	Ala	Pro	Lys	Pro	Lys	Val
1			5					10					15		
Val	Glu	Ala	Pro	Ala	Glu	Glu	Glu	Ala	Pro	Lys	Pro	Lys	Pro	Lys	Asn
			20					25					30		
Pro	Leu	Asp	Leu	Leu	Pro	Pro	Ser	Lys	Met	Val	Leu	Asp	Asp	Trp	Lys
			35				40					45			
Arg	Leu	Tyr	Ser	Asn	Thr	Lys	Thr	Asn	Phe	Arg	Glu	Val	Ala	Ile	Lys

(2) INFORMATION FOR SEQ ID NO:2177:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1502482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2177:

(2) INFORMATION FOR SEQ ID NO:2178:

(A) LENGTH: 455 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: sing

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g)

(ix) FEATURE:

(A) NAM

(B) LOCATION: 1

(D) OTHER INFORMATION

SEQUENCE DESCRIPTION: SEQ ID NO:2178:

gatgttt tcctattaat ttgacttga tccaaaaggt cg

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino ac

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: lin

MOLECULE TYPE: peptid

FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2179:

Met	Gly	Leu	Leu	Ser	Ile	Ile	Arg	Lys	Ile	Lys	Arg	Lys	Glu	Lys	Glu
1			5				10						15		

Met Arg Ile Leu Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile
20 25 30
Val Leu Lys Ile Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu
35 40 45
Gly Phe Asn Ile Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile
50 55 60
Trp Asp Val Gly Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr
65 70 75 80
Phe Glu Gln Thr Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile
85 90 95
Arg Arg Leu Asp Asp Cys Arg Ala Glu Leu His Asn Leu Leu Lys Glu
100 105 110
Glu Arg Leu Val Gly Ala
115

(2) INFORMATION FOR SEQ ID NO:2180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2180:

Met Arg Ile Leu Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile
1 5 10 15
Val Leu Lys Ile Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu
20 25 30
Gly Phe Asn Ile Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile
35 40 45
Trp Asp Val Gly Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr
50 55 60
Phe Glu Gln Thr Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile
65 70 75 80
Arg Arg Leu Asp Asp Cys Arg Ala Glu Leu His Asn Leu Leu Lys Glu
85 90 95
Glu Arg Leu Val Gly Ala
100

(2) INFORMATION FOR SEQ ID NO:2181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2181:

Met Val Gly Leu Asp Asn Ser Gly Lys Thr Thr Ile Val Leu Lys Ile
1 5 10 15
Asn Gly Glu Asp Thr Ser Val Ile Ser Pro Thr Leu Gly Phe Asn Ile
20 25 30
Lys Thr Ile Lys Tyr His Lys Tyr Ser Leu Asn Ile Trp Asp Val Gly
35 40 45
Gly Gln Lys Thr Ile Arg Ser Tyr Trp Arg Asn Tyr Phe Glu Gln Thr
50 55 60
Asp Gly Leu Val Trp Val Val Asp Ser Ser Asp Ile Arg Arg Leu Asp

(2) INFORMATION FOR SEQ ID NO:2182:

(A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..462
(D) OTHER INFORMATION: / Ceres Seq. ID 1502514

aacatcctaa	tcgaaaaaaa	gctctctgct	tccctctcca	ttttttcatc	tcattcggcg	60
ccgcggcacc	ccctgctcgt	cactcgcgat	ggcccgcatc	aaggtgcacg	agctgcgcgg	120
aaagagcaag	acggatctgc	aagcgmsst	caaggagctt	aaatcggagc	tctccctcct	180
acgcgtcgcc	awggtcaccg	gcggggctcc	caacaagctc	tccaaaatca	agattgtgcg	240
cacctccatc	gctcgcgtgc	tcaccgttat	ctcgcagaag	cagaagtcgg	cgctgcgtga	300
ggcgtacaa	aagaagaagc	ttctcccgt	cgatctccgc	cccaagaaga	cccgcgccat	360
tcgcaggcgc	ctcaccaagc	accagctctc	cttgaaagcc	gagagggaaa	agaagcgtga	420
gaagtatttt	cccatgcqga	agtacgctat	caagqcctag	at		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..130
(D) OTHER INFORMATION: / Ceres Seq. ID 1502515

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1502516

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2184:

```
Met Ala Arg Ile Lys Val His Glu Leu Arg Gly Lys Ser Lys Thr Asp
1          5          10          15
Leu Gln Ala Xaa Xaa Lys Glu Leu Lys Ser Glu Leu Ser Leu Leu Arg
20          25          30
Val Ala Xaa Val Thr Gly Gly Ala Pro Asn Lys Leu Ser Lys Ile Lys
35          40          45
Ile Val Arg Thr Ser Ile Ala Arg Val Leu Thr Val Ile Ser Gln Lys
50          55          60
Gln Lys Ser Ala Leu Arg Glu Ala Tyr Lys Lys Lys Lys Leu Leu Pro
65          70          75          80
Leu Asp Leu Arg Pro Lys Lys Thr Arg Ala Ile Arg Arg Arg Leu Thr
85          90          95
Lys His Gln Leu Ser Leu Lys Thr Glu Arg Glu Lys Lys Arg Glu Lys
100         105         110
Tyr Phe Pro Met Arg Lys Tyr Ala Ile Lys Ala
115         120
```

(2) INFORMATION FOR SEQ ID NO:2185:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..437

(D) OTHER INFORMATION: / Ceres Seq. ID 1502517

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2185:

```
tccattgcag tgcaggaatc ggaaggactg gtacttacat cacaatccat actacaattg      60
agcgaattct tcttgagatg aaaagctctt acgatcttgc caaaactgta aagaatttta      120
gatcccaacg acctgggatg gtccaaacag aggaacaata caagttctgc tacagggcaa      180
ttgctgtacg agctgaaaga cctgctaaat tcagatcatt gaggtgggtc acatgagacg      240
gacagcaacg ckkctagcat ttattacgtt tttttagaca tttctatgtg aaggaacact      300
taccctttag aggagtgaat tagtcaatct cagttctctt taaactatgt ttgttctagt      360
caaaatctat gtaataaaaa atctatcata tgtgaagcta tgctatgttt ttgactaatc      420
gttgctatta ctaccgt
```

(2) INFORMATION FOR SEQ ID NO:2186:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1502518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2186:

```
His Cys Ser Ala Gly Ile Gly Arg Thr Gly Thr Tyr Ile Thr Ile His
1          5          10          15
Thr Thr Ile Glu Arg Ile Leu Leu Gly Asp Lys Ser Ser Tyr Asp Leu
20          25          30
Ala Lys Thr Val Lys Asn Phe Arg Ser Gln Arg Pro Gly Met Val Gln
35          40          45
Thr Glu Glu Gln Tyr Lys Phe Cys Tyr Arg Ala Ile Ala Val Arg Ala
```

(2) INFORMATION FOR SEQ ID NO:2187:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..469
(D) OTHER INFORMATION: / Ceres Seq. ID 1502519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2187:

attctcccag	ccacaaatcg	atcggaaacg	cacgccctt	tctcttcgcc	ttttcgcgtc	60
gtccagatct	cagtcgttct	tcgtcccatg	agctaggaat	ccgaggtgtc	ctctaggcta	120
agcgaagttg	gccggcggcg	gctaggatgg	ggttgatata	cgggatgatg	atgggggtca	180
ttgttggcgt	cgcatacatg	ccggctggag	ccgcgtcatg	cgccgacgca	gcacgaagcg	240
catcgccaag	gctgcggata	tcaaggtgct	tgggtctctc	agcagggacg	acctcaggaa	300
gctgtgcgnt	gataacttcc	cggagtggat	atccttcccg	cagtttgacg	aggttaaattg	360
gttgaaacaag	catctgagca	aactttggcc	ttttgttgta	gaaagtgcga	cagtagtggt	420
taagggaatc	cgttgaaacca	ctgctagatg	attaccqgcc	tccaqqaat		

(2) INFORMATION FOR SEQ ID NO:2188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..72
(D) OTHER INFORMATION: / Ceres Seq. ID 1502520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2188:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..79
(D) OTHER INFORMATION: / Ceres Seq. ID 1502521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2189:

Met	Ala	Gly	Trp	Ser	Arg	Val	Met	Arg	Arg	Arg	Ser	Thr	Lys	Arg	Ile
1				5					10					15	
Ala	Lys	Ala	Ala	Asp	Ile	Lys	Val	Leu	Gly	Ser	Leu	Ser	Arg	Asp	Asp
			20					25					30		

Leu Arg Lys Leu Cys Xaa Asp Asn Phe Pro Glu Trp Ile Ser Phe Pro
35 40 45
Gln Phe Glu Gln Val Lys Trp Leu Asn Lys His Leu Ser Lys Leu Trp
50 55 60
Pro Phe Val Val Glu Ala Ala Thr Val Val Val Lys Gly Ile Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2190:

Met Arg Arg Arg Ser Thr Lys Arg Ile Ala Lys Ala Ala Asp Ile Lys
1 5 10 15
Val Leu Gly Ser Leu Ser Arg Asp Asp Leu Arg Lys Leu Cys Xaa Asp
20 25 30
Asn Phe Pro Glu Trp Ile Ser Phe Pro Gln Phe Glu Gln Val Lys Trp
35 40 45
Leu Asn Lys His Leu Ser Lys Leu Trp Pro Phe Val Val Glu Ala Ala
50 55 60
Thr Val Val Val Lys Gly Ile Arg
65 70

(2) INFORMATION FOR SEQ ID NO:2191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..419
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2191:

atagacagga agattgaatt tccaaatcct aacgaggatt cacgtttcga tatcttgaag	60
atccattcaa gaaaaatgaa cttgatgcgt ggcattgata tgaaaaagat cgcggaaaaag	120
atgaatgggg cctcaggagc tgagctcaag gccgtctgca cagaggctgg aatgtttgct	180
cttcgtgaga gaagggtgca cgttaccagc gaggacttcg agatggcagt ggccaagggtg	240
atgaagaaag acacggagaa gaacatgtcc ctgcgcaass tctggaagtg aggctcgtgc	300
ccacctttca cggcctcccc gaagctagtgc gcagtgcctt catatccata tcttttacca	360
aagcagtggga atggtgtaac ggcattgctct ggacaatgtt atctcaagtt ggcgcgcgcg	

(2) INFORMATION FOR SEQ ID NO:2192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2192:

Ile Asp Arg Lys Ile Glu Phe Pro Asn Pro Asn Glu Asp Ser Arg Phe
1 5 10 15

Asp	Ile	Leu	Lys	Ile	His	Ser	Arg	Lys	Met	Asn	Leu	Met	Arg	Gly	Ile
		20						25					30		
Asp	Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met	Asn	Gly	Ala	Ser	Gly	Ala	Glu
		35					40					45			
Leu	Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala	Leu	Arg	Glu	Arg
		50				55				60					
Arg	Val	His	Val	Thr	Gln	Glu	Asp	Phe	Glu	Met	Ala	Val	Ala	Lys	Val
		65			70				75					80	
Met	Lys	Lys	Asp	Thr	Glu	Lys	Asn	Met	Ser	Leu	Arg	Xaa	Xaa	Trp	Lys
			85					90						95	

(2) INFORMATION FOR SEQ ID NO:2193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1502529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2193:

Met	Asn	Leu	Met	Arg	Gly	Ile	Asp	Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met
1			5					10				15			
Asn	Gly	Ala	Ser	Gly	Ala	Glu	Leu	Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly
		20					25				30				
Met	Phe	Ala	Leu	Arg	Glu	Arg	Arg	Val	His	Val	Thr	Gln	Glu	Asp	Phe
		35				40					45				
Glu	Met	Ala	Val	Ala	Lys	Val	Met	Lys	Lys	Asp	Thr	Glu	Lys	Asn	Met
		50			55					60					
Ser	Leu	Arg	Xaa	Xaa	Trp	Lys									
65			70												

(2) INFORMATION FOR SEQ ID NO:2194:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1502530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2194:

Met	Arg	Gly	Ile	Asp	Leu	Lys	Lys	Ile	Ala	Glu	Lys	Met	Asn	Gly	Ala
1			5					10				15			
Ser	Gly	Ala	Glu	Leu	Lys	Ala	Val	Cys	Thr	Glu	Ala	Gly	Met	Phe	Ala
		20					25				30				
Leu	Arg	Glu	Arg	Arg	Val	His	Val	Thr	Gln	Glu	Asp	Phe	Glu	Met	Ala
		35				40					45				
Val	Ala	Lys	Val	Met	Lys	Lys	Asp	Thr	Glu	Lys	Asn	Met	Ser	Leu	Arg
		50			55					60					
Xaa	Xaa	Trp	Lys												
65															

(2) INFORMATION FOR SEQ ID NO:2195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..511
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502542
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2195:
gcaccgcggc cacagcctcg cgtcgtcgcc ccacagccac gcgagc ssnc gccgatccgc 60
gagcgcagat cgcgaagcca ggcggcgnag agggagctcg aggcggcgga ggaaggcggt 120
cgcacagtcg ctgatttccc tggggaagag atggggctct cctttggtaa gctgttcagc 180
cgccctcttcg ccaagaagga gatgaggatt ctcattggtcg ggctc gatgc cgccggtaag 240
accaccatcc tctacaagct caagctcggc gagatcgtca ccaccatccc cactatcgga 300
ttcaatgttg aaactgttga gtataagaac attagcttca ctgtttggga tgttggtggc 360
caggacaaga tcaggcccct gtggaggcac tactttcaga acacacaggg acttattttt 420
gtttagtaga gcaacgcacag ggaacgtgtt gttgaggcta gagatgagct ccacaggatg 480
ctgaatgagg atgagctgcg tgacgctgtg c
(2) INFORMATION FOR SEQ ID NO:2196:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..170
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502543
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2196:
Ala Pro Arg Pro Gln Pro Arg Val Val Ala Pro Gln Pro Arg Glu Xaa
1 5 10 15
Xaa Pro Ile Arg Glu Arg Arg Ser Arg Ser Gln Ala Ala Xaa Arg Glu
 20 25 30
Leu Glu Ala Ala Glu Glu Gly Val Arg Thr Val Ala Asp Phe Pro Gly
 35 40 45
Glu Glu Met Gly Leu Ser Phe Gly Lys Leu Phe Ser Arg Leu Phe Ala
 50 55 60
Lys Lys Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys
65 70 75 80
Thr Thr Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile
 85 90 95
Pro Thr Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser
 100 105 110
Phe Thr Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp
 115 120 125
Arg His Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser
 130 135 140
Asn Asp Arg Glu Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met
145 150 155 160
Leu Asn Glu Asp Glu Leu Arg Asp Ala Val
 165 170
(2) INFORMATION FOR SEQ ID NO:2197:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..120
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2197:

Met	Gly	Leu	Ser	Phe	Gly	Lys	Leu	Phe	Ser	Arg	Leu	Phe	Ala	Lys	Lys
1				5					10					15	
Glu	Met	Arg	Ile	Leu	Met	Val	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr
			20					25					30		
Ile	Leu	Tyr	Lys	Leu	Lys	Leu	Gly	Glu	Ile	Val	Thr	Thr	Ile	Pro	Thr
		35					40					45			
Ile	Gly	Phe	Asn	Val	Glu	Thr	Val	Glu	Tyr	Lys	Asn	Ile	Ser	Phe	Thr
	50					55					60				
Val	Trp	Asp	Val	Gly	Gly	Gln	Asp	Lys	Ile	Arg	Pro	Leu	Trp	Arg	His
65					70					75					80
Tyr	Phe	Gln	Asn	Thr	Gln	Gly	Leu	Ile	Phe	Val	Val	Asp	Ser	Asn	Asp
			85						90					95	
Arg	Glu	Arg	Val	Val	Glu	Ala	Arg	Asp	Glu	Leu	His	Arg	Met	Leu	Asn
			100					105					110		
Glu	Asp	Glu	Leu	Arg	Asp	Ala	Val								
			115				120								

(2) INFORMATION FOR SEQ ID NO:2198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1502545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2198:

Met	Arg	Ile	Leu	Met	Val	Gly	Leu	Asp	Ala	Ala	Gly	Lys	Thr	Thr	Ile
1				5					10					15	
Leu	Tyr	Lys	Leu	Lys	Leu	Gly	Glu	Ile	Val	Thr	Thr	Ile	Pro	Thr	Ile
			20					25				30			
Gly	Phe	Asn	Val	Glu	Thr	Val	Glu	Tyr	Lys	Asn	Ile	Ser	Phe	Thr	Val
		35					40					45			
Trp	Asp	Val	Gly	Gly	Gln	Asp	Lys	Ile	Arg	Pro	Leu	Trp	Arg	His	Tyr
	50					55					60				
Phe	Gln	Asn	Thr	Gln	Gly	Leu	Ile	Phe	Val	Val	Asp	Ser	Asn	Asp	Arg
65					70					75					80
Glu	Arg	Val	Val	Glu	Ala	Arg	Asp	Glu	Leu	His	Arg	Met	Leu	Asn	Glu
			85					90						95	
Asp	Glu	Leu	Arg	Asp	Ala	Val									
			100												

(2) INFORMATION FOR SEQ ID NO:2199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 488 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..488

(D) OTHER INFORMATION: / Ceres Seq. ID 1502573

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2199:

aggaggagcg	cgccatggag	cgggggcatc	ctgccgctgc	tccgccgcgc	cacgctgggtg	60
cagacgttcg	gccagcgcaa	ccacgtgtgc	ctgcaggacg	gctccatcac	cgccccgccc	120
tacgccgacc	cgggcaagat	gcaggcgcac	ctcatcagcc	ccggcacgcc	gcgctccatc	180
ttcgtctact	tcaggggcct	cttctacgac	atgggcaacg	accccgaggg	cggctactac	240
gccagggggc	tcgcgcgtcg	gtgtggggaga	acttcaagga	caaccgcgtg	ttcgacatct	300
cgacggagca	cccgctcgacg	tactacgagg	acatgcagcg	cgccatcttc	tgctgtgcc	360

cgctgggggtg ggcgccttg agcccccggc tgggtggaggc ggtgggtgttc ggggtgcatcc 420
cogtcatcat cgccgacgac atcgtgctgc cgttcgcgga cgccatcccc tgggaggaca 480
tcagcgtg

(2) INFORMATION FOR SEQ ID NO:2200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1502574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2200:

Arg	Arg	Ser	Ala	Pro	Trp	Ser	Gly	Gly	Ile	Leu	Pro	Leu	Leu	Arg	Arg
1				5					10					15	
Ala	Thr	Leu	Val	Gln	Thr	Phe	Gly	Gln	Arg	Asn	His	Val	Cys	Leu	Gln
			20					25					30		
Asp	Gly	Ser	Ile	Thr	Val	Pro	Pro	Tyr	Ala	Asp	Pro	Gly	Lys	Met	Gln
		35					40					45			
Ala	His	Leu	Ile	Ser	Pro	Gly	Thr	Pro	Arg	Ser	Ile	Phe	Val	Tyr	Phe
	50					55					60				
Arg	Gly	Leu	Phe	Tyr	Asp	Met	Gly	Asn	Asp	Pro	Glu	Gly	Gly	Tyr	Tyr
65					70				75					80	
Ala	Arg	Gly	Leu	Ala	Arg	Arg	Cys	Gly	Arg	Thr	Ser	Arg	Thr	Thr	Arg
			85						90					95	
Cys	Ser	Thr	Ser	Arg	Arg	Ser	Thr	Arg	Arg	Arg	Thr	Thr	Arg	Thr	Cys
			100					105					110		
Ser	Ala	Pro	Ser	Ser	Ala	Cys	Ala	Arg	Trp	Gly	Gly	Arg	Pro	Gly	Ala
		115					120					125			
Pro	Gly	Trp	Trp	Arg	Arg	Trp	Cys	Ser	Gly	Ala	Ser	Pro	Ser	Ser	Ser
	130					135						140			
Pro	Thr	Thr	Ser	Cys	Cys	Arg	Ser	Arg	Thr	Pro	Ser	Pro	Gly	Arg	Thr
145					150					155					160
Ser	Ala														

(2) INFORMATION FOR SEQ ID NO:2201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1502575

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2201:

Gly	Gly	Ala	Arg	His	Gly	Ala	Gly	Ala	Ser	Cys	Arg	Cys	Ser	Ala	Ala
1				5					10					15	
Pro	Arg	Trp	Cys	Arg	Arg	Ser	Ala	Ser	Ala	Thr	Thr	Cys	Ala	Cys	Arg
			20					25					30		
Thr	Ala	Pro	Ser	Pro	Ser	Arg	Pro	Thr	Pro	Thr	Arg	Ala	Arg	Cys	Arg
		35					40					45			
Arg	Thr	Ser	Ser	Ala	Pro	Ala	Arg	Arg	Ala	Pro	Ser	Ser	Ser	Thr	Ser
	50					55					60				
Gly	Ala	Ser	Ser	Thr	Thr	Trp	Ala	Thr	Thr	Pro	Arg	Ala	Ala	Thr	Thr
65					70					75				80	
Pro	Gly	Ala	Ser	Arg	Val	Gly	Val	Gly	Glu	Leu	Gln	Gly	Gln	Pro	Ala
				85					90					95	

Val Arg His Leu Asp Gly Ala Pro Val Asp Val Leu Arg Gly His Ala
100 105 110
Ala Arg His Leu Leu Pro Val Pro Ala Gly Val Gly Ala Leu Glu Pro
115 120 125
Pro Ala Gly Gly Gly Gly Val Arg Val His Pro Arg His His Arg
130 135 140
Arg Arg His Arg Ala Ala Val Arg Gly Arg His Pro Leu Gly Gly His
145 150 155 160
Gln Arg

(2) INFORMATION FOR SEQ ID NO:2202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1502576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2202:

Glu Glu Arg Ala Met Glu Arg Gly His Pro Ala Ala Ala Pro Pro Arg
1 5 10 15
His Ala Gly Ala Asp Val Arg Pro Ala Gln Pro Arg Val Pro Ala Gly
20 25 30
Arg Leu His His Arg Pro Ala Leu Arg Arg Pro Gly Gln Asp Ala Gly
35 40 45
Ala Pro His Gln Pro Arg His Ala Ala Leu His Leu Arg Leu Leu Gln
50 55 60
Gly Pro Leu Leu Arg His Gly Gln Arg Pro Arg Gly Arg Leu Leu Arg
65 70 75 80
Gln Gly Pro Arg Ala Ser Val Trp Glu Asn Phe Lys Asp Asn Pro Leu
85 90 95
Phe Asp Ile Ser Thr Glu His Pro Ser Thr Tyr Tyr Glu Asp Met Gln
100 105 110
Arg Ala Ile Phe Cys Leu Cys Pro Leu Gly Trp Ala Pro Trp Ser Pro
115 120 125
Arg Leu Val Glu Ala Val Val Phe Gly Cys Ile Pro Val Ile Ile Ala
130 135 140
Asp Asp Ile Val Leu Pro Phe Ala Asp Ala Ile Pro Trp Glu Asp Ile
145 150 155 160
Ser Val

(2) INFORMATION FOR SEQ ID NO:2203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 493 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..493

(D) OTHER INFORMATION: / Ceres Seq. ID 1502613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2203:

ctctccgtct cccgtctcca gtctcgctgc ttccacaagt ccacaaccgt accagcacca 60
ccgcgccatg gcgtcctccg ccgatccmga tgccgccacg ccaccatccg cncgcgagcc 120
ggagcccgca cggaaaggcag tccgcgtggt ggtgaagggg cgcgtcacgg gggtgggggt 180
ccgcgactgg actgcgtcac ggccgagtcg ctccggctcg cggtgggtc cgcaaccgcc 240
gtgacggcag tgtggaggcc ctctctccg gagacccgc gaagatcgaa gacatgataa 300

```
ccgcgcgcct cccgcgcgc cccccagccg ccaccgtcac cgccgtcgtc ccgtccackg 360
ccgagcccggt ggtatccgtc caccggcttc ggagatcaag ttcaccgtct gacccccccg 420
tcccgcgaca ggttcgcgtc tcgcccgcgc ggtcttgaac ggtctattcg tgcactacta 480
ctgcgaatct gcg
```

(2) INFORMATION FOR SEQ ID NO:2204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1502614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2204:

```
Leu Ser Val Ser Gly Leu Gln Ser Arg Cys Phe His Lys Ser Thr Thr
1          5          10          15
Val Pro Ala Pro Pro Arg His Gly Val Leu Arg Arg Ser Xaa Cys Arg
          20          25          30
His Ala Thr Ile Arg Xaa Ala Ala Gly Ala Arg Thr Glu Gly Ser Pro
          35          40          45
Arg Gly Gly Glu Gly Ala Arg His Gly Gly Gly Val Pro Arg Leu Asp
          50          55          60
Cys Val Thr Ala Glu Ser Leu Gly Ser Pro Ala Gly Ser Ala Thr Ala
          65          70          75          80
Val Thr Ala Val Trp Arg Pro Ser Ser Pro Glu Thr Pro Arg Arg Ser
          85          90          95
Lys Thr
```

(2) INFORMATION FOR SEQ ID NO:2205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1502615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2205:

```
Ser Pro Ser Pro Val Ser Ser Leu Ala Ala Ser Thr Ser Pro Gln Pro
1          5          10          15
Tyr Gln His His Arg Ala Met Ala Ser Ser Ala Asp Xaa Asp Ala Ala
          20          25          30
Thr Pro Pro Ser Xaa Pro Gln Pro Glu Pro Ala Arg Lys Ala Val Arg
          35          40          45
Val Val Val Lys Gly Arg Val Thr Gly Val Gly Phe Arg Asp Trp Thr
          50          55          60
Ala Ser Arg Pro Ser Arg Ser Ala Arg Arg Leu Gly Pro Gln Pro Pro
          65          70          75          80
```

(2) INFORMATION FOR SEQ ID NO:2206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..58
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2206:

Met Ala Ser Ser Ala Asp Xaa Asp Ala Ala Thr Pro Pro Ser Xaa Pro
1 5 10 15
Gln Pro Glu Pro Ala Arg Lys Ala Val Arg Val Val Val Lys Gly Arg
20 25 30
Val Thr Gly Val Gly Phe Arg Asp Trp Thr Ala Ser Arg Pro Ser Arg
35 40 45
Ser Ala Arg Arg Leu Gly Pro Gln Pro Pro
50 55

(2) INFORMATION FOR SEQ ID NO:2207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..192
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2207:

aagatcaagc caccaccacc gccagcaaga gcagagagggc gagaccgcga gagtgtacgt 60
gccaccagca gcagcagcaa tggccgcccgc cgccaccacc tctcctcct cccacctgct 120
cctcctctcc cgccacagg sscctcccta cgatgccgcc tctccttct cggccagccc 180
agaaggcccg gc

(2) INFORMATION FOR SEQ ID NO:2208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2208:

Lys Ile Lys Pro Pro Pro Pro Ala Arg Ala Glu Arg Arg Asp Arg
1 5 10 15
Glu Ser Val Arg Ala Thr Ser Ser Ser Ser Asn Gly Arg Arg Arg His
20 25 30
His Leu Leu Ile Leu Pro Pro Ala Pro Pro Leu Pro Pro Ala Xaa Xaa
35 40 45
Ser Leu Arg Cys Arg Leu Ser Phe Leu Gly Gln Pro Arg Arg Pro Gly
50 55 60

(2) INFORMATION FOR SEQ ID NO:2209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1502623

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2209:

Arg Ser Ser His His His Arg Gln Gln Glu Gln Arg Gly Glu Thr Ala
1 5 10 15
Arg Val Tyr Val Pro Pro Ala Ala Ala Met Ala Ala Ala Thr
20 25 30
Thr Ser Ser Ser Ser His Leu Leu Leu Leu Ser Arg Gln Gln Xaa Pro
35 40 45
Pro Tyr Asp Ala Ala Ser Pro Ser Ser Ala Ser Pro Glu Gly Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:2210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1502624

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2210:

Asp Gln Ala Thr Thr Thr Ala Ser Lys Ser Arg Glu Ala Arg Pro Arg
1 5 10 15
Glu Cys Thr Cys His Gln Gln Gln Gln Gln Trp Pro Pro Pro Pro Pro
20 25 30
Pro Pro His Pro Pro Thr Cys Ser Ser Pro Ala Ser Arg Xaa Leu
35 40 45
Pro Thr Met Pro Pro Leu Leu Pro Arg Pro Ala Gln Lys Ala Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO:2211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..327

(D) OTHER INFORMATION: / Ceres Seq. ID 1502635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2211:

agtgttggtgt cctagcgccg ccgcccgcctt gcgtgactga aagctcgctg	60
gcttccgctcc acgcgagaag cgagagcatg gacaccagg tgaagcttg tgttggtggtg	120
aaggtgatgg gcaggaccgg ctccaggggt caggbgacct aggtcagagt taagttcttg	180
gatgaccaga accggctcat catgaggaat gtcaaggggc ccgtccgcga gggtgacatc	240
ctcaccctgc tcgagtcga gatggatgcc akgaggctgc gctgaagccc tagcgttctt	300
ggtcattccaa gaacttaact ctgacct	

(2) INFORMATION FOR SEQ ID NO:2212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1502636

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2212:

Met Asp Thr Gln Val Lys Leu Ala Val Val Val Lys Val Met Gly Arg

1 5 10 15
Thr Gly Ser Arg Gly Gln Xaa Thr Gln Val Arg Val Lys Phe Leu Asp
20 25 30
Asp Gln Asn Arg Leu Ile Met Arg Asn Val Lys Gly Pro Val Arg Glu
35 40 45
Gly Asp Ile Leu Thr Leu Leu Glu Ser Glu Met Asp Ala Xaa Arg Leu
50 55 60

Arg
65

(2) INFORMATION FOR SEQ ID NO:2213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502637

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2213:

Met Gly Arg Thr Gly Ser Arg Gly Gln Xaa Thr Gln Val Arg Val Lys
1 5 10 15
Phe Leu Asp Asp Gln Asn Arg Leu Ile Met Arg Asn Val Lys Gly Pro
20 25 30
Val Arg Glu Gly Asp Ile Leu Thr Leu Leu Glu Ser Glu Met Asp Ala
35 40 45
Xaa Arg Leu Arg
50

(2) INFORMATION FOR SEQ ID NO:2214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..39
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2214:

Met Ser Arg Gly Pro Ser Ala Arg Val Thr Ser Ser Pro Cys Ser Ser
1 5 10 15
Pro Arg Trp Met Pro Xaa Gly Cys Ala Glu Ala Leu Ala Phe Leu Val
20 25 30
Ile Gln Glu Leu Asn Ser Asp
35

(2) INFORMATION FOR SEQ ID NO:2215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..454
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502643

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2215:

gctgttgcaa attacgttcc ctctagtctc tactctagcc ccctctctct ctcacacaca 60
cacacacccc tatcacttgg actgtgctag tataggtagc cgccgtgtaa tggagcagga 120

gctcagcctt gagctcaccc tcttcacccc ctcggtctcg ccggaaccgc cgggctattt 180
cgtctgcacg tactgcgacc gcaagttctt cacctcgcag gctctcgggtg gccaccagaa 240
cgcgcacaaag tacgagcgcm ssctggccaa gcgccggcgg agatcgccac cgccctgcgc 300
gcgcacgggg cggccgccac cgccacgggc gtccaggacg cgccgctatg ggctctcgcg 360
atgtccccgc cagccccaaag gcacgggtag cggtgccgac aagagcgcaa caaggatgga 420
taagcacaag gcgcctgctg atgatgccgc tccc

(2) INFORMATION FOR SEQ ID NO:2216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1502644

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2216:

Leu Leu Gln Ile Thr Phe Pro Leu Val Ser Thr Leu Ala Pro Ser Leu
1 5 10 15
Ser His Thr His Thr His Pro Tyr His Leu Asp Cys Ala Ser Ile Gly
20 25 30
Ser Arg Arg Val Met Glu Gln Glu Leu Ser Leu Glu Leu Thr Leu Phe
35 40 45
His Pro Ser Val Ser Pro Glu Pro Pro Gly Tyr Phe Val Cys Thr Tyr
50 55 60
Cys Asp Arg Lys Phe Phe Thr Ser Gln Ala Leu Gly Gly His Gln Asn
65 70 75 80
Ala His Lys Tyr Glu Arg Xaa Leu Ala Lys Arg Arg Arg Arg Ser Pro
85 90 95
Pro Pro Cys Ala Arg Thr Gly Arg Pro Pro Pro Arg Ala Ser Arg
100 105 110
Thr Arg Arg Tyr Gly Leu Ser Arg Cys Pro Arg Gln Pro Gln Gly Thr
115 120 125
Gly Ser Gly Ala Asp Lys Ser Ala Thr Arg Met Asp Lys His Lys Ala
130 135 140
Pro Ala Asp Asp Ala Ala Pro
145 150

(2) INFORMATION FOR SEQ ID NO:2217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1502645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2217:

Met Glu Gln Glu Leu Ser Leu Glu Leu Thr Leu Phe His Pro Ser Val
1 5 10 15
Ser Pro Glu Pro Pro Gly Tyr Phe Val Cys Thr Tyr Cys Asp Arg Lys
20 25 30
Phe Phe Thr Ser Gln Ala Leu Gly Gly His Gln Asn Ala His Lys Tyr
35 40 45
Glu Arg Xaa Leu Ala Lys Arg Arg Arg Arg Ser Pro Pro Pro Cys Ala
50 55 60
Arg Thr Gly Arg Pro Pro Pro Arg Ala Ser Arg Thr Arg Arg Tyr
65 70 75 80
Gly Leu Ser Arg Cys Pro Arg Gln Pro Gln Gly Thr Gly Ser Gly Ala

85 90 95
Asp Lys Ser Ala Thr Arg Met Asp Lys His Lys Ala Pro Ala Asp Asp
100 105 110
Ala Ala Pro
115

(2) INFORMATION FOR SEQ ID NO:2218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..451
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2218:

atcagcagac	caccacccaa	tcacaccagc	tctctctaga	gctagccctc	tcttcctcca	60
acacttggtg	atccccctcc	atctcctcaa	gccttcttca	ctgaatttct	ggccgggtcg	120
tcgtcatgca	cagctacaga	gccatgcacc	cgtacactca	tcactcgtac	cagcaccaca	180
ccgcggccgn	gcgcccacca	agcacggcca	cggccacgga	catggacatg	gccatggcga	240
cgaggaggac	gaccagtcac	gctgctcctc	tccctctggc	ctcctggcac	caccacggca	300
acgcgctgct	tcacgcggcg	gctcgtctcc	cccgatctgc	gccassgcca	ccaccacctc	360
tatggcagcc	gctgcctcct	cccccgcttc	ttacccttgg	gctcaccacc	caaagccttt	420
acaataatgc	cggtgcggc	ggtaggggag	c			

(2) INFORMATION FOR SEQ ID NO:2219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2219:

Ser	Ala	Asp	His	His	Pro	Ile	Thr	Pro	Ala	Leu	Ser	Arg	Ala	Ser	Pro
1			5					10						15	
Leu	Phe	Leu	Gln	His	Leu	Leu	Ile	Pro	Ser	His	Leu	Leu	Lys	Pro	Ser
			20					25					30		
Ser	Leu	Asn	Phe	Trp	Pro	Val	Asp	Arg	His	Ala	Gln	Leu	Gln	Ser	His
		35					40					45			
Ala	Pro	Val	His	Ser	Ser	Leu	Val	Pro	Ala	Pro	His	Arg	Gly	Xaa	Ala
	50					55					60				
Pro	Thr	Lys	His	Gly	His	Gly	His	Gly	His	Gly	His	Gly	His	Gly	Asp
65					70				75					80	
Glu	Glu	Asp	Asp	Gln	Ser	Cys	Cys	Ser	Ser	Pro	Ser	Gly	Leu	Leu	Ala
			85					90					95		
Pro	Pro	Arg	Gln	Arg	Ala	Ala	Ser	Ser	Ala	Cys	Ser	Ser	Pro	Pro	Ile
		100					105						110		
Cys	Ala	Xaa	Ala	Thr	Thr	Thr	Ser	Met	Ala	Ala	Ala	Ala	Ser	Ser	Pro
	115					120						125			
Ala	Ser	Tyr	Pro	Trp	Ala	His	Pro	Pro	Lys	Pro	Leu	Gln			
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:2220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1502651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2220:

```
Met His Ser Tyr Arg Ala Met His Pro Tyr Thr His His Ser Tyr Gln
1          5          10          15
His His Thr Ala Ala Xaa Arg Pro Pro Ser Thr Ala Thr Ala Thr Asp
20          25          30
Met Asp Met Ala Met Ala Thr Arg Arg Thr Thr Ser His Ala Ala Pro
35          40          45
Leu Pro Leu Ala Ser Trp His His His Gly Asn Ala Leu Leu His Arg
50          55          60
Arg Ala Arg Leu Pro Arg Ser Ala Pro Xaa Pro Pro Pro Pro Leu Trp
65          70          75          80
Gln Pro Leu Pro Pro Pro Leu Leu Thr Leu Gly Leu Thr His Gln
85          90          95
Ser Leu Tyr Asn Asn Ala Gly Cys Gly Gly Arg Gly
100          105
```

(2) INFORMATION FOR SEQ ID NO:2221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1502652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2221:

```
Met His Pro Tyr Thr His His Ser Tyr Gln His His Thr Ala Ala Xaa
1          5          10          15
Arg Pro Pro Ser Thr Ala Thr Ala Thr Asp Met Asp Met Ala Met Ala
20          25          30
Thr Arg Arg Thr Thr Ser His Ala Ala Pro Leu Pro Leu Ala Ser Trp
35          40          45
His His His Gly Asn Ala Leu Leu His Arg Arg Ala Arg Leu Pro Arg
50          55          60
Ser Ala Pro Xaa Pro Pro Pro Pro Leu Trp Gln Pro Leu Pro Pro Pro
65          70          75          80
Pro Leu Leu Thr Leu Gly Leu Thr His Gln Ser Leu Tyr Asn Asn Ala
85          90          95
Gly Cys Gly Gly Arg Gly
100
```

(2) INFORMATION FOR SEQ ID NO:2222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 443 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..443

(D) OTHER INFORMATION: / Ceres Seq. ID 1502653

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2222:

```
ggggaggtag tggatatcaa ggggtgataat ccagatgctg ttgttcctgg tctaattggct      60
gctggtgaag casstgtgca tctgttcattg gtgcgaatag gctaggcgca aattcgcttc      120
ttgacatagt tgtttttggc agagcttctg caaacagggt agcagatatt tctaaaccag      180
```

gtgagaagca gaaacctctg gaaaaagatg ctggagaaaa gaccatagcc tgggttgaca 240
agctgaggaa tgcgaatggg tcattgccaa cttccaagat ccgtctcaac atgcagcgtg 300
ttatgcaaaa taatgctgct gtattccgta cacaagaata cacttgaaga aggttgtgag 360
ctgattagca aaacatggga aagttttcca tgatgtgaag ctcagttgac cggagtctca 420
tttggaaactc tgacctgata gag

(2) INFORMATION FOR SEQ ID NO:2223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..34

(D) OTHER INFORMATION: / Ceres Seq. ID 1502654

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2223:

Gly Glu Val Val Asp Ile Lys Gly Asp Asn Pro Asp Ala Val Val Pro
1 5 10 15
Gly Leu Met Ala Ala Gly Glu Ala Xaa Val His Leu Phe Met Val Arg
20 25 30
Ile Gly

(2) INFORMATION FOR SEQ ID NO:2224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1502655

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2224:

Met Arg Met Gly His Cys Gln Leu Pro Arg Ser Val Ser Thr Cys Ser
1 5 10 15
Val Leu Cys Lys Ile Met Leu Leu Tyr Ser Val His Lys Asn Thr Leu
20 25 30
Glu Glu Gly Cys Glu Leu Ile Ser Lys Thr Trp Glu Ser Phe Pro
35 40 45

(2) INFORMATION FOR SEQ ID NO:2225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1502656

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2225:

Met Gly His Cys Gln Leu Pro Arg Ser Val Ser Thr Cys Ser Val Leu
1 5 10 15
Cys Lys Ile Met Leu Leu Tyr Ser Val His Lys Asn Thr Leu Glu Glu
20 25 30
Gly Cys Glu Leu Ile Ser Lys Thr Trp Glu Ser Phe Pro
35 40 45

(2) INFORMATION FOR SEQ ID NO:2226:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..386
(D) OTHER INFORMATION: / Ceres Seq. ID 1502682
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2226:
ttccccctcc ctctgccaat ctggccagct agccagccca gtccccacgc ccatcccatc 60
ccatctaaaa actgcatcga atcctcgccg ccgcaccgct agactcagcc gacgssatgc 120
cgccgccc aa ctccgctccc cgctcgccg ttcccgcaat ggcccgatcc cagaccaga 180
cccagtccca gggagacctc gacttcccgt cctcatctc cgacctcacc tccctgctcc 240
tccactcccc cgccagcgcc ggcgcgggtg gctccggacc cgtcttctcc tcctcctccc 300
tttccatccc cactcccaaa cccaagccga accccagtcc cacatcagca gcgccgccga 360
ccccgctggc gcgcgcggcc atcggg
(2) INFORMATION FOR SEQ ID NO:2227:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..128
(D) OTHER INFORMATION: / Ceres Seq. ID 1502683
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2227:
Ser Pro Ser Leu Cys Gln Ser Gly Gln Leu Ala Ser Pro Val Pro Thr
1 5 10 15
Pro Ile Pro Ser His Leu Lys Thr Ala Ser Asn Pro Arg Arg Arg Thr
20 25 30
Ala Arg Leu Ser Arg Xaa Xaa Ala Ala Ala Gln Leu Arg Ser Pro Pro
35 40 45
Arg Ala Ser Arg Asn Gly Pro Ile Pro Asp Pro Asp Pro Val Pro Gly
50 55 60
Arg Pro Arg Leu Pro Val Pro His Leu Arg Pro His Leu Pro Ala Pro
65 70 75 80
Pro Leu Pro Arg Gln Arg Arg Arg Arg Trp Leu Arg Thr Arg Leu Leu
85 90 95
Leu Leu Leu Pro Phe His Pro His Ser Gln Thr Gln Ala Glu Pro Gln
100 105 110
Ser His Ile Ser Ser Ala Ala Asp Pro Ala Gly Ala Arg Gly His Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:2228:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..90
(D) OTHER INFORMATION: / Ceres Seq. ID 1502684
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2228:
Met Pro Pro Pro Asn Ser Ala Pro Arg Leu Ala Leu Pro Ala Met Ala
1 5 10 15

Arg Ser Gln Thr Gln Thr Gln Ser Gln Gly Asp Leu Asp Phe Pro Ser
20 25 30
Leu Ile Ser Asp Leu Thr Ser Leu Leu Leu His Ser Pro Ala Ser Ala
35 40 45
Gly Ala Gly Gly Ser Gly Pro Val Phe Ser Ser Ser Ser Leu Ser Ile
50 55 60
Pro Thr Pro Lys Pro Lys Pro Asn Pro Ser Pro Thr Ser Ala Ala Pro
65 70 75 80
Pro Thr Pro Leu Ala Arg Ala Ala Ile Gly
85 90

(2) INFORMATION FOR SEQ ID NO:2229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1502685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2229:

Met Ala Arg Ser Gln Thr Gln Thr Gln Ser Gln Gly Asp Leu Asp Phe
1 5 10 15
Pro Ser Leu Ile Ser Asp Leu Thr Ser Leu Leu Leu His Ser Pro Ala
20 25 30
Ser Ala Gly Ala Gly Gly Ser Gly Pro Val Phe Ser Ser Ser Ser Leu
35 40 45
Ser Ile Pro Thr Pro Lys Pro Lys Pro Asn Pro Ser Pro Thr Ser Ala
50 55 60
Ala Pro Pro Thr Pro Leu Ala Arg Ala Ala Ile Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:2230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..491

(D) OTHER INFORMATION: / Ceres Seq. ID 1502713

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2230:

ttgatgatga	ggagaggccc	tatttaccta	agcacattct	ctacaggcaa	aaggaacagt	60
tcagtgatgg	tggtgggtat	agttggatcg	atggattgaa	ggaccatgcc	agccaacatg	120
tctccgattc	catgatgatg	aatgctggct	ttgtttaccc	agagaacaca	cccacaacaa	180
aagaagggta	ctactacaga	atgatattcg	agaaattcct	tcccaagcct	gcagcaagggt	240
caactgttcc	tggaggtcct	agtgtggcct	gcagcactgc	caaagctggt	gaatgggatg	300
catcctggtc	caagaacctt	gacccctctg	ggcgtgctgc	tttgggtggt	cacgatgctg	360
cgtatgaaga	cactgcaggg	gaaactcctg	cctctgctga	tcctgtctca	gacaagggcc	420
ttcgtccagc	tattggcgaa	asstagggac	accggttgct	tcagccacag	ctgtctaacc	480
ttatgtttat	c					

(2) INFORMATION FOR SEQ ID NO:2231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2231:

Asp Asp Glu Glu Arg Pro Tyr Leu Pro Lys His Ile Leu Tyr Arg Gln
1 5 10 15
Lys Glu Gln Phe Ser Asp Gly Val Gly Tyr Ser Trp Ile Asp Gly Leu
20 25 30
Lys Asp His Ala Ser Gln His Val Ser Asp Ser Met Met Met Asn Ala
35 40 45
Gly Phe Val Tyr Pro Glu Asn Thr Pro Thr Thr Lys Glu Gly Tyr Tyr
50 55 60
Tyr Arg Met Ile Phe Glu Lys Phe Phe Pro Lys Pro Ala Ala Arg Ser
65 70 75 80
Thr Val Pro Gly Gly Pro Ser Val Ala Cys Ser Thr Ala Lys Ala Val
85 90 95
Glu Trp Asp Ala Ser Trp Ser Lys Asn Leu Asp Pro Ser Gly Arg Ala
100 105 110
Ala Leu Gly Val His Asp Ala Ala Tyr Glu Asp Thr Ala Gly Glu Thr
115 120 125
Pro Ala Ser Ala Asp Pro Val Ser Asp Lys Gly Leu Arg Pro Ala Ile
130 135 140
Gly Glu Xaa
145

(2) INFORMATION FOR SEQ ID NO:2232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1502715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2232:

Met Met Met Asn Ala Gly Phe Val Tyr Pro Glu Asn Thr Pro Thr Thr
1 5 10 15
Lys Glu Gly Tyr Tyr Tyr Arg Met Ile Phe Glu Lys Phe Phe Pro Lys
20 25 30
Pro Ala Ala Arg Ser Thr Val Pro Gly Gly Pro Ser Val Ala Cys Ser
35 40 45
Thr Ala Lys Ala Val Glu Trp Asp Ala Ser Trp Ser Lys Asn Leu Asp
50 55 60
Pro Ser Gly Arg Ala Ala Leu Gly Val His Asp Ala Ala Tyr Glu Asp
65 70 75 80
Thr Ala Gly Glu Thr Pro Ala Ser Ala Asp Pro Val Ser Asp Lys Gly
85 90 95
Leu Arg Pro Ala Ile Gly Glu Xaa
100

(2) INFORMATION FOR SEQ ID NO:2233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1502716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2233:

```
Met Met Asn Ala Gly Phe Val Tyr Pro Glu Asn Thr Pro Thr Thr Lys
1          5          10          15
Glu Gly Tyr Tyr Tyr Arg Met Ile Phe Glu Lys Phe Phe Pro Lys Pro
20          25          30
Ala Ala Arg Ser Thr Val Pro Gly Gly Pro Ser Val Ala Cys Ser Thr
35          40          45
Ala Lys Ala Val Glu Trp Asp Ala Ser Trp Ser Lys Asn Leu Asp Pro
50          55          60
Ser Gly Arg Ala Ala Leu Gly Val His Asp Ala Ala Tyr Glu Asp Thr
65          70          75          80
Ala Gly Glu Thr Pro Ala Ser Ala Asp Pro Val Ser Asp Lys Gly Leu
85          90          95
Arg Pro Ala Ile Gly Glu Xaa
100
```

(2) INFORMATION FOR SEQ ID NO:2234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..384
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2234:

```
atcatctaca ccgccgaggc gccgacaacc acttggcgac catgagcacg ggcacggacg      60
ccgtccggtc gccgtggssc cggcgaassc ccgcccatca acaagtacgc cttcgccctgc      120
gccctgctcg cctccatgaa ctccgtcctc ctccggtatg acatctcggg gatgagcggc      180
gcgcasstgt ttcatgaagg aggacctcaa gatcacggac acgctagatc gagatcctcg      240
ccggcgtcac caacatctac tcgctcttcg gmtccctcgc cgcgggcytc acctccgamt      300
ggytcggccg ccgctacacc atggtgctgg cggccgccat cttcttcacg ggcgcgctcc      360
tcatgggcct cgcccgggac tacg
```

(2) INFORMATION FOR SEQ ID NO:2235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2235:

```
Met Asn Ser Val Leu Leu Gly Tyr Asp Ile Ser Val Met Ser Gly Ala
1          5          10          15
Xaa Xaa Phe His Glu Gly Gly Pro Gln Asp His Gly His Ala Arg Ser
20          25          30
Arg Ser Ser Pro Ala Ser Ser Thr Ser Thr Arg Ser Ser Xaa Pro Ser
35          40          45
Pro Arg Xaa Ser Pro Pro Xaa Xaa Ser Ala Ala Ala Thr Pro Trp Cys
50          55          60
Trp Arg Pro Pro Ser Ser Arg Ala Arg Ser Ser Trp Ala Ser Pro
65          70          75          80
Gly Thr Thr
```

(2) INFORMATION FOR SEQ ID NO:2236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..71
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502719
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2236:

Met Ser Gly Ala Xaa Xaa Phe His Glu Gly Gly Pro Gln Asp His Gly
1 5 10 15
His Ala Arg Ser Arg Ser Ser Pro Ala Ser Ser Thr Ser Thr Arg Ser
20 25 30
Ser Xaa Pro Ser Pro Arg Xaa Ser Pro Pro Xaa Xaa Ser Ala Ala Ala
35 40 45
Thr Pro Trp Cys Trp Arg Pro Ser Ser Ser Arg Ala Arg Ser Ser
50 55 60
Trp Ala Ser Pro Gly Thr Thr
65 70

- (2) INFORMATION FOR SEQ ID NO:2237:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..63
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502720
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2237:

Met Lys Glu Asp Leu Lys Ile Thr Asp Thr Leu Asp Arg Asp Pro Arg
1 5 10 15
Arg Arg His Gln His Leu Leu Ala Leu Arg Xaa Pro Arg Arg Gly Xaa
20 25 30
His Leu Arg Xaa Xaa Arg Pro Pro Leu His His Gly Ala Gly Gly Arg
35 40 45
His Leu Leu His Gly Arg Ala Pro His Gly Pro Arg Pro Gly Leu
50 55 60

- (2) INFORMATION FOR SEQ ID NO:2238:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 484 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..484
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502721
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2238:

tatgcaatca gagagaacat tgagaaggat attgagaggg aaaggcggag aaaggacaac 60
cctgaggcga tggaggaaga tgaagtggat gagatcgccg agatcagggc ccctcacttc 120
gaggagtcca tgaagtatgc tcggcgtagt gtcagtgatg ctgatatccg caagtaccag 180
gcgtttgccc agactttgca gcagtcgccg gggtttgcca gtgagttccg cttctcgat 240
cagccggcga casstggtgc tgctgctgca sscgatccgt ttgcttctgc ggggtgctgcg 300
gctgatgacg acgatctata cagctagttg gggtgctcaa tatcagtcgc gtcactcatc 360
tgtttaaaac tgatcatact aaacacgcat gtcatgcaat gatatttatt tgccgtacat 420
ttggacgtcg ctgagatgat gcaactctcg ccttcggtta ccttttcatg ccatattctc 480
catg

- (2) INFORMATION FOR SEQ ID NO:2239:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..108
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502722
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2239:
Tyr Ala Ile Arg Glu Asn Ile Glu Lys Asp Ile Glu Arg Glu Arg Arg
1 5 10 15
Arg Lys Asp Asn Pro Glu Ala Met Glu Glu Asp Glu Val Asp Glu Ile
 20 25 30
Ala Glu Ile Arg Ala Pro His Phe Glu Glu Ser Met Lys Tyr Ala Arg
 35 40 45
Arg Ser Val Ser Asp Ala Asp Ile Arg Lys Tyr Gln Ala Phe Ala Gln
 50 55 60
Thr Leu Gln Gln Ser Arg Gly Phe Gly Ser Glu Phe Arg Phe Ser Asp
65 70 75 80
Gln Pro Ala Thr Xaa Gly Ala Ala Ala Ala Xaa Asp Pro Phe Ala Ser
 85 90 95
Ala Gly Ala Ala Ala Asp Asp Asp Asp Leu Tyr Ser
 100 105

(2) INFORMATION FOR SEQ ID NO:2240:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..85
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502723
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2240:
Met Glu Glu Asp Glu Val Asp Glu Ile Ala Glu Ile Arg Ala Pro His
1 5 10 15
Phe Glu Glu Ser Met Lys Tyr Ala Arg Arg Ser Val Ser Asp Ala Asp
 20 25 30
Ile Arg Lys Tyr Gln Ala Phe Ala Gln Thr Leu Gln Gln Ser Arg Gly
 35 40 45
Phe Gly Ser Glu Phe Arg Phe Ser Asp Gln Pro Ala Thr Xaa Gly Ala
 50 55 60
Ala Ala Ala Xaa Asp Pro Phe Ala Ser Ala Gly Ala Ala Ala Asp Asp
65 70 75 80
Asp Asp Leu Tyr Ser
 85

(2) INFORMATION FOR SEQ ID NO:2241:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..76
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502724
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2241:

Met Leu Gly Val Val Ser Val Met Leu Ile Ser Ala Ser Thr Arg Arg
1 5 10 15
Leu Pro Arg Leu Cys Ser Ser Pro Gly Gly Leu Ala Val Ser Ser Ala
20 25 30
Ser Arg Ile Ser Arg Arg Xaa Xaa Val Leu Leu Leu Xaa Xaa Ile Arg
35 40 45
Leu Leu Leu Arg Val Leu Arg Leu Met Thr Thr Ile Tyr Thr Ala Ser
50 55 60
Trp Val Ala Gln Tyr Gln Ser Arg His Ser Ser Val
65 70 75

(2) INFORMATION FOR SEQ ID NO:2242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..309
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2242:

gaagcgagcc aaccagcca tggagaagcg gatcgatcg cagcggtcc tctggcgca	60
cctcctcccc tccccctccg ccgcctcctc gcagcctcag cttgcggcgt cggcgtgcgc	120
ggccggggac agcgccgcct accagagggtc ctcctccttc ggggacgatg tctgctgctg	180
cgctgcctac aggacgccga tatgcaagcg caagcgagga ggcttcaagg acacctaccc	240
agaggacctc ctactgttg ttctcaagcg tgttctggac aacactagaa tcaatccagc	300
tgacatcgg	

(2) INFORMATION FOR SEQ ID NO:2243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502727

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2243:

Lys Arg Ala Asn Pro Ala Met Glu Lys Ala Ile Asp Arg Gln Arg Val
1 5 10 15
Leu Leu Ala His Leu Leu Pro Ser Pro Ser Ala Ala Ser Ser Gln Pro
20 25 30
Gln Leu Ala Ala Ser Ala Cys Ala Ala Gly Asp Ser Ala Ala Tyr Gln
35 40 45
Arg Ser Ser Ser Phe Gly Asp Asp Val Val Val Val Ala Ala Tyr Arg
50 55 60
Thr Pro Ile Cys Lys Ala Lys Arg Gly Gly Phe Lys Asp Thr Tyr Pro
65 70 75 80
Glu Asp Leu Leu Thr Val Val Leu Lys Ala Val Leu Asp Asn Thr Arg
85 90 95
Ile Asn Pro Ala Asp Ile
100

(2) INFORMATION FOR SEQ ID NO:2244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..102
(D) OTHER INFORMATION: / Ceres Seq. ID 1502728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2244:

```
Ser Glu Pro Thr Gln Pro Trp Arg Arg Ser Ile Gly Ser Gly Ser
1          5          10          15
Ser Trp Arg Thr Ser Ser Pro Pro Pro Pro Pro Pro Pro Arg Ser Leu
20          25          30
Ser Leu Arg Arg Arg Arg Ala Arg Pro Gly Thr Ala Pro Thr Arg
35          40          45
Gly Pro Pro Pro Ser Gly Thr Met Ser Ser Ser Ser Leu Pro Thr Gly
50          55          60
Arg Arg Tyr Ala Arg Pro Ser Glu Glu Ala Ser Arg Thr Pro Thr Gln
65          70          75          80
Arg Thr Ser Ser Leu Leu Phe Ser Arg Leu Phe Trp Thr Thr Leu Glu
85          90          95
Ser Ile Gln Leu Thr Ser
100
```

(2) INFORMATION FOR SEQ ID NO:2245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..96
(D) OTHER INFORMATION: / Ceres Seq. ID 1502729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2245:

```
Met Glu Lys Ala Ile Asp Arg Gln Arg Val Leu Leu Ala His Leu Leu
1          5          10          15
Pro Ser Pro Ser Ala Ala Ser Ser Gln Pro Gln Leu Ala Ala Ser Ala
20          25          30
Cys Ala Ala Gly Asp Ser Ala Ala Tyr Gln Arg Ser Ser Ser Phe Gly
35          40          45
Asp Asp Val Val Val Val Ala Ala Tyr Arg Thr Pro Ile Cys Lys Ala
50          55          60
Lys Arg Gly Gly Phe Lys Asp Thr Tyr Pro Glu Asp Leu Leu Thr Val
65          70          75          80
Val Leu Lys Ala Val Leu Asp Asn Thr Arg Ile Asn Pro Ala Asp Ile
85          90          95
```

(2) INFORMATION FOR SEQ ID NO:2246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..496
(D) OTHER INFORMATION: / Ceres Seq. ID 1502730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2246:

```
gagaatcgag cagagccacc gatcgctcct gagcactttc cacattccag ttccactccg      60
cctccgctgc cggtcgccgt ctccgagact ccgacagtcc gaccgcaaga aggatgagtg      120
aagaggataa gactgctgct tctgctgagc agccgaagag ggcccctaag ctcaatgaaa      180
ggatcctctc ttctctgtcc aggaggtccg tagctgctca tccatggcat gatcttgaga      240
```

tcggtcctga tgctcctgct gttttcaatg ttgtaagtac cagcattacc ttagaaccgt 300
ttgatgtggt atatgttcgg tgctgtgggg acttaggttg tctggaacca tctacgggaa 360
ggttgttgag atcacaaagg gaagcaaagt taaatatgag cttgacaaga aaactggact 420
gattaagggt gatcgagtc tggtactcat cagttgtata ccctcacaat tatggtttcg 480
ttccaaagga ctcttt

(2) INFORMATION FOR SEQ ID NO:2247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..102
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502731

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2247:

Met Ser Glu Glu Asp Lys Thr Ala Ala Ser Ala Glu Gln Pro Lys Arg
1 5 10 15
Ala Pro Lys Leu Asn Glu Arg Ile Leu Ser Ser Leu Ser Arg Arg Ser
20 25 30
Val Ala Ala His Pro Trp His Asp Leu Glu Ile Gly Pro Asp Ala Pro
35 40 45
Ala Val Phe Asn Val Val Ser Thr Ser Ile Thr Leu Glu Pro Phe Asp
50 55 60
Val Leu Tyr Val Arg Cys Cys Gly Asp Leu Gly Cys Leu Glu Pro Ser
65 70 75 80
Thr Gly Arg Leu Leu Arg Ser Gln Arg Glu Ala Lys Leu Asn Met Ser
85 90 95
Leu Thr Arg Lys Leu Asp
100

(2) INFORMATION FOR SEQ ID NO:2248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..266
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2248:

acatcaatcc attccctttc ctctcccgct ccacttccat gggcaagggt cggctccttct 60
tctcgcgctc ccgcagcggc aagcgcgggc gscggagag caggctcgtc ctgcccgcac 120
tcttcgcgcg ccagcgcgcc gccgtccccg tccccactcc cgaggaggtc achgtcgctg 180
tcgtcaacca caaccagggg acgagacgga gcgcgtgttc cgcaagttcg acgcgaacgg 240
cgacgggcag atctcgcggt ccgagc

(2) INFORMATION FOR SEQ ID NO:2249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2249:

Thr Ser Ile His Ser Leu Ser Ser Pro Ala Pro Leu Pro Trp Ala Arg

1 5 10 15
Phe Gly Pro Ser Ser Arg Ala Pro Ala Ala Ala Ser Ala Ala Xaa Arg
20 25 30
Arg Ala Gly Ser Ser Ser Pro His Ser Ser Ala Ala Ser Ala Pro Pro
35 40 45
Ser Pro Ser Pro Leu Pro Arg Arg Ser Xaa Ser Ser Ser Thr Thr
50 55 60
Thr Arg Gly Arg Asp Gly Ala Arg Val Pro Gln Val Arg Arg Glu Arg
65 70 75 80
Arg Arg Ala Asp Leu Ala Val Arg
85

(2) INFORMATION FOR SEQ ID NO:2250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1502757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2250:

His Gln Ser Ile Pro Phe Pro Leu Pro Leu His Phe His Gly Gln Gly
1 5 10 15
Ser Val Leu Leu Leu Ala Leu Pro Gln Arg Gln Ala Arg Gln Xaa Gly
20 25 30
Glu Gln Ala Arg Pro Arg Arg Thr Pro Arg Pro Ala Arg Arg Arg
35 40 45
Pro Arg Pro His Ser Arg Gly Gly His Xaa Arg Arg Arg Gln Pro Gln
50 55 60
Pro Gly Asp Glu Thr Glu Arg Val Phe Arg Lys Phe Asp Ala Asn Gly
65 70 75 80
Asp Gly Gln Ile Ser Arg Ser Glu
85

(2) INFORMATION FOR SEQ ID NO:2251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1502758

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2251:

Ile Asn Pro Phe Pro Phe Leu Ser Arg Ser Thr Ser Met Gly Lys Val
1 5 10 15
Arg Ser Phe Phe Ser Arg Ser Arg Ser Gly Lys Arg Gly Xaa Pro Glu
20 25 30
Ser Arg Leu Val Leu Ala Ala Leu Leu Arg Gly Gln Arg Ala Ala Val
35 40 45
Pro Val Pro Thr Pro Glu Glu Val Xaa Val Val Val Asn His Asn
50 55 60
Gln Gly Thr Arg Arg Ser Ala Cys Ser Ala Ser Ser Thr Arg Thr Ala
65 70 75 80
Thr Gly Arg Ser Arg Gly Pro Ser
85

(2) INFORMATION FOR SEQ ID NO:2252:

(i) SEQUENCE CHARACTERISTICS:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..43
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502762

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2255:

Met Leu Cys Asp Ser Arg Arg Gly Val Ala Leu Val Ala Leu Leu Val
1 5 10 15
Gly Thr Asn Asn Asn Leu Gly Asn Ile Thr Asn Lys Gly Ser Val Arg
20 25 30
Lys Gly Phe Glu Glu Ile Asn Phe Phe Leu Phe
35 40

(2) INFORMATION FOR SEQ ID NO:2256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502763

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2256:

agatcagatg gcagacaaaa taaggatcac ggakttgcag agatatccaa tccaagcaca 60
tcggaggtgc tcattgaaga gagaagatcc ttgggtccgg aaaaggagac gagatcctgt 120
cctgggcagc gcaggagggg aggagttaat acctgcgtcc cctggcacgt gtgggtcgcc 180
ctgccccgcc ccgcaagaag cgcgcccccc gcsstggtat ataagcgcgc mssaccggcc 240
caaggctggg caagacggcg ggtcgtcgga gtcgacaggg gagtccaagc ttcagatggc 300
cagcgtcggg ggagcagttg ccggggggcgt gggggcgccg acgcgcacgt cctcgcggtg 360
gacgacagct ccgtcgaccg cgccatcatc gccgccatac tccggagctc ccggtttcgt 420
gtgactgcgg tggaaagtgg gaagagggcc ctggaactgt taggcacgga gccgaacg

(2) INFORMATION FOR SEQ ID NO:2257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2257:

Arg Ser Asp Gly Arg Gln Asn Lys Asp His Gly Xaa Ala Glu Ile Ser
1 5 10 15
Asn Pro Ser Thr Ser Glu Val Leu Ile Glu Glu Arg Arg Ser Leu Gly
20 25 30
Pro Glu Lys Glu Thr Arg Ser Cys Pro Gly Gln Arg Arg Arg Gly Gly
35 40 45
Val Asn Thr Cys Val Pro Trp His Val Trp Val Ala Leu Pro Arg Pro
50 55 60
Ala Arg Ser Ala Pro Pro Xaa Xaa Val Tyr Lys Arg Xaa Xaa Pro Ala
65 70 75 80

Gln Gly Trp Ala Arg Arg Arg Val Val Gly Val Asp Arg Gly Val Gln
85 90 95
Ala Ser Asp Gly Gln Arg Arg Trp Ser Ser Gly Arg Gly Arg Gly Gly
100 105 110
Ala Asp Ala His Val Leu Ala Val Asp Asp Ser Ser Val Asp Arg Ala
115 120 125
Ile Ile Ala Ala Ile Leu Arg Ser Ser Arg Phe Arg Val Thr Ala Val
130 135 140
Glu Ser Gly Lys Arg Ala Leu Glu Leu Leu Gly Thr Glu Pro Asn
145 150 155

(2) INFORMATION FOR SEQ ID NO:2258:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1502765

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2258:

Asp Gln Met Ala Asp Lys Ile Arg Ile Thr Xaa Leu Gln Arg Tyr Pro
1 5 10 15
Ile Gln Ala His Arg Arg Cys Ser Leu Lys Arg Glu Asp Pro Trp Val
20 25 30
Arg Lys Arg Arg Arg Asp Pro Val Leu Gly Ser Ala Gly Gly Glu Glu
35 40 45
Leu Ile Pro Ala Ser Pro Gly Thr Cys Gly Ser Pro Cys Pro Ala Pro
50 55 60
Gln Glu Ala Arg Pro Pro Xaa Trp Tyr Ile Ser Ala Xaa Xaa Arg Pro
65 70 75 80
Lys Ala Gly Gln Asp Gly Gly Ser Ser Glu Ser Thr Gly Glu Ser Lys
85 90 95
Leu Gln Met Ala Ser Val Gly Gly Ala Val Ala Gly Gly Val Gly Ala
100 105 110
Pro Thr Arg Thr Ser Ser Arg Trp Thr Thr Ala Pro Ser Thr Ala Pro
115 120 125
Ser Ser Pro Pro Tyr Ser Gly Ala Pro Gly Phe Val
130 135 140

(2) INFORMATION FOR SEQ ID NO:2259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..138

(D) OTHER INFORMATION: / Ceres Seq. ID 1502766

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2259:

Met Ala Asp Lys Ile Arg Ile Thr Xaa Leu Gln Arg Tyr Pro Ile Gln
1 5 10 15
Ala His Arg Arg Cys Ser Leu Lys Arg Glu Asp Pro Trp Val Arg Lys
20 25 30
Arg Arg Arg Asp Pro Val Leu Gly Ser Ala Gly Gly Glu Glu Leu Ile
35 40 45
Pro Ala Ser Pro Gly Thr Cys Gly Ser Pro Cys Pro Ala Pro Gln Glu
50 55 60
Ala Arg Pro Pro Xaa Trp Tyr Ile Ser Ala Xaa Xaa Arg Pro Lys Ala

(2) INFORMATION FOR SEQ ID NO:2260:

(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..459

(D) OTHER INFORMATION: / Ceres Seq. ID 1502767

atcgcacccg	tctccccgtt	ctgactccgc	cckcgccgc	dctccgcac	gccccaggjc	60
ttcatctccg	ccgccgtcgc	cgccgcacgc	ctccgatcga	cccccgaaac	tccggaaacc	120
gtgggcttcg	cgagatggat	ctcaaggata	gcctctccaa	atttaagcaa	cagcaggaga	180
gatgccagtc	atcactggcg	agcatagctg	cttcgacctc	aaagccaaag	cacagggcc:	240
aaccagcgca	tgctcccaac	gtcccagcaa	gaccatcaca	acctattaag	ttttcaaattg	300
atacagaaag	gctgcagcac	atcaattcga	ttaggaattc	tccgtgttga	gcacagatca	360
agcttgctat	cgaacttcct	tacaagacaa	gacaagcttt	tactgcagag	cagantaaat	420
gaagcaactt	atgttgatat	tcatggtaat	aaagctgtc			

(2) INFORMATION FOR SEQ ID NO:2261:

(A) LENGTH: 139 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ix) FEATURE:

(B) LOCATION: 1..139

(D) OTHER INFORMATION: / Ceres Seq. ID 1502768

Arg 1	Thr	Arg	Leu 5	Pro	Val	Leu	Thr	Pro 10	Pro	Xaa	Pro	Xaa	Leu 15	Pro	His
Ala	Pro	Arg	Leu 20	His	Leu	Arg	Arg	Arg 25	Arg	Arg	Arg	Ile 30	Ala	Pro	Ile
Asp	Pro	Arg	Asn 35	Ser	Gly	Asn	Arg 40	Gly	Leu	Arg	Glu	Met 45	Asp	Leu	Lys
Asp	Ser 50	Leu	Ser	Lys	Phe	Lys 55	Gln	Gln	Gln	Glu 60	Arg	Cys	Gln	Ser	Ser
Leu 65	Ala	Ser	Ile	Ala	Ala 70	Ser	Thr	Ser	Lys	Pro 75	Lys	His	Arg	Ala	Gln 80
Pro	Ala	His	Ala 85	Pro	Asn	Val	Pro	Ala	Arg 90	Pro	Ser	Gln	Pro	Ile 95	Lys
Phe	Ser	Asn	Asp 100	Thr	Glu	Arg	Leu	Gln 105	His	Ile	Asn	Ser	Ile 110	Arg	Lys
Ser	Pro	Val	Gly 115	Ala	Gln	Ile	Lys 120	Leu	Val	Ile	Glu	Leu 125	Leu	Tyr	Lys
Thr	Arg 130	Gln	Ala	Phe	Thr	Ala 135	Glu	Gln	Xaa	Lys					

(2) INFORMATION FOR SEQ ID NO:2262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..95
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2262:

```
Met Asp Leu Lys Asp Ser Leu Ser Lys Phe Lys Gln Gln Gln Glu Arg
1          5          10          15
Cys Gln Ser Ser Leu Ala Ser Ile Ala Ala Ser Thr Ser Lys Pro Lys
          20          25          30
His Arg Ala Gln Pro Ala His Ala Pro Asn Val Pro Ala Arg Pro Ser
          35          40          45
Gln Pro Ile Lys Phe Ser Asn Asp Thr Glu Arg Leu Gln His Ile Asn
          50          55          60
Ser Ile Arg Lys Ser Pro Val Gly Ala Gln Ile Lys Leu Val Ile Glu
65          70          75          80
Leu Leu Tyr Lys Thr Arg Gln Ala Phe Thr Ala Glu Gln Xaa Lys
          85          90          95
```

(2) INFORMATION FOR SEQ ID NO:2263:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..70
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2263:

```
Met Leu Pro Thr Ser Gln Gln Asp His His Asn Leu Leu Ser Phe Gln
1          5          10          15
Met Ile Gln Lys Gly Cys Ser Thr Ser Ile Arg Leu Gly Asn Leu Leu
          20          25          30
Leu Glu His Arg Ser Ser Leu Ser Ser Asn Phe Phe Thr Arg Gln Asp
          35          40          45
Lys Leu Leu Leu Gln Ser Arg Xaa Asn Glu Ala Thr Tyr Val Asp Ile
          50          55          60
His Gly Asn Lys Ala Val
65          70
```

(2) INFORMATION FOR SEQ ID NO:2264:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 486 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..486
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502771

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2264:

```
gtgggacgag aacaagttca cagctgatga gctgcagact ctgacaaaca acctatgcta      60
cacgtacgct aggtgcaccc gtcctgtgtc aattgtgtccc ccggcatact atgctcatct      120
ggcagccttc cgagctcgct tctacatgga gccagatacc tctgacagtg gctcaatggc      180
cagtggtgcc cgtggccctc caccaggtgc ggcacssagc atgagaggag cggggagtgt      240
tgcggtcagg cccctacctg ctctcaagga aaacgtgaag cgtgtcatgt tttactgctg      300
```

agatgctgag ctaccttcac caagaaaata tcctgacttg ttccatgtac ccgcactggt 360
tcggtgatac tatctgacac cgaatttatg cattaagtct tccagtgggc tggagatttt 420
aagtaacgcc tgtttttatt cgtgagttgt aacgctgcag ttcgaggagc ttcagtgctg 480
tatgat

(2) INFORMATION FOR SEQ ID NO:2265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2265:

Trp Asp Glu Asn Lys Phe Thr Ala Asp Glu Leu Gln Thr Leu Thr Asn
1 5 10 15
Asn Leu Cys Tyr Thr Tyr Ala Arg Cys Thr Arg Ser Val Ser Ile Val
20 25 30
Pro Pro Ala Tyr Tyr Ala His Leu Ala Ala Phe Arg Ala Arg Phe Tyr
35 40 45
Met Glu Pro Asp Thr Ser Asp Ser Gly Ser Met Ala Ser Gly Ala Arg
50 55 60
Gly Pro Pro Pro Gly Ala Ala Xaa Ser Met Arg Gly Ala Gly Ser Val
65 70 75 80
Ala Val Arg Pro Leu Pro Ala Leu Lys Glu Asn Val Lys Arg Val Met
85 90 95
Phe Tyr Cys

(2) INFORMATION FOR SEQ ID NO:2266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2266:

Met Glu Pro Asp Thr Ser Asp Ser Gly Ser Met Ala Ser Gly Ala Arg
1 5 10 15
Gly Pro Pro Pro Gly Ala Ala Xaa Ser Met Arg Gly Ala Gly Ser Val
20 25 30
Ala Val Arg Pro Leu Pro Ala Leu Lys Glu Asn Val Lys Arg Val Met
35 40 45
Phe Tyr Cys
50

(2) INFORMATION FOR SEQ ID NO:2267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502781

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2267:
atcagyaaya acttcaggct tggagaaaga agaaaggcat agcagcgggc agcggcatgg 60
gcaccakccc cgctcatccct ggcagcatgc tcttcgtcgc tcttcttgtg nctgtctgct 120
tc

(2) INFORMATION FOR SEQ ID NO:2268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2268:

Ser	Xaa	Xaa	Thr	Ser	Gly	Leu	Glu	Lys	Glu	Glu	Arg	His	Ser	Ser	Gly
1				5				10					15		
Gln	Arg	His	Gly	His	Xaa	Pro	Arg	His	Pro	Cys	Asp	Asp	Ala	Leu	Arg
		20					25						30		
Arg	Ser	Ser	Cys	Xaa	Cys	Leu	Leu								
		35					40								

(2) INFORMATION FOR SEQ ID NO:2269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2269:

Gln	Xaa	Xaa	Leu	Gln	Ala	Trp	Arg	Lys	Lys	Lys	Gly	Ile	Ala	Ala	Gly
1			5					10					15		
Ser	Gly	Met	Gly	Thr	Xaa	Pro	Val	Ile	Pro	Ala	Thr	Met	Leu	Phe	Val
		20					25						30		
Ala	Leu	Leu	Xaa	Xaa	Val	Cys	Phe								
		35					40								

(2) INFORMATION FOR SEQ ID NO:2270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2270:

accttactas	sagcagacgg	tatcggttcaa	ggccccata	ctgctacaga	agacgcaggt	60
ssaccttctg	tttcgccata	ctaccgccgg	cacaggtaca	gatctgtctc	caagtcatcc	120
agttcatctc	c					

(2) INFORMATION FOR SEQ ID NO:2271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: / Ceres Seq. ID 1502785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2271:

Thr	Leu	Leu	Xaa	Ala	Asp	Gly	Ile	Val	Gln	Gly	Pro	His	Thr	Ala	Thr
1				5					10					15	
Glu	Asp	Ala	Gly	Xaa	Pro	Ser	Val	Ser	Pro	Tyr	Tyr	Arg	Arg	His	Arg
			20					25					30		
Tyr	Arg	Ser	Val	Ser	Lys	Ser	Ser	Ser	Ser	Ser	Ser				
			35				40								

(2) INFORMATION FOR SEQ ID NO:2272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: / Ceres Seq. ID 1502786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2272:

Pro	Tyr	Xaa	Xaa	Gln	Thr	Val	Ser	Phe	Lys	Val	Pro	Ile	Leu	Leu	Gln
1				5					10					15	
Lys	Thr	Gln	Xaa	Xaa	Leu	Leu	Phe	Arg	His	Thr	Thr	Ala	Gly	Thr	Gly
			20					25					30		
Thr	Asp	Leu	Ser	Pro	Ser	His	Pro	Val	His	Leu					
			35				40								

(2) INFORMATION FOR SEQ ID NO:2273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: / Ceres Seq. ID 1502787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2273:

Leu	Thr	Xaa	Ser	Arg	Arg	Tyr	Arg	Ser	Arg	Ser	Pro	Tyr	Cys	Tyr	Arg
1				5					10					15	
Arg	Arg	Arg	Xaa	Thr	Phe	Cys	Phe	Ala	Ile	Leu	Pro	Pro	Ala	Gln	Val
			20					25					30		
Gln	Ile	Cys	Leu	Gln	Val	Ile	Gln	Phe	Ile	Ser					
			35				40								

(2) INFORMATION FOR SEQ ID NO:2274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..473

(D) OTHER INFORMATION: / Ceres Seq. ID 1502805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2274:

agattccttt ccctttccgt tagcaggata gagagggaga ggagcagaag atagcagagg

gccagaggcg cagaaggcag tgcgggacag gaggaagagg aagaagaagc ggcavsgcga 120
ggatgccgtg cctgaacgtg tgcaccaacg tgaacctgga ggggggtggac acctccgcca 180
tcctcgccga agcctccaag tccgtcgcca acatcatcgg caagcccagag gcctacgtga 240
tggttggtct caagggttcg gtgcctatgg catttgagg taccaggag ccagcagctt 300
acggtgagct ggtttccatc ggaggcctga accctgatgt gaacaagaag cttagtgtg 360
gcacgcttc taccctggag tcaaagctgt ctgttcccaa gtcacgcttc tacctcaagt 420
tctatgactc gaaggctcat cctgcacaag aaaatgctca atgtttgcat gct

(2) INFORMATION FOR SEQ ID NO:2275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1502806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2275:

Met Pro Cys Leu Asn Val Ser Thr Asn Val Asn Leu Glu Gly Val Asp
1 5 10 15
Thr Ser Ala Ile Leu Ala Glu Ala Ser Lys Ser Val Ala Asn Ile Ile
20 25 30
Gly Lys Pro Glu Ala Tyr Val Met Val Val Leu Lys Gly Ser Val Pro
35 40 45
Met Ala Phe Gly Gly Thr Gln Glu Pro Ala Ala Tyr Gly Glu Leu Val
50 55 60
Ser Ile Gly Gly Leu Asn Pro Asp Val Asn Lys Lys Leu Ser Ala Gly
65 70 75 80
Ile Ala Ser Ile Leu Glu Ser Lys Leu Ser Val Pro Lys Ser Arg Phe
85 90 95
Tyr Leu Lys Phe Tyr Asp Ser Lys Ala His Pro Ala Gln Glu Asn Ala
100 105 110
Gln Cys Leu His Ala
115

(2) INFORMATION FOR SEQ ID NO:2276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1502807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2276:

Met Val Val Leu Lys Gly Ser Val Pro Met Ala Phe Gly Gly Thr Gln
1 5 10 15
Glu Pro Ala Ala Tyr Gly Glu Leu Val Ser Ile Gly Gly Leu Asn Pro
20 25 30
Asp Val Asn Lys Lys Leu Ser Ala Gly Ile Ala Ser Ile Leu Glu Ser
35 40 45
Lys Leu Ser Val Pro Lys Ser Arg Phe Tyr Leu Lys Phe Tyr Asp Ser
50 55 60
Lys Ala His Pro Ala Gln Glu Asn Ala Gln Cys Leu His Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:2277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..69
(D) OTHER INFORMATION: / Ceres Seq. ID 1502808
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2277:
Met Ala Phe Gly Gly Thr Gln Glu Pro Ala Ala Tyr Gly Glu Leu Val
1 5 10 15
Ser Ile Gly Gly Leu Asn Pro Asp Val Asn Lys Lys Leu Ser Ala Gly
20 25 30
Ile Ala Ser Ile Leu Glu Ser Lys Leu Ser Val Pro Lys Ser Arg Phe
35 40 45
Tyr Leu Lys Phe Tyr Asp Ser Lys Ala His Pro Ala Gln Glu Asn Ala
50 55 60
Gln Cys Leu His Ala
65
(2) INFORMATION FOR SEQ ID NO:2278:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 410 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..410
(D) OTHER INFORMATION: / Ceres Seq. ID 1502809
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2278:
agactgtctg ccagtggacg cgagggagcg cctccgcctc agatccaacc cccaccgatg 60
cgagctccgg cgatgtcccg ctgggcccgc gcgssctcg cggggctcct cgccgctcac 120
cgccgcccgc gttttaccta cccggcgtgg cgcccaacga cttccataag aaagatccac 180
ttttggtgaa ggtgaataag ctgacatcca cgaagacgca acttccctac tcatattact 240
ctcttccttt ctgtaaacca aacacgatag ttgacagtgc agagaatctt ggagaagttc 300
tgcgtggtga tcgcattgag aactctcctt atgtggtcag tactagatta ctgcttgtca 360
catattcagc attgtaattt gtaatgtacc aaatcactta gtcgtcatgc
(2) INFORMATION FOR SEQ ID NO:2279:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..62
(D) OTHER INFORMATION: / Ceres Seq. ID 1502810
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2279:
Arg Leu Ser Ala Ser Gly Arg Glu Gly Ala Pro Pro Pro Gln Ile Gln
1 5 10 15
Pro Pro Pro Met Arg Ala Pro Ala Met Leu Arg Trp Ala Ala Xaa
20 25 30
Leu Ala Gly Leu Leu Ala Ala His Arg Pro Pro Arg Phe Thr Tyr Pro
35 40 45
Ala Trp Arg Pro Thr Thr Ser Ile Arg Lys Ile His Phe Trp
50 55 60
(2) INFORMATION FOR SEQ ID NO:2280:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..124
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502811
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2280:

Thr	Val	Cys	Gln	Trp	Thr	Arg	Gly	Ser	Ala	Ser	Ala	Ser	Asp	Pro	Thr
1			5						10					15	
Pro	Thr	Asp	Ala	Ser	Ser	Gly	Asp	Ala	Pro	Leu	Gly	Arg	Gly	Xaa	Xaa
			20					25					30		
Arg	Gly	Ala	Pro	Arg	Arg	Ser	Pro	Ala	Ala	Ala	Phe	Tyr	Leu	Pro	Gly
			35				40					45			
Val	Ala	Pro	Asn	Asp	Phe	His	Lys	Lys	Asp	Pro	Leu	Leu	Val	Lys	Val
			50			55					60				
Asn	Lys	Leu	Thr	Ser	Thr	Lys	Thr	Gln	Leu	Pro	Tyr	Ser	Tyr	Tyr	Ser
65					70				75					80	
Leu	Pro	Phe	Cys	Lys	Pro	Asn	Thr	Ile	Val	Asp	Ser	Ala	Glu	Asn	Leu
			85					90					95		
Gly	Glu	Val	Leu	Arg	Gly	Asp	Arg	Ile	Glu	Asn	Ser	Pro	Tyr	Val	Val
			100				105						110		
Ser	Thr	Arg	Leu	Leu	Leu	Val	Thr	Tyr	Ser	Ala	Leu				
			115				120								

(2) INFORMATION FOR SEQ ID NO:2281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..443
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2281:

aacatcctaa	tcgaaaaacg	gaagtttcgg	cggcgssgcg	tgctcgtgat	ctcaacccaa	60
ggcgtgcctc	cgctccggtc	accgctcgct	ccacgcaacc	atgtcgagga	ggaagaccag	120
ggagcccaag	gaggagaacg	tcacccttgg	accactgtc	cgtgaaggag	agtatgtctt	180
tggtgtcgct	cacatctttg	catccttcaa	tgacaccttc	attcatatca	ctgatttgtc	240
tgggagggaa	actctgggtc	ggatcaccgg	tggcatgaag	gtgaaggctg	accgtgacga	300
gtcgtcacct	tacgttgcta	tgcttgctgc	tcaagacgtc	gcacagcgct	gcaaggagct	360
tggcattact	gcactgcaca	ttaagcttcg	cgccaccgga	gcaacaagac	caagacccct	420
ggacctggtg	cccagtcctgc	cct				

(2) INFORMATION FOR SEQ ID NO:2282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2282:

His	Pro	Asn	Arg	Lys	Thr	Glu	Val	Ser	Ala	Ala	Xaa	Arg	Ala	Arg	Asp
1				5					10					15	
Leu	Asn	Pro	Arg	Arg	Ala	Ser	Ala	Pro	Val	Thr	Arg	Arg	Ser	Thr	Gln
			20				25					30			
Pro	Cys	Arg	Gly	Gly	Arg	Pro	Gly	Ser	Pro	Arg	Arg	Arg	Thr	Ser	Pro

35 40 45
Leu Asp Pro Leu Ser Val Lys Glu Ser Met Ser Leu Val Ser Leu Thr
50 55 60
Ser Leu His Pro Ser Met Thr Pro Ser Phe Ile Ser Leu Ile Cys Leu
65 70 75 80
Gly Gly Lys Leu Trp Phe Gly Ser Pro Val Ala
85 90

(2) INFORMATION FOR SEQ ID NO:2283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1502822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2283:

Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu
1 5 10 15
Gly Pro Thr Val Arg Glu Gly Glu Tyr Val Phe Gly Val Ala His Ile
20 25 30
Phe Ala Ser Phe Asn Asp Thr Phe Ile His Ile Thr Asp Leu Ser Gly
35 40 45
Arg Glu Thr Leu Val Arg Ile Thr Gly Gly Met Lys Val Lys Ala Asp
50 55 60
Arg Asp Glu Ser Ser Pro Tyr Ala Ala Met Leu Ala Ala Gln Asp Val
65 70 75 80
Ala Gln Arg Cys Lys Glu Leu Gly Ile Thr Ala Leu His Ile Lys Leu
85 90 95
Arg Ala Thr Gly Ala Thr Arg Pro Arg Pro Leu Asp Leu Val Pro Ser
100 105 110
Leu Pro

(2) INFORMATION FOR SEQ ID NO:2284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..442

(D) OTHER INFORMATION: / Ceres Seq. ID 1502834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2284:

ttaactcgag aggaggtgaa gcatcccgga atggagatcc tgatgctttg gcaacaatga 60
acgcaactgc agaagctcct gaagcaaaaag awaagcaaaa gccatcgctt gaattgtctg 120
gaaagcttgc tgaggagacc aacagagttg cagggtgtaaa tctattatat tcagaacccc 180
cagaggctcg aaagtcagag attagatgga ggctctatgt atttaaagat ggtgaaccac 240
tgaatgaacc actgtatggt catcggtatga cctgctacct ttttggaaga gaaakgaaag 300
ttgcagatgt cccacagat catccctcct gcagcaagca acatgcagtt cttcaatata 360
gacttgtgga gaaggagcaa ctagatggca tactgacgaa gagaataagg ccttawctga 420
tggatcttga tagtacaat gg

(2) INFORMATION FOR SEQ ID NO:2285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1502835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2285:

Asn	Ser	Arg	Gly	Gly	Glu	Ala	Ser	Arg	Asn	Gly	Asp	Pro	Asp	Ala	Leu
1			5						10					15	
Ala	Thr	Met	Asn	Ala	Thr	Ala	Glu	Ala	Leu	Glu	Ala	Lys	Xaa	Lys	Gln
			20					25					30		
Lys	Pro	Ser	Phe	Glu	Leu	Ser	Gly	Lys	Leu	Ala	Glu	Glu	Thr	Asn	Arg
			35				40					45			
Val	Ala	Gly	Val	Asn	Leu	Leu	Tyr	Ser	Glu	Pro	Pro	Glu	Ala	Arg	Lys
			50				55					60			
Ser	Glu	Ile	Arg	Trp	Arg	Leu	Tyr	Val	Phe	Lys	Asp	Gly	Glu	Pro	Leu
65					70				75					80	
Asn	Glu	Pro	Leu	Tyr	Val	His	Arg	Met	Thr	Cys	Tyr	Leu	Phe	Gly	Arg
			85						90					95	
Glu	Xaa	Lys	Val	Ala	Asp	Val	Pro	Thr	Asp	His	Pro	Ser	Cys	Ser	Lys
			100					105					110		
Gln	His	Ala	Val	Leu	Gln	Tyr	Arg	Leu	Val	Glu	Lys	Glu	Gln	Leu	Asp
			115				120					125			
Gly	Ile	Leu	Thr	Lys	Arg	Ile	Arg	Pro	Xaa	Leu	Met	Asp	Leu	Asp	Ser
			130				135					140			
Thr	Asn														
145															

(2) INFORMATION FOR SEQ ID NO:2286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1502836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2286:

Met	Asn	Ala	Thr	Ala	Glu	Ala	Leu	Glu	Ala	Lys	Xaa	Lys	Gln	Lys	Pro
1			5						10					15	
Ser	Phe	Glu	Leu	Ser	Gly	Lys	Leu	Ala	Glu	Glu	Thr	Asn	Arg	Val	Ala
			20					25					30		
Gly	Val	Asn	Leu	Leu	Tyr	Ser	Glu	Pro	Pro	Glu	Ala	Arg	Lys	Ser	Glu
			35				40					45			
Ile	Arg	Trp	Arg	Leu	Tyr	Val	Phe	Lys	Asp	Gly	Glu	Pro	Leu	Asn	Glu
			50				55				60				
Pro	Leu	Tyr	Val	His	Arg	Met	Thr	Cys	Tyr	Leu	Phe	Gly	Arg	Glu	Xaa
65					70				75					80	
Lys	Val	Ala	Asp	Val	Pro	Thr	Asp	His	Pro	Ser	Cys	Ser	Lys	Gln	His
			85					90						95	
Ala	Val	Leu	Gln	Tyr	Arg	Leu	Val	Glu	Lys	Glu	Gln	Leu	Asp	Gly	Ile
			100				105						110		
Leu	Thr	Lys	Arg	Ile	Arg	Pro	Xaa	Leu	Met	Asp	Leu	Asp	Ser	Thr	Asn
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:2287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 461 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..461
(D) OTHER INFORMATION: / Ceres Seq. ID 1502844

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2287:

tacgacctgc	tcgggatctc	agcggatggg	agccccgatg	atgttcggggc	gtcctacagg	60
cggctggcgc	taaagtacca	cccagacgtg	tccccctcgg	cgccgcggcc	gagaacacgc	120
gccgcttcat	cgaggtgcag	gaggcctacg	agacgctctc	cgacccaagc	cgccgctcca	180
gctacgaccg	tgcactcgcc	cgcggsstct	gccgctcgcc	ttctccgggc	gccgttccca	240
atcccaccac	gcctactacc	accaccagga	gcagggagag	agatctgggt	ggagaaggtc	300
ctgggaggac	cagatcgag	agctgaagag	gaggagcgtg	gcgaaggatt	cagaagagaa	360
cctgtcgtgg	ggcgctcgca	tgcggagaag	ggccgaggcg	tcacagcgna	gtagctgcga	420
caagcgaccc	tgccaaatgc	agctgtactc	gtacgtagca	t		

(2) INFORMATION FOR SEQ ID NO:2288:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..137
(D) OTHER INFORMATION: / Ceres Seq. ID 1502845

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2288:

Tyr	Asp	Leu	Leu	Gly	Ile	Ser	Ala	Asp	Gly	Ser	Pro	Asp	Asp	Val	Arg
1			5						10					15	
Ala	Ser	Tyr	Arg	Arg	Leu	Ala	Leu	Lys	Tyr	His	Pro	Asp	Val	Ser	Pro
			20					25					30		
Pro	Ala	Pro	Arg	Pro	Arg	Thr	Arg	Ala	Ala	Ser	Ser	Arg	Cys	Arg	Arg
			35				40					45			
Pro	Thr	Arg	Arg	Ser	Pro	Thr	Gln	Ala	Ala	Ala	Pro	Ala	Thr	Thr	Val
			50				55					60			
His	Ser	Pro	Ala	Xaa	Ser	Ala	Ala	Arg	Leu	Leu	Arg	Ala	Pro	Phe	Pro
65					70					75				80	
Ile	Pro	Pro	Arg	Leu	Leu	Pro	Pro	Pro	Gly	Ala	Gly	Arg	Glu	Ile	Trp
			85						90					95	
Val	Glu	Lys	Val	Leu	Gly	Gly	Pro	Asp	Arg	Arg	Ala	Glu	Glu	Glu	Glu
			100				105						110		
Arg	Gly	Glu	Gly	Phe	Arg	Arg	Glu	Pro	Val	Val	Gly	Arg	Ser	His	Ala
			115				120					125			
Glu	Lys	Gly	Arg	Gly	Val	Thr	Ala	Xaa							
			130				135								

(2) INFORMATION FOR SEQ ID NO:2289:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 503 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..503
(D) OTHER INFORMATION: / Ceres Seq. ID 1502850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2289:

atgcgtgcat	ggcgtgctag	ctaggtacct	tgcggccaag	agcgaggcgg	accactacaa	60
gcgggagatg	agaaggkagc	aggaggagat	catcgccgtc	ccagacaccg	aggcckctga	120
gattggagat	atcatgtcac	ggtatgggct	cgagccgcag	agtacggccc	tgctgctgcc	180
gggctcaggc	ggaaccctca	agcttkgcta	gacttcatgr	tgaggttcga	gctgggactg	240

gagagaccgg atcccagaag ggctctgcag acgccttcac gatcgcaactg tcctacgtgg 300
tcggcggggt ggtccctctc ctgccctacg tgctcgtctc cgccgcgcag gatgccatgc 360
tcacatccgt cggagtcacg ctggccgcgc tgcttttctt cggctacgtc aagggccgct 420
tcacggggga accgkccgtt cgccagtgcc gtccagaccg ctgtcattgg agcgctcgct 480
tcggcggggt cgtacssgga tgg

(2) INFORMATION FOR SEQ ID NO:2290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2290:

Cys Val His Gly Val Leu Ala Arg Tyr Leu Ala Ala Lys Ser Glu Ala
1 5 10 15
Asp His Tyr Lys Arg Glu Met Arg Arg Xaa Gln Glu Glu Ile Ile Ala
20 25 30
Val Pro Asp Thr Glu Ala Xaa Glu Ile Gly Asp Ile Met Ser Arg Tyr
35 40 45
Gly Leu Glu Pro Gln Ser Thr Ala Leu Ser Ser Pro Gly Ser Gly Gly
50 55 60
Thr Leu Lys Leu Xaa
65

(2) INFORMATION FOR SEQ ID NO:2291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..120
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502852

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2291:

Met Gly Ser Ser Arg Arg Val Arg Pro Cys Arg Arg Arg Ala Gln Ala
1 5 10 15
Glu Pro Ser Ser Xaa Ala Arg Leu His Xaa Glu Val Arg Ala Gly Thr
20 25 30
Gly Glu Thr Gly Ser Gln Lys Gly Ser Ala Asp Ala Phe Thr Ile Ala
35 40 45
Leu Ser Tyr Val Val Gly Gly Leu Val Pro Leu Leu Pro Tyr Val Leu
50 55 60
Val Ser Ala Ala Gln Asp Ala Met Leu Thr Ser Val Gly Val Thr Leu
65 70 75 80
Ala Ala Leu Leu Phe Gly Tyr Val Lys Gly Arg Phe Thr Gly Glu
85 90 95
Pro Xaa Val Arg Gln Cys Arg Pro Asp Arg Cys His Trp Ser Ala Arg
100 105 110
Phe Gly Gly Gly Val Xaa Gly Trp
115 120

(2) INFORMATION FOR SEQ ID NO:2292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1502853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2292:

```
Met Xaa Arg Phe Glu Leu Gly Leu Glu Arg Pro Asp Pro Arg Arg Ala
1          5          10          15
Leu Gln Thr Pro Ser Arg Ser His Cys Pro Thr Trp Ser Ala Gly Trp
20          25          30
Ser Leu Ser Cys Pro Thr Cys Ser Ser Pro Pro Arg Arg Met Pro Cys
35          40          45
Ser His Pro Ser Glu Ser Arg Trp Pro Arg Cys Phe Ser Ser Ala Thr
50          55          60
Ser Arg Ala Ala Ser Arg Gly Asn Xaa Pro Phe Ala Ser Ala Val Gln
65          70          75          80
Thr Ala Val Ile Gly Ala Leu Ala Ser Ala Ala Ala Tyr Xaa Asp
85          90          95
```

(2) INFORMATION FOR SEQ ID NO:2293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..475

(D) OTHER INFORMATION: / Ceres Seq. ID 1502860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2293:

```
atcccaaagc acaagagcac gcaactgcagc accacttcct gcgctgctgc tcatcacaca      60
ccgtagtact aacactccat cgccacaatg gctcccaagg ttgcgctctt ccttgccctc      120
agcctcctct tcgctgccgc cgcgcattggc tgcgaaccct actgtcccgg ccagtcgctc      180
ccaacgccgc ccgtcgtgcc gtcgcacagc cacggggcgct gcssatcgac gcactaaagc      240
tcaaggtgtg cgccaacgtg ctggacctcg tcaaggctcg cctaccccag cagcagcaat      300
gttgcccgtc gctggagggg ctggtggacc tcgacgccgc actgtgcctc tgcaccgcca      360
tcaaggctaa cgtcctcggc atccacctca acgtgcccc tagcctcaac ctcactctca      420
acaattgcgg caagatttgc ccaaagact ttacttgccc caactaattg agctg
```

(2) INFORMATION FOR SEQ ID NO:2294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..122

(D) OTHER INFORMATION: / Ceres Seq. ID 1502861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2294:

```
Ser Gln Ser Thr Arg Ala Arg Thr Ala Ala Pro Leu Pro Ala Leu Leu
1          5          10          15
Leu Ile Thr His Arg Ser Thr Asn Thr Pro Ser Pro Gln Trp Leu Pro
20          25          30
Arg Leu Arg Ser Ser Leu Pro Ser Ala Ser Ser Ser Leu Pro Pro Arg
35          40          45
Met Ala Ala Asn Pro Thr Val Pro Ala Gln Ser Ser Gln Arg Arg Pro
50          55          60
Ser Cys Arg Arg Thr Ala Thr Gly Ala Xaa Xaa Arg Arg Thr Lys Ala
65          70          75          80
Gln Gly Val Arg Gln Arg Ala Gly Pro Arg Gln Gly Arg Pro Thr Pro
```

85 90 95
Ala Arg Ala Met Leu Pro Ala Ala Gly Gly Ala Gly Gly Pro Arg Arg
100 105 110
Arg Thr Val Pro Leu His Arg His Gln Gly
115 120

(2) INFORMATION FOR SEQ ID NO:2295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..154
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2295:

Pro Lys Ala Gln Glu His Ala Leu Gln His His Phe Leu Arg Cys Cys
1 5 10 15
Ser Ser His Thr Val Val Leu Thr Leu His Arg His Asn Gly Ser Gln
20 25 30
Gly Cys Ala Leu Pro Cys Pro Gln Pro Pro Leu Arg Cys Arg Arg Ala
35 40 45
Trp Leu Arg Thr Leu Leu Ser Arg Pro Ser Arg Pro Asn Ala Ala Arg
50 55 60
Arg Ala Val Ala Gln Pro Arg Ala Leu Xaa Ile Asp Ala Leu Lys Leu
65 70 75 80
Lys Val Cys Ala Asn Val Leu Asp Leu Val Lys Val Gly Leu Pro Gln
85 90 95
His Glu Gln Cys Cys Pro Leu Leu Glu Gly Leu Val Asp Leu Asp Ala
100 105 110
Ala Leu Cys Leu Cys Thr Ala Ile Lys Ala Asn Val Leu Gly Ile His
115 120 125
Leu Asn Val Pro Leu Ser Leu Asn Leu Ile Leu Asn Asn Cys Gly Lys
130 135 140
Ile Cys Pro Lys Asp Phe Thr Cys Pro Asn
145 150

(2) INFORMATION FOR SEQ ID NO:2296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..334
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2296:

cactttctta agacgagttg tggtagcccg aattatgcag cacctgaggt catatctggt 60
aaactatatg ctggtcctga agttgacgtc tggagctgtg gagttattct ttatgctctt 120
ctttgtggca ctctccatt tgacgatgag aatattccaa accttttcaa gaaaataaag 180
ggtggaatat atacccttcc tagtcatttg tcaccttcag cgagggactt gattcccaga 240
atgctgggtg ttgatccaat gaaaaggatt acaatacgtg aaatccgtga acatgtgtgg 300
ttcaagatcc gacttcgcgc ctatttggct gtgc

(2) INFORMATION FOR SEQ ID NO:2297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..111
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502897
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2297:
His Phe Leu Lys Thr Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
1 5 10 15
Val Ile Ser Gly Lys Leu Tyr Ala Gly Pro Glu Val Asp Val Trp Ser
 20 25 30
Cys Gly Val Ile Leu Tyr Ala Leu Leu Cys Gly Thr Leu Pro Phe Asp
 35 40 45
Asp Glu Asn Ile Pro Asn Leu Phe Lys Lys Ile Lys Gly Gly Ile Tyr
 50 55 60
Thr Leu Pro Ser His Leu Ser Pro Ser Ala Arg Asp Leu Ile Pro Arg
65 70 75 80
Met Leu Val Val Asp Pro Met Lys Arg Ile Thr Ile Arg Glu Ile Arg
 85 90 95
Glu His Val Trp Phe Lys Ile Arg Leu Pro Arg Tyr Leu Ala Val
 100 105 110
(2) INFORMATION FOR SEQ ID NO:2298:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..58
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502898
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2298:
Thr Phe Leu Arg Arg Val Val Val Ala Arg Ile Met Gln His Leu Arg
1 5 10 15
Ser Tyr Leu Val Asn Tyr Met Leu Val Leu Lys Leu Thr Ser Gly Ala
 20 25 30
Val Glu Leu Phe Phe Met Leu Phe Phe Val Ala Leu Ser His Leu Thr
 35 40 45
Met Arg Ile Phe Gln Thr Phe Ser Arg Lys
 50 55
(2) INFORMATION FOR SEQ ID NO:2299:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..315
 (D) OTHER INFORMATION: / Ceres Seq. ID 1502902
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2299:
atcagtcctg tccaccagca ccgcnaccac actgcgcgac cgnnaatgaa ccacggcggc 60
ggcgggagga gcagcagccg gctccgggac cggctggccc ggatgttccg cccgagcgcg 120
ctgctccgct ccacctgcaa cacggccgcc gccgcatact cctgtctctc ctgctctccc 180
gcgtccacgg ccaagcctcc gcctccgcct gtggttgccg cggcctccgc gtgctctccc 240
agccgcgcgc tgcctggcgc cgctgctcgc ggggactcgt cgttctctgc ctctctcgcg 300
cgcgacctcg ccgtc
(2) INFORMATION FOR SEQ ID NO:2300:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..105
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502903
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2300:

Ile	Ser	Pro	Val	His	Gln	His	Arg	Xaa	His	Thr	Arg	Arg	Pro	Xaa	Met
1				5					10					15	
Asn	His	Gly	Gly	Gly	Gly	Arg	Ser	Ser	Ser	Arg	Leu	Arg	Asp	Arg	Leu
		20						25					30		
Ala	Arg	Met	Phe	Arg	Pro	Ser	Ala	Leu	Leu	Arg	Ser	Thr	Cys	Asn	Thr
		35					40					45			
Ala	Ala	Ala	Ala	Ser	Ser	Cys	Ser	Ser	Ser	Ser	Pro	Ala	Ser	Thr	Ala
	50					55					60				
Lys	Pro	Pro	Pro	Pro	Pro	Val	Ala	Ala	Ala	Ala	Ser	Ala	Cys	Ser	Ser
65					70					75				80	
Ser	Arg	Ala	Leu	Leu	Gly	Ala	Val	Val	Asp	Gly	Asp	Ser	Ser	Phe	Leu
			85						90					95	
Ala	Ser	Ser	Arg	Arg	Asp	Leu	Ala	Val							
			100				105								

(2) INFORMATION FOR SEQ ID NO:2301:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..104
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502904
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2301:

Gln	Ser	Cys	Pro	Pro	Ala	Pro	Xaa	Pro	His	Ser	Pro	Thr	Xaa	Asn	Glu
1			5						10					15	
Pro	Arg	Arg	Arg	Arg	Glu	Glu	Gln	Gln	Pro	Ala	Pro	Gly	Pro	Ala	Gly
			20					25					30		
Pro	Asp	Val	Pro	Pro	Glu	Arg	Ala	Ala	Pro	Leu	His	Leu	Gln	His	Gly
		35					40					45			
Arg	Arg	Arg	Ile	Leu	Leu	Leu	Leu	Val	Ser	Arg	Val	His	Gly	Gln	
	50				55					60					
Ala	Ser	Ala	Ser	Ala	Cys	Gly	Cys	Gly	Gly	Leu	Arg	Val	Leu	Leu	Gln
65				70					75					80	
Pro	Arg	Ala	Ala	Arg	Arg	Arg	Arg	Arg	Arg	Gly	Leu	Val	Val	Pro	Arg
			85					90						95	
Leu	Leu	Ala	Ala	Arg	Pro	Arg	Arg								
			100												

(2) INFORMATION FOR SEQ ID NO:2302:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..90
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502905
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2302:

Met Asn His Gly Gly Gly Arg Ser Ser Arg Leu Arg Asp Arg
1 5 10 15
Leu Ala Arg Met Phe Arg Pro Ser Ala Leu Leu Arg Ser Thr Cys Asn
20 25 30
Thr Ala Ala Ala Ala Ser Ser Cys Ser Ser Ser Ser Pro Ala Ser Thr
35 40 45
Ala Lys Pro Pro Pro Pro Val Ala Ala Ala Ala Ser Ala Cys Ser
50 55 60
Ser Ser Arg Ala Leu Leu Gly Ala Val Val Asp Gly Asp Ser Ser Phe
65 70 75 80
Leu Ala Ser Ser Arg Arg Asp Leu Ala Val
85 90

(2) INFORMATION FOR SEQ ID NO:2303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..337
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502937

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2303:

aaaacccatt	gtgtgcccgc	cgtcgacgca	gcctccgtcc	tcccccgcat	ccgaatcacg	60
cacgccaacg	tcccaccct	gtcatggcca	cctccagcga	cggcgcggcg	accagcgggc	120
ctcctctcca	tccccaagga	aggcgagcgc	atcatcgcg	ccacgssccg	ccccgacggc	180
acgctccgca	agggcatccg	catccgcgcc	ggttacgtgc	cccaggagga	ggtcgccatc	240
taccagtcca	agggcgccct	aatgaggaag	tcagggcccg	acgtgccgcc	ggggtacgac	300
ccggcgcyta	gtggccgacg	ccaaaccccc	ccccccc			

(2) INFORMATION FOR SEQ ID NO:2304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1502938

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2304:

Lys Thr His Cys Val Pro Ala Val Asp Ala Ala Ser Val Leu Pro Arg
1 5 10 15
Ile Arg Ile Thr His Ala Asn Val Pro Pro Leu Ser Trp Pro Pro Pro
20 25 30
Ala Thr Ala Arg Arg Pro Ala Ala Leu Leu Ser Ile Pro Lys Glu Gly
35 40 45
Glu Arg Ile Ile Ala Pro Thr Xaa Arg Pro Asp Gly Thr Leu Arg Lys
50 55 60
Ala Ile Arg Ile Arg Ala Gly Tyr Val Pro Gln Glu Glu Val Ala Ile
65 70 75 80
Tyr Gln Ser Lys Gly Ala Leu Met Arg Lys Ser Gly Pro Asp Val Pro
85 90 95
Pro Gly Tyr Asp Pro Ala Xaa Ser Gly Arg Arg Gln Thr Pro Pro Pro
100 105 110

(2) INFORMATION FOR SEQ ID NO:2305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..86
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502939
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2305:

Lys Pro Ile Val Cys Pro Pro Ser Thr Gln Pro Pro Ser Ser Pro Ala
1 5 10 15
Ser Glu Ser Arg Thr Pro Thr Ser His Pro Cys His Gly His Leu Gln
20 25 30
Arg Arg Arg Gly Asp Gln Arg Arg Ser Ser Pro Ser Pro Arg Lys Ala
35 40 45
Ser Ala Ser Ser Arg Pro Xaa Xaa Ala Pro Thr Ala Arg Ser Ala Arg
50 55 60
Pro Ser Ala Ser Ala Pro Val Thr Cys Pro Arg Arg Arg Ser Pro Ser
65 70 75 80
Thr Ser Pro Arg Ala Pro
85

(2) INFORMATION FOR SEQ ID NO:2306:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..102
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502940
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2306:

Asn Pro Leu Cys Ala Arg Arg Arg Arg Ser Leu Arg Pro Pro Pro His
1 5 10 15
Pro Asn His Ala Arg Gln Arg Pro Thr Pro Val Met Ala Thr Ser Ser
20 25 30
Asp Gly Ala Ala Thr Ser Gly Ala Pro Leu His Pro Gln Gly Arg Arg
35 40 45
Ala His His Arg Ala His Xaa Pro Pro Arg Arg His Ala Pro Gln Gly
50 55 60
His Pro His Pro Arg Arg Leu Arg Ala Pro Gly Gly Gly Arg His Leu
65 70 75 80
Pro Val Gln Gly Arg Pro Asn Glu Glu Val Arg Ala Arg Arg Ala Ala
85 90 95
Gly Val Arg Pro Gly Xaa
100

(2) INFORMATION FOR SEQ ID NO:2307:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 443 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..443
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1502981
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2307:

aatcgggtcaa tcacgtctac ttgcttgacg acgattctcc agggatacgt cccatctgct 60
gcgaccaggg cgatggggga ggaggagacc cgcgcaggcg acctcccga gccgtgcctg 120

gcgcacgccca tcgcgctcac ctgcgcgcgc gacgcctgcc gctgcgcgcgc cgtctccccc 180
gccttcgcgc cgcgcgcgcga ctccgactac gtctggggcc gcttcgtccc ggaggatcac 240
cgccgcgcga tcgccttgca tctgcatgcc gccggccggg accgtggggc gaggaaggac 300
gcgtaccttg cgctctgcga cggcggcggc ggccggcgctcc ccgtcgacgt cgacgtcgas 360
gccttggtgc aggtgtggc tggaccaggc cagcgssgcc aagtgtctac cgctgtcggc 420
gaggaggctc agcctgccgt ggg

(2) INFORMATION FOR SEQ ID NO:2308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2308:

Asn Arg Ser Ile Thr Ser Thr Cys Leu Gln Thr Ile Leu Gln Gly Tyr
1 5 10 15
Val Pro Ser Ala Thr Arg Ala Met Gly Glu Glu Glu Thr Arg Ala
20 25 30
Gly Asp Leu Pro Glu Pro Cys Leu Ala His Ala Ile Ala Leu Thr Ser
35 40 45
Pro Arg Asp Ala Cys Arg Cys Ala Ala Val Ser Pro Ala Phe Arg Ala
50 55 60
Ala Ala Asp Ser Asp Tyr Val Trp Gly Arg Phe Val Pro Glu Asp His
65 70 75 80
Arg Arg Ala Ile Ala Leu His Leu His Ala Ala Gly Arg Asp Arg Gly
85 90 95
Pro Arg Lys Asp Ala Tyr Leu Ala Leu Cys Asp Gly Gly Gly Gly Gly
100 105 110
Val Pro Val Asp Val Asp Val Xaa Ala Leu Val Gln Ala Val Ala Gly
115 120 125
Pro Gly Gln Xaa Xaa Gln Val Leu Arg Ala Val Gly Glu Glu Ala Gln
130 135 140
Pro Ala Val
145

(2) INFORMATION FOR SEQ ID NO:2309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2309:

Ile Gly Gln Ser Arg Leu Leu Ala Cys Arg Arg Phe Ser Arg Asp Thr
1 5 10 15
Ser His Leu Leu Arg Pro Gly Arg Trp Gly Arg Arg Arg Pro Ala Gln
20 25 30
Ala Thr Ser Arg Ser Arg Ala Trp Arg Thr Pro Ser Arg Ser Pro Arg
35 40 45
Arg Ala Thr Pro Ala Ala Ala Pro Pro Ser Pro Pro Ser Ala Pro
50 55 60
Pro Pro Thr Pro Thr Thr Ser Gly Ala Ala Ser Ser Arg Arg Ile Thr
65 70 75 80
Ala Ala Pro Ser Pro Cys Ile Cys Met Pro Pro Ala Gly Thr Val Gly

85 90 95
Arg Gly Arg Thr Arg Thr Leu Arg Ser Ala Thr Ala Ala Ala Ala Ala
100 105 110
Ser Pro Ser Thr Ser Thr Ser Xaa Pro Trp Cys Arg Leu Trp Leu Asp
115 120 125
Gln Ala Ser Xaa Ala Lys Cys Tyr Ala Leu Ser Ala Arg Arg Leu Ser
130 135 140
Leu Pro Trp
145

(2) INFORMATION FOR SEQ ID NO:2310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1502984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2310:

Ser Val Asn His Val Tyr Leu Leu Ala Asp Ser Pro Gly Ile Arg
1 5 10 15
Pro Ile Cys Cys Asp Gln Gly Asp Gly Gly Gly Gly Asp Pro Arg Arg
20 25 30
Arg Pro Pro Gly Ala Val Pro Gly Ala Arg His Arg Ala His Leu Ala
35 40 45
Ala Arg Arg Leu Pro Leu Arg Arg Arg Leu Pro Arg Leu Pro Arg Arg
50 55 60
Arg Arg Leu Arg Leu Arg Leu Gly Pro Leu Arg Pro Gly Gly Ser Pro
65 70 75 80
Pro Arg His Arg Pro Ala Ser Ala Cys Arg Arg Pro Gly Pro Trp Ala
85 90 95
Glu Glu Gly Arg Val Pro Cys Ala Leu Arg Arg Arg Arg Arg Arg Arg
100 105 110
Pro Arg Arg Arg Arg Arg Arg Xaa Leu Gly Ala Gly Cys Gly Trp Thr
115 120 125
Arg Pro Ala Xaa Pro Ser Ala Thr Arg Cys Arg Arg Gly Gly Ser Ala
130 135 140
Cys Arg Gly
145

(2) INFORMATION FOR SEQ ID NO:2311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..335

(D) OTHER INFORMATION: / Ceres Seq. ID 1502985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2311:

aaacggaac gggggcagtt ggtgagttgg gacttgggag ccgacgctgt cggggtgatc 60
cagtcgccgc cgacgccgcc gaacgccgcc gcgcccgagc ctccctctac gcggacssgg 120
naggaccctt ccactcccag agccgggcgt gtccgatcgt gagcccatgg cggaatccat 180
cgtctccggc gccgccgcc cgcgccggg ckcgcctcgt ttctcctacc tggccgtgtt 240
ctccaactgc ccgctcgtcg ccgcggtgct cgccttcgcc atcgcgagc ccatcaaggt 300
cctcaccacc tgggtataagg agaaccggtg ggacg

(2) INFORMATION FOR SEQ ID NO:2312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..111
(D) OTHER INFORMATION: / Ceres Seq. ID 1502986
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2312:
Thr Glu Thr Gly Ala Val Gly Glu Leu Gly Leu Gly Ser Arg Arg Cys
1 5 10 15
Arg Gly Asp Pro Val Ala Ala Asp Ala Ala Glu Arg Ala Arg Ala Arg
20 25 30
Ala Ser Leu Tyr Ala Asp Xaa Xaa Gly Pro Phe His Ser Gln Ser Arg
35 40 45
Ala Cys Pro Ile Val Ser Pro Trp Arg Asn Pro Ser Ser Pro Ala Pro
50 55 60
Pro Pro Arg Arg Arg Xaa Arg Pro Arg Ser Pro Thr Trp Pro Cys Ser
65 70 75 80
Pro Thr Ala Arg Ser Ser Pro Arg Cys Ser Pro Ser Pro Ser Arg Ser
85 90 95
Pro Ser Arg Ser Ser Pro Pro Gly Ile Arg Arg Thr Gly Gly Thr
100 105 110
(2) INFORMATION FOR SEQ ID NO:2313:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..56
(D) OTHER INFORMATION: / Ceres Seq. ID 1502987
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2313:
Met Ala Glu Ser Ile Val Ser Gly Ala Ala Ala Pro Pro Pro Gly Xaa
1 5 10 15
Pro Ser Phe Ser Tyr Leu Ala Val Phe Ser Asn Cys Pro Leu Val Ala
20 25 30
Ala Val Leu Ala Phe Ala Ile Ala Gln Ser Ile Lys Val Leu Thr Thr
35 40 45
Trp Tyr Lys Glu Asn Arg Trp Asp
50 55
(2) INFORMATION FOR SEQ ID NO:2314:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..505
(D) OTHER INFORMATION: / Ceres Seq. ID 1503000
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2314:
gaaggacttc cgcgtcgccg tcaagcaggt gtcgcacctg ttccaggaca actaccccga 60
gctcgtcgcg agaaacatct tgatcaacgt gccgttctgg tactacgcgt tcagcaccct 120
gttctaccgg ttcttgacgc agaggacgaa gagcaagttc gtcgttgctc gcccggtccaa 180
ggtcaccgag accctcctca agtacatttc gatcgaggcc atcccgggtga agtacggcgg 240
cctgaagcgc gacggcgaca ccgagttctc cgcggacgac ggcgaggtcg cggagggtcac 300

cgtcaagggg agctccacgg agaccatcga gatcgaagcc actgaggctg atgccacgct 360
gacatgggac ctgacgggtgc tgggggtggga ggtgaactac aaggaggagt tcgtgccggc 420
ggacgagggc tcctacacca tcatcgtcag gaagggaag aagatggcgt ccggcgagga 480
kgcggtccgc aactcgttcc gcacc

(2) INFORMATION FOR SEQ ID NO:2315:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1503001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2315:

Glu Gly Leu Pro Arg Arg Arg Gln Ala Gly Ala Arg Pro Val Pro Gly
1 5 10 15
Gln Leu Pro Arg Ala Arg Arg Glu Lys His Leu Asp Gln Arg Ala Val
20 25 30
Leu Val Leu Arg Val Gln His Pro Val Leu Pro Val Pro Asp Ala Glu
35 40 45
Asp Glu Glu Gln Val Arg Arg Cys Ser Pro Val Gln Gly His Arg Asp
50 55 60
Pro Pro Gln Val His Ser Asp Arg Gly His Pro Gly Glu Val Arg Arg
65 70 75 80
Pro Glu Ala Arg Arg Arg His Arg Val Leu Arg Gly Arg Arg Arg Gly
85 90 95
Arg Gly Gly His Arg Gln Gly Lys Leu His Gly Asp His Arg Asp Arg
100 105 110
Ser His

(2) INFORMATION FOR SEQ ID NO:2316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1503002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2316:

Lys Asp Phe Arg Val Ala Val Lys Gln Val Leu Asp Leu Phe Gln Asp
1 5 10 15
Asn Tyr Pro Glu Leu Val Ala Arg Asn Ile Leu Ile Asn Val Pro Phe
20 25 30
Trp Tyr Tyr Ala Phe Ser Thr Leu Phe Tyr Pro Phe Leu Thr Gln Arg
35 40 45
Thr Lys Ser Lys Phe Val Val Ala Arg Pro Ser Lys Val Thr Glu Thr
50 55 60
Leu Leu Lys Tyr Ile Pro Ile Glu Ala Ile Pro Val Lys Tyr Gly Gly
65 70 75 80
Leu Lys Arg Asp Gly Asp Thr Glu Phe Ser Ala Asp Asp Gly Glu Val
85 90 95
Ala Glu Val Thr Val Lys Gly Ser Ser Thr Glu Thr Ile Glu Ile Glu
100 105 110
Ala Thr Glu Ala Asp Ala Thr Leu Thr Trp Asp Leu Thr Val Leu Gly
115 120 125
Trp Glu Val Asn Tyr Lys Glu Glu Phe Val Pro Ala Asp Glu Gly Ser

130 135 140
Tyr Thr Ile Ile Val Arg Lys Gly Lys Lys Met Ala Ser Gly Glu Xaa
145 150 155 160
Ala Val Arg Asn Ser Phe Arg Thr
165

(2) INFORMATION FOR SEQ ID NO:2317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503010

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2317:

gtcgggtccat agcatcgatt cactccgcgc gcgccgctgt ctctctgctg tgcgccgcgtt	60
cctcgattat ctctccatgg cggccgctca tcccccgctg catccgccgc ctcccccggt	120
agggtgccgg cgaccctccc gcggcassag cggcgcgacg gctgggtgcc cctgccccat	180
atgcctcgaa gccttcaaag acgaggccta cctcgacact tgcttccatt ccttttgcta	240
caagtgtata tgccagtggg taaggatagt agcgagcaag cacgcagaac ctttgtcttc	300
agttagatgt ccactttgta agactgagaa tctatccgtc atacatgctt ttgatggcga	360
atcatttgag cgggtggtaca taaatcagga acytaggaag aggcgttctt tcagatgcac	420
acgagttggt gtcacaattc tataacatga aagagaccac aagcaacatt tctaggggtgc	480
agcaatactg ggagc	

(2) INFORMATION FOR SEQ ID NO:2318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2318:

Ser Val His Ser Ile Asp Ser Leu Arg Ala Arg Arg Cys Leu Leu Val	
1 5 10 15	
Val Ala Ala Phe Leu Asp Tyr Leu Ser Met Ala Ala Ala His Pro Pro	
20 25 30	
Leu His Pro Pro Pro Pro Pro Val Gly Cys Arg Arg Pro Ser Arg Gly	
35 40 45	
Xaa Ser Gly Ala Thr Ala Gly Cys Pro Cys Pro Ile Cys Leu Glu Ala	
50 55 60	
Phe Lys Asp Glu Ala Tyr Leu Asp Thr Cys Phe His Ser Phe Cys Tyr	
65 70 75 80	
Lys Cys Ile Cys Gln Trp Val Arg Ile Val Ala Ser Lys His Ala Glu	
85 90 95	
Pro Leu Ser Ser Val Arg Cys Pro Leu Cys Lys Thr Glu Asn Leu Ser	
100 105 110	
Val Ile His Ala Phe Asp Gly Glu Ser Phe Glu Arg Trp Tyr Ile Asn	
115 120 125	
Gln Glu Xaa Arg Lys Arg Arg Ser Phe Arg Cys Thr Arg Val Gly Val	
130 135 140	
Thr Ile Leu	
145	

(2) INFORMATION FOR SEQ ID NO:2319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503012
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2319:

```
Met Ala Ala Ala His Pro Pro Leu His Pro Pro Pro Pro Pro Val Gly
1      5      10      15
Cys Arg Arg Pro Ser Arg Gly Xaa Ser Gly Ala Thr Ala Gly Cys Pro
      20      25      30
Cys Pro Ile Cys Leu Glu Ala Phe Lys Asp Glu Ala Tyr Leu Asp Thr
      35      40      45
Cys Phe His Ser Phe Cys Tyr Lys Cys Ile Cys Gln Trp Val Arg Ile
      50      55      60
Val Ala Ser Lys His Ala Glu Pro Leu Ser Ser Val Arg Cys Pro Leu
      65      70      75      80
Cys Lys Thr Glu Asn Leu Ser Val Ile His Ala Phe Asp Gly Glu Ser
      85      90      95
Phe Glu Arg Trp Tyr Ile Asn Gln Glu Xaa Arg Lys Arg Arg Ser Phe
      100     105     110
Arg Cys Thr Arg Val Gly Val Thr Ile Leu
      115     120
```

(2) INFORMATION FOR SEQ ID NO:2320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 436 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..436
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2320:

```
cttttttcgg aggaggcggg ccaggtaagc agcagcagga accctagcac cgccgcacatcc      60
gcagccatgg gtatcgacct cgttgccggg gggaggaaca agaagaccaa gcgcacagcs      120
cgaagtccga cgatgtttat ctcaagctcc ttgtcaagct ctaccgtttc ttggtcagga      180
ggaccaagag caacttcaat gctgtcattc tcaagaggct cttcatgagc aaaaccaatc      240
gcccaccaat ctccatgcgc cgccttggtc agttcatgga aggaaaggag aagaacattg      300
ctgtgattgt tggcacagtc acagatgaca agaggatcca agagggtcca gcaatgaagg      360
gaagctcgat gactacatga agttccttga tggctcttcc gcttagatgt ttattttgtga      420
ctgctagggg cgatgt
```

(2) INFORMATION FOR SEQ ID NO:2321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503043

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2321:

```
Leu Phe Ser Glu Glu Ala Asp Gln Val Ser Ser Ser Arg Asn Pro Ser
1      5      10      15
Thr Ala Ala Ser Ala Ala Met Gly Ile Asp Leu Val Ala Gly Gly Arg
      20      25      30
```

Asn Lys Lys Thr Lys Arg Thr Xaa Arg Ser Pro Thr Met Phe Ile Ser
35 40 45
Ser Ser Leu Ser Ser Ser Thr Val Ser Trp Ser Gly Gly Pro Arg Ala
50 55 60
Thr Ser Met Leu Ser Phe Ser Arg Gly Ser Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:2322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..53
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503044

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2322:

Met Gly Ile Asp Leu Val Ala Gly Gly Arg Asn Lys Lys Thr Lys Arg
1 5 10 15
Thr Xaa Arg Ser Pro Thr Met Phe Ile Ser Ser Ser Leu Ser Ser
20 25 30
Thr Val Ser Trp Ser Gly Gly Pro Arg Ala Thr Ser Met Leu Ser Phe
35 40 45
Ser Arg Gly Ser Ser
50

(2) INFORMATION FOR SEQ ID NO:2323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503045

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2323:

Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met Arg Arg Leu Val Lys
1 5 10 15
Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val Ile Val Gly Thr Val
20 25 30
Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala Met Lys Gly Ser Ser
35 40 45
Met Thr Thr
50

(2) INFORMATION FOR SEQ ID NO:2324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..227
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503048

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2324:

aggacaggtt gcatttgcac ctgagttcct gatcggttgta ttccagtttc ttccgtgagt 60
tttgtgggat cgcgaggaag aaggatgtcg tgctgcggag gcaactgcgg gtgcggcgcc 120
ggggcassag ccggcgggca gtgcctgccg cagctgaacc gcctcctggs stgccgcgcg 180

tacctgggtgc ccggcgcgcc ggaccccagc gcggactgct gcagcgc

(2) INFORMATION FOR SEQ ID NO:2325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1503049

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2325:

Met	Ser	Cys	Cys	Gly	Asn	Cys	Gly	Cys	Gly	Ala	Gly	Xaa	Xaa	Ala
1			5				10					15		
Gly	Gly	Gln	Cys	Leu	Pro	Gln	Leu	Asn	Arg	Leu	Leu	Xaa	Cys	Arg
		20					25					30		
Tyr	Leu	Val	Pro	Gly	Ala	Pro	Asp	Pro	Ser	Ala	Asp	Cys	Cys	Ser
		35					40					45		

(2) INFORMATION FOR SEQ ID NO:2326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..512

(D) OTHER INFORMATION: / Ceres Seq. ID 1503064

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2326:

aattctcccc	gcctccccct	ccgaccctcc	gactaccgcc	gcctcctggs	scasstctcc	60
tccgcgggcc	tcttcgagcg	cgtcggcccc	acccccaggg	tacagctcgc	cctgatggcc	120
gtcctcttct	acgcggcgct	ctacctcgtc	ctcgctcgcg	ccassgcctc	ggcssacatg	180
ctcgctgggg	ggctcatcgg	cttcgctctg	atccagtcgg	gctggatggg	ccacgactcg	240
ggccaccacc	gcatcacggg	ccatccgctc	ctggaccgcg	tcgtgcaggt	gctctccgga	300
aactgcctca	ctggcctcag	catcgccctg	tggaaatgca	accacaacac	gcaccacatc	360
gcctgcaaca	gcctggacca	tgaccgcggac	ctccagcaca	tgccgctctt	cgctgtctcc	420
cccaagctgt	tcggcaacat	atggtcctac	tkctaccagc	ggaccctggc	cttcgacgcc	480
gcctcgaaat	tcctcatcag	ctaccagcac	tg			

(2) INFORMATION FOR SEQ ID NO:2327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1503065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2327:

Asn	Ser	Pro	Arg	Leu	Pro	Leu	Arg	Pro	Ser	Asp	Tyr	Arg	Arg	Leu	Leu
1				5					10					15	
Xaa	Xaa	Xaa	Ser	Ser	Ala	Gly	Leu	Phe	Glu	Arg	Val	Gly	Pro	Thr	Pro
			20				25					30			
Arg	Val	Gln	Leu	Ala	Leu	Met	Ala	Val	Leu	Phe	Tyr	Ala	Ala	Leu	Tyr
		35				40					45				
Leu	Val	Leu	Ala	Cys	Ala	Xaa	Ala	Ser	Xaa	Xaa	Met	Leu	Ala	Gly	Gly
	50					55					60				
Leu	Ile	Gly	Phe	Val	Trp	Ile	Gln	Ser	Gly	Trp	Met	Gly	His	Asp	Ser

65					70					75					80
Gly	His	His	Arg	Ile	Thr	Gly	His	Pro	Leu	Leu	Asp	Arg	Val	Val	Gln
				85					90					95	
Val	Leu	Ser	Gly	Asn	Cys	Leu	Thr	Gly	Leu	Ser	Ile	Ala	Trp	Trp	Lys
			100					105					110		
Cys	Asn	His	Asn	Thr	His	His	Ile	Ala	Cys	Asn	Ser	Leu	Asp	His	Asp
		115					120					125			
Pro	Asp	Leu	Gln	His	Met	Pro	Leu	Phe	Ala	Val	Ser	Pro	Lys	Leu	Phe
		130					135				140				
Gly	Asn	Ile	Trp	Ser	Tyr	Xaa	Tyr	Gln	Arg	Thr	Leu	Ala	Phe	Asp	Ala
145					150					155					160
Ala	Ser	Lys	Phe	Leu	Ile	Ser	Tyr	Gln	His						
				165					170						

(2) INFORMATION FOR SEQ ID NO:2328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..126
(D) OTHER INFORMATION: / Ceres Seq. ID 1503066

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2328:

Phe	Ser	Pro	Pro	Pro	Pro	Pro	Thr	Leu	Arg	Leu	Pro	Pro	Pro	Pro	Xaa
1				5				10						15	
Xaa	Xaa	Leu	Leu	Arg	Gly	Pro	Leu	Arg	Ala	Arg	Arg	Pro	His	Pro	Gln
		20						25					30		
Gly	Thr	Ala	Arg	Pro	Asp	Gly	Arg	Pro	Leu	Leu	Arg	Gly	Ala	Leu	Pro
		35				40						45			
Arg	Pro	Arg	Leu	Arg	Xaa	Xaa	Leu	Gly	Xaa	His	Ala	Arg	Trp	Gly	Ala
	50					55					60				
His	Arg	Leu	Arg	Leu	Asp	Pro	Val	Arg	Leu	Asp	Gly	Pro	Arg	Leu	Gly
65				70						75				80	
Pro	Pro	Pro	His	His	Gly	Pro	Ser	Ala	Pro	Gly	Pro	Arg	Arg	Ala	Gly
				85				90						95	
Ala	Leu	Arg	Lys	Leu	Pro	His	Trp	Pro	Gln	His	Arg	Leu	Val	Glu	Met
			100					105					110		
Gln	Pro	Gln	His	Ala	Pro	His	Arg	Leu	Gln	Gln	Pro	Gly	Pro		
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:2329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..132
(D) OTHER INFORMATION: / Ceres Seq. ID 1503067

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2329:

Met	Ala	Val	Leu	Phe	Tyr	Ala	Ala	Leu	Tyr	Leu	Val	Leu	Ala	Cys	Ala
1				5					10					15	
Xaa	Ala	Ser	Xaa	Xaa	Met	Leu	Ala	Gly	Gly	Leu	Ile	Gly	Phe	Val	Trp
			20					25					30		
Ile	Gln	Ser	Gly	Trp	Met	Gly	His	Asp	Ser	Gly	His	His	Arg	Ile	Thr
		35				40						45			
Gly	His	Pro	Leu	Leu	Asp	Arg	Val	Val	Gln	Val	Leu	Ser	Gly	Asn	Cys
	50					55					60				

[illegible]

(2) INFORMATION FOR SEQ ID NO:2330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..305
(D) OTHER INFORMATION: / Ceres Seq. ID 1503071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2330:

catgaagaaa	agaaaggcgg	tatccagacc	tcaagccctg	ctctgaagga	ggagctgcgc	60
aagaggctga	gcgttgctga	agatgatgag	gatttaagct	gggatatcga	ggatgacgat	120
gacaatgcct	gaataccatt	ggtgatatgg	aagtgtcagt	tgkattttcta	cattttgcac	180
cttccattac	tcgtgcaagt	tactgtgatt	tggccaatwa	gattggctat	ccttatgcta	240
tggacacggt	tgtatactgt	aaactctcca	gtttgatgat	atcaagtggc	aattggctaa	300
gcgc						

(2) INFORMATION FOR SEQ ID NO:2331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..43
(D) OTHER INFORMATION: / Ceres Seq. ID 1503072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2331:

His Glu Glu Lys Lys Gly Gly Ile Gln Thr Ser Ser Pro Ala Leu Lys
1 5 10 15
Glu Glu Leu Arg Lys Arg Leu Ser Val Ala Glu Asp Asp Glu Asp Leu
20 25 30
Ser Trp Asp Ile Glu Asp Asp Asp Asn Ala
35 40

(2) INFORMATION FOR SEQ ID NO:2332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1503073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2332:

Met Glu Val Ser Val Xaa Phe Leu His Phe Ala Pro Ser Ile Thr Arg
1 5 10 15
Ala Ser Tyr Cys Asp Leu Ala Asn Xaa Ile Gly Tyr Pro Tyr Ala Met

[illegible]

20 25 30
Asp Thr Phe Val Tyr Cys Lys Leu Ser Ser Leu Met Ile Ser Ser Gly
35 40 45
Asn Trp Leu Ser Ala
50

(2) INFORMATION FOR SEQ ID NO:2333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..414

(D) OTHER INFORMATION: / Ceres Seq. ID 1503104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2333:

atcccacgaa aacaagcaca gagagagaga gaaccccagc gggcaaacgc ctccctcccc	60
ctgcctccag gccccagatc cggccatccg ggtagctcca gaccttctcc aatggcggtc	120
aaggtctacg tcgtgtttta ctccacctac gggcacgttg ccaagcttgc tgaggagatg	180
aagaaaggcg ccgcttcagt tgaaggcgtg gaggtcaaag tatggcaggt cccggagatt	240
ctgtccgagg aggtgctcgg caagatgggc gcgccacca agaccgacgc gccggtcac	300
accccgacga gctggcggag gccgacggcg tcctcttcgg gttccccacg cggttcggca	360
tgatggcggc gcagatgaag gccttcttcg acgcgaccgg cgggctgtgg cgcg	

(2) INFORMATION FOR SEQ ID NO:2334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1503105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2334:

Ile Pro Arg Lys Gln Ala Gln Arg Glu Arg Glu Pro Gln Arg Ala Asn	
1 5 10 15	
Ala Ser Leu Pro Leu Pro Pro Gly Pro Arg Ser Gly His Pro Gly Ser	
20 25 30	
Ser Arg Pro Ser Pro Met Ala Val Lys Val Tyr Val Val Phe Tyr Ser	
35 40 45	
Thr Tyr Gly His Val Ala Lys Leu Ala Glu Glu Met Lys Lys Gly Ala	
50 55 60	
Ala Ser Val Glu Gly Val Glu Val Lys Val Trp Gln Val Pro Glu Ile	
65 70 75 80	
Leu Ser Glu Glu Val Leu Gly Lys Met Gly Ala Pro Pro Lys Thr Asp	
85 90 95	
Ala Pro Val Ile Thr Pro Gln Ser Trp Arg Arg Pro Thr Ala Ser Ser	
100 105 110	
Ser Gly Ser Pro Arg Gly Ser Ala	
115 120	

(2) INFORMATION FOR SEQ ID NO:2335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1503106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2335:

```
Met Ala Val Lys Val Tyr Val Val Phe Tyr Ser Thr Tyr Gly His Val
1      5      10      15
Ala Lys Leu Ala Glu Glu Met Lys Lys Gly Ala Ala Ser Val Glu Gly
20     25     30
Val Glu Val Lys Val Trp Gln Val Pro Glu Ile Leu Ser Glu Glu Val
35     40     45
Leu Gly Lys Met Gly Ala Pro Pro Lys Thr Asp Ala Pro Val Ile Thr
50     55     60
Pro Gln Ser Trp Arg Arg Pro Thr Ala Ser Ser Ser Gly Ser Pro Arg
65     70     75     80
Gly Ser Ala
```

(2) INFORMATION FOR SEQ ID NO:2336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1503107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2336:

```
Met Ala Gly Pro Gly Asp Ser Val Arg Gly Gly Ala Arg Gln Asp Gly
1      5      10      15
Arg Ala Thr Gln Asp Arg Arg Ala Gly His His Pro Ala Glu Leu Ala
20     25     30
Glu Ala Asp Gly Val Leu Phe Gly Phe Pro Thr Arg Phe Gly Met Met
35     40     45
Ala Ala Gln Met Lys Ala Phe Phe Asp Ala Thr Gly Gly Leu Trp Arg
50     55     60
```

(2) INFORMATION FOR SEQ ID NO:2337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..510

(D) OTHER INFORMATION: / Ceres Seq. ID 1503108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2337:

```
gtkattgggt tggtcgcttg gttcttcctt gccggaagat acctttcggt cggtgtcgcc      60
aactcgccat tcttgggagg tcttggtcgg gaccggtgct gatggaggag aggtacgagg      120
cgctgaagga gctgggggcc ggcaacttcg gcgtggcgag gctggtcagg gacaagcgga      180
ccaaggagct ggtagccgtc aagtacatcg agaggggcaa gaagattgat gagaacgtgc      240
agagggagat catcaatcac cagtcgctcc ggcaccctaa catcgtacgg ttcaaggagg      300
ttgtctaac acccacacat cttgctattg tcatggaata tgctgctggt ggagagctat      360
ttgagaaaat ctgctcagca gggcgattca gtgaagatgw ktccagggtat ttcttccaac      420
agctgatatc aggggttcag ctactgccat tctatggaaa tttgtcaccg tgatctttaa      480
acttkagaac accctccttg atgggagtc
```

(2) INFORMATION FOR SEQ ID NO:2338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..156
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2338:

Xaa	Trp	Val	Gly	Arg	Leu	Val	Leu	Pro	Cys	Arg	Lys	Ile	Pro	Phe	Val
1			5					10						15	
Arg	Cys	Arg	Gln	Leu	Ala	Ile	Leu	Gly	Arg	Ser	Trp	Ser	Gly	Pro	Val
			20					25					30		
Leu	Met	Glu	Glu	Arg	Tyr	Glu	Ala	Leu	Lys	Glu	Leu	Gly	Ala	Gly	Asn
			35				40					45			
Phe	Gly	Val	Ala	Arg	Leu	Val	Arg	Asp	Lys	Arg	Thr	Lys	Glu	Leu	Val
			50			55				60					
Ala	Val	Lys	Tyr	Ile	Glu	Arg	Gly	Lys	Lys	Ile	Asp	Glu	Asn	Val	Gln
65					70					75				80	
Arg	Glu	Ile	Ile	Asn	His	Gln	Ser	Leu	Arg	His	Pro	Asn	Ile	Val	Arg
				85				90					95		
Phe	Lys	Glu	Val	Cys	Leu	Thr	Pro	Thr	His	Leu	Ala	Ile	Val	Met	Glu
			100					105					110		
Tyr	Ala	Ala	Gly	Gly	Glu	Leu	Phe	Glu	Lys	Ile	Cys	Ser	Ala	Gly	Arg
		115				120						125			
Phe	Ser	Glu	Asp	Xaa	Ser	Arg	Tyr	Phe	Phe	Gln	Gln	Leu	Ile	Ser	Gly
		130				135					140				
Val	Gln	Leu	Leu	Pro	Phe	Tyr	Gly	Asn	Leu	Ser	Pro				
145				150						155					

(2) INFORMATION FOR SEQ ID NO:2339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..123
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2339:

Met	Glu	Glu	Arg	Tyr	Glu	Ala	Leu	Lys	Glu	Leu	Gly	Ala	Gly	Asn	Phe
1				5					10					15	
Gly	Val	Ala	Arg	Leu	Val	Arg	Asp	Lys	Arg	Thr	Lys	Glu	Leu	Val	Ala
			20					25				30			
Val	Lys	Tyr	Ile	Glu	Arg	Gly	Lys	Lys	Ile	Asp	Glu	Asn	Val	Gln	Arg
			35				40				45				
Glu	Ile	Ile	Asn	His	Gln	Ser	Leu	Arg	His	Pro	Asn	Ile	Val	Arg	Phe
			50			55				60					
Lys	Glu	Val	Cys	Leu	Thr	Pro	Thr	His	Leu	Ala	Ile	Val	Met	Glu	Tyr
65				70					75					80	
Ala	Ala	Gly	Gly	Glu	Leu	Phe	Glu	Lys	Ile	Cys	Ser	Ala	Gly	Arg	Phe
			85					90					95		
Ser	Glu	Asp	Xaa	Ser	Arg	Tyr	Phe	Phe	Gln	Gln	Leu	Ile	Ser	Gly	Val
			100				105						110		
Gln	Leu	Leu	Pro	Phe	Tyr	Gly	Asn	Leu	Ser	Pro					
		115				120									

(2) INFORMATION FOR SEQ ID NO:2340:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 263 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..263
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503132
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2340:

accagccggt gttggtttca gcttgatttc ccactctgtc gcacagcgtc gcccgctcgcc	60
gctgagatcc taggaagaaa tggagctctc tcgcaagctc ttcacggccg tcctcctcgt	120
catgctgctg ctgctgtccg cagaggtcgg gccggtggcg gtggcggagg cgcggacgtg	180
ccagtcgcag agccacaggt tccggggccc ctgcctccgc cggccaact gcgccaacgt	240
ctgcaggacc gaggggttcc ccg	

(2) INFORMATION FOR SEQ ID NO:2341:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..87
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503133
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2341:

Thr	Ser	Arg	Cys	Trp	Phe	Gln	Leu	Val	Phe	Pro	Leu	Cys	Arg	Thr	Ala	
1				5						10				15		
Ser	Pro	Val	Ala	Ala	Glu	Ile	Leu	Gly	Arg	Asn	Gly	Ala	Leu	Ser	Gln	
			20					25				30				
Ala	Leu	His	Gly	Arg	Pro	Pro	Arg	His	Ala	Ala	Ala	Ala	Val	Arg	Arg	
		35				40						45				
Gly	Arg	Ala	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Asp	Val	Pro	Val	Ala	Glu	
	50				55					60						
Pro	Gln	Val	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Val	Gln	Leu	Arg	Gln	Arg	
65				70						75				80		
Leu	Gln	Asp	Arg	Gly	Val	Pro										
				85												

(2) INFORMATION FOR SEQ ID NO:2342:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..61
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503134
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2342:

Met	Glu	Leu	Ser	Arg	Lys	Leu	Phe	Thr	Ala	Val	Leu	Val	Met	Leu	
1				5					10				15		
Leu	Leu	Leu	Ser	Ala	Glu	Val	Gly	Pro	Val	Ala	Val	Ala	Glu	Ala	Arg
			20					25				30			
Thr	Cys	Gln	Ser	Gln	Ser	His	Arg	Phe	Arg	Gly	Pro	Cys	Leu	Arg	Arg
		35				40						45			
Ser	Asn	Cys	Ala	Asn	Val	Cys	Arg	Thr	Glu	Gly	Phe	Pro			
50				55								60			

(2) INFORMATION FOR SEQ ID NO:2343:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..47
(D) OTHER INFORMATION: / Ceres Seq. ID 1503135
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2343:

Met Leu Leu Leu Ser Ala Glu Val Gly Pro Val Ala Val Ala Glu
1 5 10 15
Ala Arg Thr Cys Gln Ser Gln Ser His Arg Phe Arg Gly Pro Cys Leu
20 25 30
Arg Arg Ser Asn Cys Ala Asn Val Cys Arg Thr Glu Gly Phe Pro
35 40 45

(2) INFORMATION FOR SEQ ID NO:2344:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 342 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..342
(D) OTHER INFORMATION: / Ceres Seq. ID 1503136
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2344:

tccaccaccg cttcaccatc cctccaggc ccaccaccac catggcctct ccttccccctt 60
cttccccgc cgcgcctcc ggccgcgcg tgccgcgcgc gtgctggacg accgacgaga 120
cctcgcgct cgcgssgtc ctacaccgc cccgcctcgc cgtcggcccg gagcacctga 180
cctccaccga ctgggccgcc gtagccgcg cgccccgtcc aagaccgcca gcagtgccgc 240
cacaagatcg agaagctccg ccgacgcctc cgttccaacc gccgacgccc atgccgcctt 300
cctcgacgcc atggatctcc tcgacggccc tttccccgcc ct

(2) INFORMATION FOR SEQ ID NO:2345:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..113
(D) OTHER INFORMATION: / Ceres Seq. ID 1503137
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2345:

Pro Pro Pro Leu His His Pro Leu Gln Ala His His His His Gly Leu
1 5 10 15
Ser Phe Pro Phe Phe Pro Arg Pro Arg Pro Pro Arg Ala Ala
20 25 30
Ala Val Leu Asp Asp Arg Arg Asp Pro Arg Ala Arg Xaa Gly Pro Thr
35 40 45
Pro Arg Pro Pro Arg Arg Arg Pro Gly Ala Pro Asp Leu His Arg Leu
50 55 60
Gly Arg Arg Ser Arg Gly Ala Pro Ser Lys Thr Ala Ser Ser Ala Ala
65 70 75 80
Thr Arg Ser Arg Ser Ser Ala Asp Ala Ser Gly Pro Thr Ala Asp Ala
85 90 95
His Ala Arg Phe Leu Asp Ala Met Asp Leu Leu Asp Gly Pro Phe Pro
100 105 110
Ala

(2) INFORMATION FOR SEQ ID NO:2346:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..113
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503138
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2346:
His His Arg Phe Thr Ile Pro Ser Arg Pro Thr Thr Thr Met Ala Ser
1 5 10 15
Pro Ser Pro Ser Ser Pro Ala Arg Ala Ser Gly Arg Arg Val Pro Pro
 20 25 30
Pro Cys Trp Thr Thr Asp Glu Thr Leu Ala Leu Ala Xaa Val Leu His
 35 40 45
Arg Ala Arg Leu Ala Val Gly Arg Glu His Leu Thr Ser Thr Asp Trp
 50 55 60
Ala Ala Val Ala Ala Ala Pro Arg Pro Arg Pro Pro Ala Val Pro Pro
65 70 75 80
Gln Asp Arg Glu Ala Pro Pro Thr Pro Pro Val Gln Pro Pro Thr Pro
 85 90 95
Met Pro Ala Ser Ser Thr Pro Trp Ile Ser Ser Thr Ala Leu Ser Pro
 100 105 110
Pro

(2) INFORMATION FOR SEQ ID NO:2347:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..100
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503139
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2347:
Met Ala Ser Pro Ser Pro Ser Ser Pro Ala Arg Ala Ser Gly Arg Arg
1 5 10 15
Val Pro Pro Pro Cys Trp Thr Thr Asp Glu Thr Leu Ala Leu Ala Xaa
 20 25 30
Val Leu His Arg Ala Arg Leu Ala Val Gly Arg Glu His Leu Thr Ser
 35 40 45
Thr Asp Trp Ala Ala Val Ala Ala Ala Pro Arg Pro Arg Pro Pro Ala
 50 55 60
Val Pro Pro Gln Asp Arg Glu Ala Pro Pro Thr Pro Pro Val Gln Pro
65 70 75 80
Pro Thr Pro Met Pro Ala Ser Ser Thr Pro Trp Ile Ser Ser Thr Ala
 85 90 95
Leu Ser Pro Pro
 100

(2) INFORMATION FOR SEQ ID NO:2348:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..536

(D) OTHER INFORMATION: / Ceres Seq. ID 1503144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2348:

attacacacc	agcctcttga	tgcaggtttt	agtgccattg	tggaatcatg	caaggkcctc	60
agkcggtttt	ctgtttcagg	tcctttctcac	ggacagtgtg	tttaaatacca	tcggggcaca	120
tgtgaccgt	cttgagatgc	tctcgattgc	cttcgccggg	aacagtgtg	tgggcctcca	180
ttacatccta	tcgggctgca	agagcttgaa	gaagctagag	attagggact	gcccatttgg	240
tgacaagccc	ttgttgcaa	acgctgcca	gctggagaca	atgcgatccc	tttgatgtc	300
gacgtgtca	atgaccttgg	gcgcatgcgg	cagcttgccg	gcaagatgcc	ccgtcttagt	360
gtggagggtca	tgaatgatcc	tcgacgagga	ttccccttgg	actctctaac	agatgagagc	420
cctgttgaga	cgttgtatgt	ctaccggaca	atttcagggtc	caakgtccka	cacaccagct	480
tgtgtccaga	ttctctaagg	ggcagctgtg	gtctacaaaag	gtactatgga	agcatc	

(2) INFORMATION FOR SEQ ID NO:2349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2349:

Leu	His	Thr	Ser	Leu	Leu	Met	Gln	Val	Leu	Val	Pro	Leu	Trp	Asn	His	
1				5				10						15		
Ala	Arg	Xaa	Ser	Xaa	Gly	Phe	Leu	Phe	Gln	Val	Leu	Leu	Thr	Asp	Ser	
			20					25					30			
Val	Phe	Lys	Ser	Ile	Gly	Ala	His	Ala	Asp	Arg	Leu	Glu	Met	Leu	Ser	
		35					40					45				
Ile	Ala	Phe	Ala	Gly	Asn	Ser	Asp	Leu	Gly	Leu	His	Tyr	Ile	Leu	Ser	
	50					55					60					
Gly	Cys	Lys	Ser	Leu	Lys	Lys	Leu	Glu	Ile	Arg	Asp	Cys	Pro	Phe	Gly	
65					70					75				80		
Asp	Lys	Pro	Leu	Leu	Ala	Asn	Ala	Ala	Lys	Leu	Glu	Thr	Met	Arg	Ser	
				85					90					95		
Leu	Trp	Met	Ser	Thr	Cys	Ser	Met	Thr	Leu	Gly	Ala	Cys	Gly	Ser	Leu	
			100					105					110			
Arg	Ala	Arg	Cys	Pro	Val	Leu	Val	Trp	Arg	Ser						
			115					120								

(2) INFORMATION FOR SEQ ID NO:2350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1503146

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2350:

Met	Gln	Val	Leu	Val	Pro	Leu	Trp	Asn	His	Ala	Arg	Xaa	Ser	Xaa	Gly	
1				5				10						15		
Phe	Leu	Phe	Gln	Val	Leu	Leu	Thr	Asp	Ser	Val	Phe	Lys	Ser	Ile	Gly	
			20					25					30			
Ala	His	Ala	Asp	Arg	Leu	Glu	Met	Leu	Ser	Ile	Ala	Phe	Ala	Gly	Asn	
	35					40					45					
Ser	Asp	Leu	Gly	Leu	His	Tyr	Ile	Leu	Ser	Gly	Cys	Lys	Ser	Leu	Lys	
	50					55					60					

Lys Leu Glu Ile Arg Asp Cys Pro Phe Gly Asp Lys Pro Leu Leu Ala
65 70 75 80
Asn Ala Ala Lys Leu Glu Thr Met Arg Ser Leu Trp Met Ser Thr Cys
85 90 95
Ser Met Thr Leu Gly Ala Cys Gly Ser Leu Arg Ala Arg Cys Pro Val
100 105 110
Leu Val Trp Arg Ser
115

(2) INFORMATION FOR SEQ ID NO:2351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1503147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2351:

Met Leu Ser Ile Ala Phe Ala Gly Asn Ser Asp Leu Gly Leu His Tyr
1 5 10 15
Ile Leu Ser Gly Cys Lys Ser Leu Lys Lys Leu Glu Ile Arg Asp Cys
20 25 30
Pro Phe Gly Asp Lys Pro Leu Leu Ala Asn Ala Ala Lys Leu Glu Thr
35 40 45
Met Arg Ser Leu Trp Met Ser Thr Cys Ser Met Thr Leu Gly Ala Cys
50 55 60
Gly Ser Leu Arg Ala Arg Cys Pro Val Leu Val Trp Arg Ser
65 70 75

(2) INFORMATION FOR SEQ ID NO:2352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..165

(D) OTHER INFORMATION: / Ceres Seq. ID 1503148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2352:

atcaatgcgc gggtcaggct ctggaagcca atgggtggagg agatgtacgt ggaggagatg 60
aaggccgagg gcaggacggc gggggccagc agcaggtagg cgtcgcgkcg ccaacaaccc 120
taaccctagc agcgcgggcc acgcctccga ggcggcgtga ggacg

(2) INFORMATION FOR SEQ ID NO:2353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..32

(D) OTHER INFORMATION: / Ceres Seq. ID 1503149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2353:

Ile Asn Ala Arg Val Arg Leu Trp Lys Pro Met Val Glu Glu Met Tyr
1 5 10 15
Val Glu Glu Met Lys Ala Glu Gly Arg Thr Ala Gly Ala Ser Ser Arg
20 25 30

(2) INFORMATION FOR SEQ ID NO:2354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..54

(D) OTHER INFORMATION: / Ceres Seq. ID 1503150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2354:

Gln Cys Ala Gly Gln Ala Leu Glu Ala Asn Gly Gly Gly Asp Val Arg
1 5 10 15
Gly Gly Asp Glu Gly Arg Gly Gln Asp Gly Gly Gly Gln Gln Gln Val
20 25 30
Gly Val Ala Xaa Pro Thr Thr Leu Thr Leu Ala Ala Pro Ala Thr Pro
35 40 45
Pro Arg Arg Arg Glu Asp
50

(2) INFORMATION FOR SEQ ID NO:2355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..453

(D) OTHER INFORMATION: / Ceres Seq. ID 1503151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2355:

ctctccagcg gctccagcca atccggcaat cccgctcccc cagctcgctg ctcgccccgct	60
ctcctccgcc ctccgccatg gsgccttccc ctccgcctcc cgcgcgccg cgatctccgc	120
ctcgacctgg agcatggctt cctcccgtag gtccctcccc gcaactccgcc cctccccgcg	180
gggcaggctc cgttcgctcg tctcgccccg gggcggtcc acggctgcat cggtcggtg	240
cctcggggtc ttctccggcc tgcgcgccgt ctccaatctc ctctccctcg gcgctgagaa	300
ctcaagcttt gakatcggt tgtttggatt gatgcccgtg gaaggatagt tgcgatgcga	360
catgggagac gcgttcctaa acttaacagg cctccggatc aaaggaaagc actgctgcgt	420
gggcttacca cacagctgct gaagcatggg agg	

(2) INFORMATION FOR SEQ ID NO:2356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1503152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2356:

Leu Ser Ser Gly Ser Ser Gln Ser Gly Asn Pro Ala Pro Pro Ala Arg
1 5 10 15
Cys Ser Pro Ala Leu Leu Arg Pro Pro Pro Trp Xaa Leu Pro Leu Arg
20 25 30
Leu Pro Val Ala Gly Asp Leu Arg Leu Asp Leu Glu His Gly Phe Pro
35 40 45
Pro Tyr Val Pro Pro Arg Thr Pro Pro Leu Pro Arg Gly Gln Ala Pro

50 55 60
Phe Val Val Leu Ala Arg Gly Ala Val His Gly Cys Ile Gly Arg Leu
65 70 75 80
Pro Arg Val Leu Leu Arg Pro Arg Ala Arg Leu Glu Ser Pro Leu Pro
85 90 95
Arg Arg

(2) INFORMATION FOR SEQ ID NO:2357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..115

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2357:

Ser Pro Ala Ala Pro Ala Asn Pro Ala Ile Pro Leu Pro Gln Leu Ala
1 5 10 15
Ala Arg Pro Leu Ser Ser Ala Leu Arg His Xaa Ala Phe Pro Ser Ala
20 25 30
Ser Pro Ser Pro Ala Ile Ser Ala Ser Thr Trp Ser Met Ala Ser Leu
35 40 45
Arg Thr Ser Leu Pro Ala Leu Arg Pro Ser Pro Ala Gly Arg Leu Arg
50 55 60
Ser Ser Phe Ser Pro Ala Gly Arg Ser Thr Ala Ala Ser Val Gly Cys
65 70 75 80
Leu Gly Ser Phe Ser Gly Leu Ala Pro Val Ser Asn Leu Leu Ser Leu
85 90 95
Gly Ala Glu Asn Ser Ser Phe Xaa His Arg Leu Phe Gly Leu Met Pro
100 105 110
Val Glu Gly
115

(2) INFORMATION FOR SEQ ID NO:2358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..109

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2358:

Leu Gln Arg Leu Gln Pro Ile Arg Gln Ser Arg Ser Pro Ser Ser Leu
1 5 10 15
Leu Ala Arg Ser Pro Pro Pro Ser Ala Met Xaa Pro Ser Pro Pro Pro
20 25 30
Pro Arg Arg Arg Arg Ser Pro Pro Arg Pro Gly Ala Trp Leu Pro Ser
35 40 45
Val Arg Pro Ser Pro His Ser Ala Pro Pro Pro Arg Ala Gly Ser Val
50 55 60
Arg Arg Ser Arg Pro Arg Gly Gly Pro Arg Leu His Arg Ser Ala Ala
65 70 75 80
Ser Gly Pro Ser Pro Ala Ser Arg Pro Ser Arg Ile Ser Ser Pro Ser
85 90 95
Ala Leu Arg Thr Gln Ala Leu Xaa Ile Gly Cys Leu Asp
100 105

(2) INFORMATION FOR SEQ ID NO:2359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..455
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2359:

aaaggatgca ctggttccag ttcaacctcc ctgagctgtg atgggaatcg cattccctct	60
ataattccta taaatagggg cctcccgcct cccatcacia tcacccatca ctcgctatat	120
tccatttcca agtccccgct cttggattcc cgacgacgag ctcggagctt cttcttccct	180
gctcgggtgct cgccgcaaca gctgccgcca tgtctgccgc gaaccagctc gccgctctgg	240
tcagcaacat gtacgccacg ggtttgcttg acgatcagtt ccagcagctc cagctsstcc	300
aggaccccgag cgcccctgac tttcgtctcc gaggtcgtca cgctcttctg tcaggacggc	360
gagcggatca tcgaagagct ggccaaactg ctggagaagc ccaacgtgga ttttgacagg	420
gttgacgcct ytggtcatca gtcgaaggga agcag	

(2) INFORMATION FOR SEQ ID NO:2360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..151
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2360:

Lys	Gly	Cys	Thr	Gly	Ser	Ser	Ser	Ser	Ser	Leu	Ser	Cys	Asp	Gly	Asn	
1				5						10				15		
Arg	Ile	Pro	Ser	Ile	Ile	Pro	Ile	Asn	Arg	Gly	Pro	Pro	Ala	Pro	Ile	
			20					25					30			
Thr	Ile	Thr	His	His	Ser	Leu	Tyr	Ser	His	Ser	Lys	Ser	Pro	Leu	Leu	
			35				40					45				
Asp	Ser	Arg	Arg	Arg	Ala	Arg	Ser	Phe	Phe	Phe	Pro	Ala	Arg	Cys	Ser	
			50			55					60					
Pro	Gln	Gln	Leu	Pro	Pro	Cys	Leu	Pro	Arg	Thr	Ser	Ser	Pro	Leu	Trp	
65					70				75					80		
Ser	Ala	Thr	Cys	Thr	Pro	Arg	Val	Cys	Leu	Thr	Ile	Ser	Ser	Ser	Ser	
			85					90						95		
Ser	Ser	Xaa	Ser	Arg	Thr	Pro	Ala	Pro	Leu	Thr	Phe	Val	Ser	Glu	Val	
			100				105						110			
Val	Thr	Leu	Phe	Cys	Gln	Asp	Gly	Glu	Arg	Ile	Ile	Glu	Glu	Leu	Ala	
			115			120						125				
Lys	Leu	Leu	Glu	Lys	Pro	Asn	Val	Asp	Phe	Asp	Arg	Val	Asp	Ala	Xaa	
			130			135					140					
Val	His	Gln	Leu	Lys	Gly	Ser										
145					150											

(2) INFORMATION FOR SEQ ID NO:2361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..461

(D) OTHER INFORMATION: / Ceres Seq. ID 1503170

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2361:

ctatggactt	cgttgaaggt	ttgcctcgct	cacagcatgc	tgattgcac	ctggttattg	60
tgacaaaatt	ctctaaatat	ggccacttcc	ttccactcag	tcattccctat	actgctcact	120
cggttgctca	cagcttcttg	ttcaatgttt	acaagatcca	tggcctttct	tcagttatta	180
tttcggatcg	tgacctagtg	ttcaccagcc	agttttggca	acaaccgttt	cgtcttgccg	240
gcattgagct	taagccgagt	tcttcttacc	atccccaaac	cgacggacag	accgaacaag	300
tcaatcaatg	cttggaacaa	tatctgcgct	gcttcgcaaa	tgtctgccca	acgaaatgga	360
aagagtgggt	gcctgtgggc	gagtactggt	acaacaccag	cctccactct	gcactggggc	420
gtgcaccatt	tgaggttctt	tatggccgcc	aaccccgta	c		

(2) INFORMATION FOR SEQ ID NO:2362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1503171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2362:

Met	Asp	Phe	Val	Glu	Gly	Leu	Pro	Arg	Ser	Gln	His	Ala	Asp	Cys	Ile	
1			5					10						15		
Leu	Val	Ile	Val	Asp	Lys	Phe	Ser	Lys	Tyr	Gly	His	Phe	Leu	Pro	Leu	
			20					25					30			
Ser	His	Pro	Tyr	Thr	Ala	His	Ser	Val	Ala	His	Ser	Phe	Leu	Phe	Asn	
			35				40					45				
Val	Tyr	Lys	Ile	His	Gly	Leu	Ser	Ser	Val	Ile	Ile	Ser	Asp	Arg	Asp	
			50			55					60					
Leu	Val	Phe	Thr	Ser	Gln	Phe	Trp	Gln	Gln	Pro	Phe	Arg	Leu	Ala	Gly	
65					70				75					80		
Ile	Glu	Leu	Lys	Pro	Ser	Ser	Ser	Tyr	His	Pro	Gln	Thr	Asp	Gly	Gln	
				85				90					95			
Thr	Glu	Gln	Val	Asn	Gln	Cys	Leu	Glu	Thr	Tyr	Leu	Arg	Cys	Phe	Ala	
			100					105					110			
Asn	Val	Cys	Pro	Thr	Lys	Trp	Lys	Glu	Trp	Leu	Pro	Val	Gly	Glu	Tyr	
			115				120					125				
Trp	Tyr	Asn	Thr	Ser	Leu	His	Ser	Ala	Leu	Gly	Arg	Ala	Pro	Phe	Glu	
			130			135					140					
Val	Leu	Tyr	Gly	Arg	Gln	Pro	Arg	Thr								
145					150											

(2) INFORMATION FOR SEQ ID NO:2363:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1503172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2363:

Met	Asp	Phe	Val	Glu	Gly	Leu	Pro	Arg	Ser	Gln	His	Ala	Asp	Cys	Ile	
1			5					10						15		
Leu	Val	Ile	Val	Asp	Lys	Phe	Ser	Lys	Tyr	Gly	His	Phe	Leu	Pro	Leu	
			20					25					30			
Ser	His	Pro	Tyr	Thr	Ala	His	Ser	Val	Ala	His	Ser	Phe	Leu	Phe	Asn	
			35				40					45				

Val Tyr Lys Ile His Gly Leu Ser Ser Val Ile Ile Ser Asp Arg Asp
50 55 60
Leu Val Phe Thr Ser Gln Phe Trp Gln Gln Pro Phe Arg Leu Ala Gly
65 70 75 80
Ile Glu Leu Lys Pro Ser Ser Ser Tyr His Pro Gln Thr Asp Gly Gln
85 90 95
Thr Glu Gln Val Asn Gln Cys Leu Glu Thr Tyr Leu Arg Cys Phe Ala
100 105 110
Asn Val Cys Pro Thr Lys Trp Lys Glu Trp Leu Pro Val Gly Glu Tyr
115 120 125
Trp Tyr Asn Thr Ser Leu His Ser Ala Leu Gly Arg Ala Pro Phe Glu
130 135 140
Val Leu Tyr Gly Arg Gln Pro Arg Thr
145 150

(2) INFORMATION FOR SEQ ID NO:2364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..456
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2364:

acacttcgat	cagtgtcgcc	aacaagtagc	tagacgatga	gcagaggagc	tgagaagaag	60
aattggccgc	cgtctcggtc	ttcttcctcc	tcctcttctt	caccgacgtc	gtcgtnggggt	120
cgccagcagg	tccatggcgg	ggttctaccg	ctacccgccc	tccactcgca	cctccggcaw	180
kgacagaacc	cagccgcccgc	cagcaccagc	tgcaccgaca	caacaacaag	gcgacaagag	240
cagcagcaag	aagaagagga	ggagtatcag	catcgggccg	agcatcacgt	gcgcgggctc	300
catctgcagt	accaaggaga	gctcggtcat	gagccgggac	cgccgcggcg	cctccagcag	360
gtcgctcagg	gcaccctacg	tcgacgtcga	cgtcaacgac	gcctctgccc	ccgccatctc	420
cgccacgtcg	tccttcaact	cggagaccac	cgtggc			

(2) INFORMATION FOR SEQ ID NO:2365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2365:

Met Ser Arg Gly Ala Glu Lys Lys Asn Trp Pro Pro Ser Arg Ser Ser
1 5 10 15
Ser Ser Ser Ser Ser Ser Pro Thr Ser Ser Xaa Gly Arg Gln Gln Val
20 25 30
His Gly Gly Val Leu Pro Leu Pro Val Leu His Ser His Leu Arg Xaa
35 40 45
Xaa Gln Asn Pro Ala Ala Ala Ser Thr Ser Cys Thr Asp Thr Thr Thr
50 55 60
Arg Arg Gln Glu Gln Gln Gln Glu Glu Glu Glu Tyr Gln His Arg
65 70 75 80
Pro Glu His His Val Arg Gly Leu His Leu Gln Tyr Gln Gly Glu Leu
85 90 95
Gly His Glu Pro Gly Pro Pro Arg Arg Leu Gln Gln Val Ala Gln Gly
100 105 110
Thr Leu Arg Arg Arg Arg Arg Gln Arg Arg Leu Cys Arg Arg His Leu

115 120 125
Arg His Val Val Leu Gln Leu Gly Asp His Arg Gly
130 135 140

(2) INFORMATION FOR SEQ ID NO:2366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..107
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2366:

Met	Ala	Gly	Phe	Tyr	Arg	Tyr	Pro	Ser	Ser	Thr	Arg	Thr	Ser	Gly	Xaa
1				5					10					15	
Asp	Arg	Thr	Gln	Pro	Pro	Pro	Ala	Pro	Ala	Ala	Pro	Thr	Gln	Gln	Gln
			20					25					30		
Gly	Asp	Lys	Ser	Ser	Ser	Lys	Lys	Lys	Arg	Arg	Ser	Ile	Ser	Ile	Gly
		35				40					45				
Arg	Ser	Ile	Thr	Cys	Ala	Gly	Ser	Ile	Cys	Ser	Thr	Lys	Glu	Ser	Ser
		50				55				60					
Val	Met	Ser	Arg	Asp	Arg	Arg	Gly	Ala	Ser	Ser	Arg	Ser	Leu	Arg	Ala
65				70					75					80	
Pro	Tyr	Val	Asp	Val	Asp	Val	Asn	Asp	Ala	Ser	Ala	Ala	Ala	Ile	Ser
			85				90							95	
Ala	Thr	Ser	Ser	Phe	Asn	Ser	Glu	Thr	Thr	Val					
			100				105								

(2) INFORMATION FOR SEQ ID NO:2367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..512
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2367:

atgcatgctg	aaactgtggc	aaattggaac	cacttattca	gttggtgttt	tgcaaattca	60
gatttgggtg	aattactgac	tctcaactgc	cctgctgaca	gagcaatggt	gctgctgatg	120
taccaaattg	agttgagact	gctcaattgg	gcctgggcag	acgagtgtgt	cttcaacctg	180
tgtctacttc	gattacacag	tgttgttcat	agcagcctag	ccaatgctta	taaatacctg	240
ttgataacag	tgattaccag	aacacactca	attggccaag	atcatTTTTg	gcataacgtg	300
gataggggtg	tggtgtgtgg	aattaaggat	agatgctgtg	caagattggc	aaagctagtt	360
ttatctgcta	cactgacaca	agattctggc	aagctttctc	aacttgaatt	gcaccatcca	420
ttgttggtga	atactcagtc	aagcggcttg	aggacaagcc	ggatttcaag	cggtggggaa	480
tatcagcata	tcattcttct	ctcaagtcaa	ag			

(2) INFORMATION FOR SEQ ID NO:2368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..170
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2368:

Met His Ala Glu Thr Val Ala Asn Trp Asn His Leu Phe Ser Trp Cys
1 5 10 15
Phe Ala Asn Ser Asp Leu Gly Glu Leu Thr Leu Asn Cys Pro Ala
20 25 30
Asp Arg Ala Met Val Leu Leu Met Tyr Gln Ile Glu Leu Arg Leu Leu
35 40 45
Asn Trp Ala Trp Ala Asp Glu Cys Val Phe Asn Leu Cys Leu Leu Arg
50 55 60
Leu His Ser Val Val His Ser Ser Leu Ala Asn Ala Tyr Lys Ser Trp
65 70 75 80
Leu Ile Thr Val Ile His Arg Thr His Ser Ile Gly Gln Asp His Phe
85 90 95
Trp His Asn Val Asp Arg Gly Val Val Cys Gly Ile Lys Asp Arg Cys
100 105 110
Cys Ala Arg Leu Ala Lys Leu Val Leu Ser Ala Thr Leu Thr Gln Asp
115 120 125
Ser Gly Lys Leu Ser Gln Leu Glu Leu His His Pro Leu Leu Leu Asn
130 135 140
Thr Gln Ser Ser Gly Leu Arg Thr Ser Arg Ile Ser Ser Gly Gly Glu
145 150 155 160
Tyr Gln His Ile Ile Phe Ser Ser Ser Gln
165 170

(2) INFORMATION FOR SEQ ID NO:2369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1503202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2369:

Met His Ala Glu Thr Val Ala Asn Trp Asn His Leu Phe Ser Trp Cys
1 5 10 15
Phe Ala Asn Ser Asp Leu Gly Glu Leu Leu Thr Leu Asn Cys Pro Ala
20 25 30
Asp Arg Ala Met Val Leu Leu Met Tyr Gln Ile Glu Leu Arg Leu Leu
35 40 45
Asn Trp Ala Trp Ala Asp Glu Cys Val Phe Asn Leu Cys Leu Leu Arg
50 55 60
Leu His Ser Val Val His Ser Ser Leu Ala Asn Ala Tyr Lys Ser Trp
65 70 75 80
Leu Ile Thr Val Ile His Arg Thr His Ser Ile Gly Gln Asp His Phe
85 90 95
Trp His Asn Val Asp Arg Gly Val Val Cys Gly Ile Lys Asp Arg Cys
100 105 110
Cys Ala Arg Leu Ala Lys Leu Val Leu Ser Ala Thr Leu Thr Gln Asp
115 120 125
Ser Gly Lys Leu Ser Gln Leu Glu Leu His His Pro Leu Leu Leu Asn
130 135 140
Thr Gln Ser Ser Gly Leu Arg Thr Ser Arg Ile Ser Ser Gly Gly Glu
145 150 155 160
Tyr Gln His Ile Ile Phe Ser Ser Ser Gln
165 170

(2) INFORMATION FOR SEQ ID NO:2370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

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(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..135
(D) OTHER INFORMATION: / Ceres Seq. ID 1503203
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2370:
Met Val Leu Leu Met Tyr Gln Ile Glu Leu Arg Leu Leu Asn Trp Ala
1 5 10 15
Trp Ala Asp Glu Cys Val Phe Asn Leu Cys Leu Leu Arg Leu His Ser
20 25 30
Val Val His Ser Ser Leu Ala Asn Ala Tyr Lys Ser Trp Leu Ile Thr
35 40 45
Val Ile His Arg Thr His Ser Ile Gly Gln Asp His Phe Trp His Asn
50 55 60
Val Asp Arg Gly Val Val Cys Gly Ile Lys Asp Arg Cys Cys Ala Arg
65 70 75 80
Leu Ala Lys Leu Val Leu Ser Ala Thr Leu Thr Gln Asp Ser Gly Lys
85 90 95
Leu Ser Gln Leu Glu Leu His His Pro Leu Leu Asn Thr Gln Ser
100 105 110
Ser Gly Leu Arg Thr Ser Arg Ile Ser Ser Gly Gly Glu Tyr Gln His
115 120 125
Ile Ile Phe Ser Ser Ser Gln
130 135

(2) INFORMATION FOR SEQ ID NO:2371:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..345

(D) OTHER INFORMATION: / Ceres Seq. ID 1503237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2371:

tctccgcgca	ctccacccca	ctcgccgccc	ccgctgccac	cgccgcttgc	tgccgcagcc	60
gccatggggg	cgtacaagta	cgtatcgga	ctatggagga	ggaagcagtc	ggacgtgatg	120
gcggtacagg	cgccggcgcc	ggcggtgga	gggactgatg	tgtgggcccc	tcctggcttc	180
ggccgagtta	tcttatctat	ctatagtatc	gtgttaccgt	tcgcttctgt	caccgtgtta	240
gtgtccgttc	tacctttgga	ttaggtgttg	gtacccctgt	tgttcccttt	ggttgctccc	300
gctatgaaac	gagacgagag	aagaatgagc	aaggtttttg	ttcgc		

(2) INFORMATION FOR SEQ ID NO:2372:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1503238

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2372:

Ser	Pro	Arg	Thr	Pro	Pro	His	Ser	Pro	Pro	Pro	Leu	Pro	Pro	Leu
1	5	10	15											
Ala	Ala	Ala	Ala	Ala	Met	Gly	Ala	Tyr	Lys	Tyr	Val	Ser	Glu	Leu
	20	25	30											
Arg	Arg	Lys	Gln	Ser	Asp	Val	Met	Ala	Ala	Thr	Ala	Ala	Ala	Ala

35 40 45
Ala Gly Gly Thr Asp Val Trp Ala His Pro Gly Phe Gly Arg Val Ile
50 55 60
Leu Ser Ile Tyr Ser Ile Val Leu Pro Phe Ala Ser Val Thr Val Leu
65 70 75 80
Val Ser Val Leu Pro Leu Asp
85

(2) INFORMATION FOR SEQ ID NO:2373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..51

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2373:

Ser Ala His Ser Thr Pro Leu Ala Ala Ala Thr Ala Ala Cys
1 5 10 15
Cys Arg Ser Arg His Gly Gly Val Gln Val Arg Ile Gly Thr Met Glu
20 25 30
Glu Glu Ala Val Gly Arg Asp Gly Gly Tyr Gly Gly Gly Gly Gly
35 40 45
Trp Arg Asp
50

(2) INFORMATION FOR SEQ ID NO:2374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

- (B) LOCATION: 1..66

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2374:

Met Gly Ala Tyr Lys Tyr Val Ser Glu Leu Trp Arg Arg Lys Gln Ser
1 5 10 15
Asp Val Met Ala Ala Thr Ala Ala Ala Ala Ala Gly Gly Thr Asp
20 25 30
Val Trp Ala His Pro Gly Phe Gly Arg Val Ile Leu Ser Ile Tyr Ser
35 40 45
Ile Val Leu Pro Phe Ala Ser Val Thr Val Leu Val Ser Val Leu Pro
50 55 60
Leu Asp
65

(2) INFORMATION FOR SEQ ID NO:2375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..400

- (D) OTHER INFORMATION: / Ceres Seq. ID 1503268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2375:

cccggttaaaa tcacgacgcg gtggtgactg gtgagtccac agtccacact cccactcca 60
ttttctacca tcacactgac acgttcatag ctagctagtc ttcagctagt aacgtacgac 120
ggactaatct cgatctggga gcgaggagga ggacgacgat aatgaagatg agctccgtgc 180
ccgcggcass cgggtgatgg tgggtggtgt gctgctctct gcggcgggcg cgactgtgac 240
ggggcaggcg cttgtgccgg gcgtgatgat cttcggcgac tcggtggttg acgcaggcaa 300
caacaaccgg ctagcgacgc tggcgcgcg cgacttccc ccctacggcc gcgacttccc 360
ggcgacgcac gcgcccacgg gntnnctgc aacggcaagc

(2) INFORMATION FOR SEQ ID NO:2376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1503269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2376:

Met Val Val Val Val Leu Leu Ser Ala Ala Ala Thr Val Thr Gly
1 5 10 15
Gln Ala Leu Val Pro Gly Val Met Ile Phe Gly Asp Ser Val Val Asp
20 25 30
Ala Gly Asn Asn Asn Arg Leu Ala Thr Leu Val Arg Ala Asp Phe Pro
35 40 45
Pro Tyr Gly Arg Asp Phe Pro Ala Thr His Ala Pro Thr Xaa Xaa Pro
50 55 60
Ala Thr Ala Ser
65

(2) INFORMATION FOR SEQ ID NO:2377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1503270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2377:

Met Ile Phe Gly Asp Ser Val Val Asp Ala Gly Asn Asn Asn Arg Leu
1 5 10 15
Ala Thr Leu Val Arg Ala Asp Phe Pro Pro Tyr Gly Arg Asp Phe Pro
20 25 30
Ala Thr His Ala Pro Thr Xaa Xaa Pro Ala Thr Ala Ser
35 40 45

(2) INFORMATION FOR SEQ ID NO:2378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463

(D) OTHER INFORMATION: / Ceres Seq. ID 1503275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2378:

ctctttctcc ccagtagcaa cgaccgcgcg tcctccgcn ccgcactaaa ccctactcca 60
tgtaccacagg tctgctcgg gcccccggc gatgagaacc cgtcagttcc aaagatggct 120

cgctcgtggat tgatggaaca kgacttaagc aaactggatg tgacgaagct tcacccctg 180
tcacctgaag ttatctcacg ccaagcaaca atcaatatgg gtaccattgg ccatgtggct 240
kcatggaaag tccactgttg ttaaagctat atctggtgtt cagactgttc ggttcaagaa 300
tgagctggaa cgtaacatta ctataaagct gggttacgct aatgcaaaaa tctacaaatg 360
tgaggatgac agatgtccgc gaccaatgtg ctacaaggcc tatggaagcg gaaaakaaga 420
tagccctcta tgtgatgtgc ctggatttga aaacactaga atg

(2) INFORMATION FOR SEQ ID NO:2379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1503276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2379:

Leu Phe Leu Pro Ser Ser Asn Asp Arg Ala Ser Ser Ala Xaa Ala Leu
1 5 10 15
Asn Pro Thr Pro Cys Thr Gln Val Cys Val Gly Pro Pro Gly Asp Glu
20 25 30
Asn Pro Ser Val Pro Lys Met Ala Arg Arg Gly Leu Met Glu Xaa Asp
35 40 45
Leu Ser Lys Leu Asp Val Thr Lys Leu His Pro Leu Ser Pro Glu Val
50 55 60
Ile Ser Arg Gln Ala Thr Ile Asn Met Gly Thr Ile Gly His Val Ala
65 70 75 80
Xaa Trp Lys Val His Cys Cys
85

(2) INFORMATION FOR SEQ ID NO:2380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1503277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2380:

Met Ala Arg Arg Gly Leu Met Glu Xaa Asp Leu Ser Lys Leu Asp Val
1 5 10 15
Thr Lys Leu His Pro Leu Ser Pro Glu Val Ile Ser Arg Gln Ala Thr
20 25 30
Ile Asn Met Gly Thr Ile Gly His Val Ala Xaa Trp Lys Val His Cys
35 40 45
Cys

(2) INFORMATION FOR SEQ ID NO:2381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1503278

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2381:
Met Trp Xaa His Gly Lys Ser Thr Val Val Lys Ala Ile Ser Gly Val
1 5 10 15
Gln Thr Val Arg Phe Lys Asn Glu Leu Glu Arg Asn Ile Thr Ile Lys
20 25 30
Leu Gly Tyr Ala Asn Ala Lys Ile Tyr Lys Cys Glu Asp Asp Arg Cys
35 40 45
Pro Arg Pro Met Cys Tyr Lys Ala Tyr Gly Ser Gly Lys Xaa Asp Ser
50 55 60
Pro Leu Cys Asp Val Pro Gly Phe Glu Asn Thr Arg Met
65 70 75

(2) INFORMATION FOR SEQ ID NO:2382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2382:

ttgttgatga	ttagtgcaa	tctgggggaa	ctcttagaga	atgccagaad	agttctagct	60
ttgcatggcg	ctgcaaaagt	cagtgcctat	gtgactcatg	ctgtgtttcc	taagcagtc	120
tatgaacggt	tcattggcgtc	tagttctgct	gggccagggtg	acagatttgc	ttacttctgg	180
atcacggact	catgcccaca	cacagtaaaa	gctattgggc	aaagacctcc	atttgagggt	240
ctgagcctcg	ctggctcaat	tgcagatgct	cttcagatat	gagcgtacac	tggtagatgg	300
gcatgggctt	ggattgttga	tgcccaccag	attgaaactt	gtactatgag	gtggaatgct	360
cccgtttttc	ctaaatgtaa	gagttgggtt	ccagttcctg	gaaaagcaaa	taatgtgtag	420
taagtttaag	tacctgaagg	ttccataaac	agccctgtgg	ctt		

(2) INFORMATION FOR SEQ ID NO:2383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2383:

Val Asp Asp Leu Val Gln Ser Gly Gly Thr Leu Arg Glu Cys Gln Xaa	
1 5 10 15	
Ser Ser Ser Phe Ala Trp Arg Cys Lys Ser Gln Cys Leu Cys Asp Ser	
20 25 30	
Cys Cys Val Ser	
35	

(2) INFORMATION FOR SEQ ID NO:2384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..36
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2384:

Met Leu Cys Phe Leu Ser Ser His Met Asn Val Ser Trp Arg Leu Val
1 5 10 15
Leu Leu Gly Gln Val Thr Asp Leu Leu Thr Ser Gly Ser Arg Thr His
20 25 30
Ala His Thr Gln
35

(2) INFORMATION FOR SEQ ID NO:2385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503282

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2385:

Met Ala Ser Ser Ser Ala Gly Pro Gly Asp Arg Phe Ala Tyr Phe Trp
1 5 10 15
Ile Thr Asp Ser Cys Pro His Thr Val Lys Ala Ile Gly Gln Arg Pro
20 25 30
Pro Phe Glu Val Leu Ser Leu Ala Gly Ser Ile Ala Asp Ala Leu Gln
35 40 45
Ile

(2) INFORMATION FOR SEQ ID NO:2386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2386:

cacaggggtgc	tgatgtgata	gagaaagctc	cagatggcac	tccagctggt	ggtggcttgc	60
tttatgttgt	tgttcatgaa	gcccaagatc	ttgaggggaa	gcaccatata	aaccatata	120
caaaaataat	tttcaaagc	gaggagaaga	aaactaaggt	catcaagaag	aatagggatc	180
caagatggga	ggatgagttt	gagttcgtgt	gtgaggagcc	tcctgtgaat	gataaactgc	240
atgttgaagt	cataagtaaa	gccccgaagc	agggctgata	catggcaagg	aaactttggg	300
ctatatgat	attagccttg	cagacgtgat	cagcaacaag	cggattaatg	aaaagtacca	360
tctcatagac	tcgaaaaatg	gtcagatcca	gatcgagttg	cagtggagaa	cttcctagac	420
aggaaggwgc	cagaatgcct	tgatgttcct	ctattcagtt	tgcgtatata	tgtgattgag	480
gattgaggtc	atgtagataa	tttcttttt				

(2) INFORMATION FOR SEQ ID NO:2387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2387:

Gln Gly Ala Asp Val Ile Glu Lys Ala Pro Asp Gly Thr Pro Ala Gly
1 5 10 15

Gly Gly Leu Leu Tyr Val Val Val His Glu Ala Gln Asp Leu Glu Gly
20 25 30
Lys His His Thr Asn Pro Tyr Ala Lys Ile Ile Phe Lys Gly Glu Glu
35 40 45
Lys Lys Thr Lys Val Ile Lys Lys Asn Arg Asp Pro Arg Trp Glu Asp
50 55 60
Glu Phe Glu Phe Val Cys Glu Glu Pro Pro Val Asn Asp Lys Leu His
65 70 75 80
Val Glu Val Ile Ser Lys Ala Pro Lys Gln Gly
85 90

(2) INFORMATION FOR SEQ ID NO:2388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2388:

tacatcgtga	tattaagtct	agcaacatct	tgcttgatgg	cagtttcgag	gcccgtgtat	60
cagactttgg	acttgcaaag	cttttagagg	atgaagaatc	acatattact	acaatagttg	120
caggaacatt	tggtacatt	gcaccagagt	atatgcaatt	tggcagagca	ccgagaagac	180
tgatgtctac	agttttgggg	ttttggtact	cgaaatactc	agtggaaagc	ggcctactga	240
tgcacccctc	attgagaagg	gactaaacat	tggtggatgg	ttaaattttc	ttgctagtga	300
gaaccggggag	agggaaattg	tcgacctgaa	ctgtgaagga	gtgcagactg	agaccttaga	360
tgccctgctc	tctcttgcca	agcaatgtgt	tagctcctcg	ccagagagag	gccgacaatg	420
cacaggggtg	tacatatgct	gggagtcgga	tgtaattaca	ccgtgcccta	gcgacttcta	480
tg						

(2) INFORMATION FOR SEQ ID NO:2389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..87
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2389:

His Arg Asp Ile Lys Ser Ser Asn Ile Leu Leu Asp Gly Ser Phe Glu	
1 5 10 15	
Ala Arg Val Ser Asp Phe Gly Leu Ala Lys Leu Leu Glu Asp Glu Glu	
20 25 30	
Ser His Ile Thr Thr Ile Val Ala Gly Thr Phe Gly Tyr Leu Ala Pro	
35 40 45	
Glu Tyr Met Gln Phe Gly Arg Ala Pro Arg Arg Leu Met Ser Thr Val	
50 55 60	
Leu Gly Phe Trp Tyr Ser Lys Tyr Ser Val Glu Ser Gly Leu Leu Met	
65 70 75 80	
His Pro Ser Leu Arg Arg Asp	
85	

(2) INFORMATION FOR SEQ ID NO:2390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..448

(D) OTHER INFORMATION: / Ceres Seq. ID 1503305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2390:

Sequence alignment 1 (100%)						
aagcagcaac	atatcaagct	cagagcctca	gagcgccass	caagtcttgc	ggtcgcggaag	60
agcaacgcaa	caagatggtg	aagctcgcat	tcggaagcgt	cggcgactcc	ttcagcgctca	120
cctccatcaa	ggcctacgtn	gcggagtcca	tcgccaccct	cctcttcgtc	ttcgccggcg	180
tgggttccgc	catcgccctc	gggcaactga	cgaatggcgg	cgcgctggac	cctgcggggac	240
tgggtggcga	cgcggtggcg	cacgcgctgg	ccctcttcgt	gggcgtctcc	gtggccgcga	300
acacctccgg	cggccacctg	aaccgcccg	tgacgttcgg	cctggccgtg	ggcggcacat	360
tcaccgtcct	caccggcctc	ttctactggg	tgggccccag	tgctgggcgc	gtccgtggcg	420
tgccctggctc	ctcaggttcg	tgaccac				

(2) INFORMATION FOR SEQ ID NO:2391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1503306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2391:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1503307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2392:

Ala Ala Thr Tyr Gln Ala Gln Ser Leu Arg Ala Pro Xaa Lys Ser Cys
1 5 10 15
Gly Arg Glu Glu Gln Arg Asn Lys Met Val Lys Leu Ala Phe Gly Ser

20 25 30
Val Gly Asp Ser Phe Ser Val Thr Ser Ile Lys Ala Tyr Xaa Ala Glu
35 40 45
Phe Ile Ala Thr Leu Leu Phe Val Phe Ala Gly Val Gly Ser Ala Ile
50 55 60
Ala Phe Gly Gln Leu Thr Asn Gly Gly Ala Leu Asp Pro Ala Gly Leu
65 70 75 80
Val Ala Ile Ala Val Ala His Ala Leu Ala Leu Phe Val Gly Val Ser
85 90 95
Val Ala Ala Asn Thr Ser Gly Gly His Leu Asn Pro Ala Val Thr Phe
100 105 110
Gly Leu Ala Val Gly Gly Thr Phe Thr Val Leu Thr Gly Leu Phe Tyr
115 120 125
Trp Val Gly Pro Ala Ala Gly Arg Val Arg Gly Val Pro Gly Ser Ser
130 135 140
Gly Ser
145

(2) INFORMATION FOR SEQ ID NO:2393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..122
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2393:

Met Val Lys Leu Ala Phe Gly Ser Val Gly Asp Ser Phe Ser Val Thr
1 5 10 15
Ser Ile Lys Ala Tyr Xaa Ala Glu Phe Ile Ala Thr Leu Leu Phe Val
20 25 30
Phe Ala Gly Val Gly Ser Ala Ile Ala Phe Gly Gln Leu Thr Asn Gly
35 40 45
Gly Ala Leu Asp Pro Ala Gly Leu Val Ala Ile Ala Val Ala His Ala
50 55 60
Leu Ala Leu Phe Val Gly Val Ser Val Ala Ala Asn Thr Ser Gly Gly
65 70 75 80
His Leu Asn Pro Ala Val Thr Phe Gly Leu Ala Val Gly Gly Thr Phe
85 90 95
Thr Val Leu Thr Gly Leu Phe Tyr Trp Val Gly Pro Ala Ala Gly Arg
100 105 110
Val Arg Gly Val Pro Gly Ser Ser Gly Ser
115 120

(2) INFORMATION FOR SEQ ID NO:2394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503322

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2394:

gtggcctcgt ctccttcccc acttcggcct cggcagttcc gacttccgcg tgccgggccgg 60
agcctcgtcc cgcttcgcat ctgcacattc gcgccttcgc cgctgcgatt ccttagcagc 120
tcctcggccg ctccaccac ccttcgcgcg gcgagatgga gctcaagccc ggcattgtcg 180
cgctcgtcac cggcgggcgc tccggcatcg ggaaagcact ttgtattgct tttgcaagga 240

gggggtttatt tgtgactgtc gttgatttct cagaggaaaa tggaagagaa gttgctacat 300
tagttcaaaa agaaaatagc aaatttcacg gagatcttag aattccatct tcaatatttg 360
ttaagtgtga tgtagtaat gcagataatc ttgctgcttg ttttgagaag catgtacaga 420
catacaatgg actagatatc tgcataact gtgctggaat tgct

(2) INFORMATION FOR SEQ ID NO:2395:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1503323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2395:

Trp	Pro	Arg	Leu	Leu	Pro	His	Phe	Gly	Leu	Gly	Ser	Ser	Asp	Phe	Arg
1			5						10					15	
Val	Pro	Ala	Gly	Ala	Ser	Ser	Arg	Phe	Ala	Ser	Arg	Thr	Ser	Arg	Leu
			20					25					30		
Arg	Arg	Cys	Asp	Ser	Leu	Ala	Ala	Pro	Arg	Pro	Leu	His	Pro	Pro	Leu
		35					40					45			
Arg	Arg	Arg	Asp	Gly	Ala	Gln	Ala	Arg	His	Val	Gly	Ala	Arg	His	Arg
		50				55					60				
Arg	Arg	Leu	Arg	His	Arg	Glu	Ser	Thr	Leu	Tyr	Cys	Phe	Cys	Lys	Glu
65					70					75					80
Gly	Phe	Ile	Cys	Asp	Cys	Arg									
					85										

(2) INFORMATION FOR SEQ ID NO:2396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1503324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2396:

Met	Glu	Leu	Lys	Pro	Gly	Met	Ser	Ala	Leu	Val	Thr	Gly	Gly	Ala	Ser
1			5						10					15	
Gly	Ile	Gly	Lys	Ala	Leu	Cys	Ile	Ala	Phe	Ala	Arg	Arg	Gly	Leu	Phe
			20					25					30		
Val	Thr	Val	Val	Asp	Phe	Ser	Glu	Asn	Gly	Arg	Glu	Val	Ala	Thr	
		35					40					45			
Leu	Val	Gln	Lys	Glu	Asn	Ser	Lys	Phe	His	Gly	Asp	Leu	Arg	Ile	Pro
		50				55					60				
Ser	Ser	Ile	Phe	Val	Lys	Cys	Asp	Val	Ser	Asn	Ala	Asp	Asn	Leu	Ala
65					70					75					80
Ala	Cys	Phe	Glu	Lys	His	Val	Gln	Thr	Tyr	Asn	Gly	Leu	Asp	Ile	Cys
				85					90					95	
Ile	Asn	Cys	Ala	Gly	Ile	Ala									
					100										

(2) INFORMATION FOR SEQ ID NO:2397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..97

(D) OTHER INFORMATION: / Ceres Seq. ID 1503325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2397:

```
Met Ser Ala Leu Val Thr Gly Gly Ala Ser Gly Ile Gly Lys Ala Leu
1           5           10           15
Cys Ile Ala Phe Ala Arg Arg Gly Leu Phe Val Thr Val Val Asp Phe
20           25           30
Ser Glu Glu Asn Gly Arg Glu Val Ala Thr Leu Val Gln Lys Glu Asn
35           40           45
Ser Lys Phe His Gly Asp Leu Arg Ile Pro Ser Ser Ile Phe Val Lys
50           55           60
Cys Asp Val Ser Asn Ala Asp Asn Leu Ala Ala Cys Phe Glu Lys His
65           70           75           80
Val Gln Thr Tyr Asn Gly Leu Asp Ile Cys Ile Asn Cys Ala Gly Ile
85           90           95
Ala
```

(2) INFORMATION FOR SEQ ID NO:2398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 489 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..489

(D) OTHER INFORMATION: / Ceres Seq. ID 1503330

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2398:

```
tgtagagagt ttcaggtgct cagcaacaag gataggatct gatggtggag tcgcatttgt      60
ctgaggcatt ggggacatgc actcgtctga agaaacttga tcttagggac aacttgtttg      120
gtgttgatgc agggtttagct ctcagcgaaa cccttccaaa actacctgat cttgttgagc      180
tttatctcag tgatctcaat cttgagaaca aggtactat agcaattgca aaagccctca      240
aacagtcagc actgcagttg gaggtccttg aaattgctgg aaatgaaata aatgccaaaag      300
cagccccaga tttggctgaa tgtctagcag taatgcagtc actcaagaag ctgaccttgg      360
ctgaaaatga actgaaggac aatggtgctg tgataattgc aaaatcattg gaagatggcc      420
actcagatct caaggaactt gatgtgagca cgaacatgct gcagaggggt ggagctcggt      480
gctttacgc
```

(2) INFORMATION FOR SEQ ID NO:2399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1503331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2399:

```
Met Val Glu Ser His Leu Ser Glu Ala Leu Gly Thr Cys Thr Arg Leu
1           5           10           15
Lys Lys Leu Asp Leu Arg Asp Asn Leu Phe Gly Val Asp Ala Gly Leu
20           25           30
Ala Leu Ser Glu Thr Leu Pro Lys Leu Pro Asp Leu Val Glu Leu Tyr
35           40           45
Leu Ser Asp Leu Asn Leu Glu Asn Lys Gly Thr Ile Ala Ile Ala Lys
50           55           60
Ala Leu Lys Gln Ser Ala Leu Gln Leu Glu Val Leu Glu Ile Ala Gly
```

[illegible]

(2) INFORMATION FOR SEQ ID NO:2400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..449
(D) OTHER INFORMATION: / Ceres Seq. ID 1503332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2400:

(12) SEQUENCE DESCRIPTION: SEQ ID NO:2400:							
tctcttcttc	caatcattgg	tggttgtgct	ctagctgctg	tcacagagct	gaactttaat		60
atggttggat	ttatgggtgc	catgatatcc	aaccttgcat	ttgttttccg	caacatcttc		120
tcgaagaggg	catgaagggg	aagtccgtca	gtggcatgaa	ttactacgct	tgccgtgcaa		180
ttatgtccct	ggtcatactg	actccatttg	ctatagctat	ggaaggccct	caaatgtggg		240
ctgctggttg	gcaaaaggct	cttgacagaag	ttggacccaa	tgttgtctgg	tggattgctg		300
cacagagcgt	gttctaccac	ttataatacc	aggtgtccta	catgtctctc	gatcagattt		360
ctccattgac	attcagcatt	ggcataacaa	tgaagcgtat	atcagtgatt	gtttcatcaa		420
tcattatcct	ccacactcct	atccagcgt					

(2) INFORMATION FOR SEQ ID NO:2401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..106
(D) OTHER INFORMATION: / Ceres Seq. ID 1503333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2401:

SEQUENCE IDENTIFICATION: SEQ ID NO:2401:															
Met	Lys	Gly	Lys	Ser	Val	Ser	Gly	Met	Asn	Tyr	Tyr	Ala	Cys	Leu	Ser
1				5				10						15	
Ile	Met	Ser	Leu	Val	Ile	Leu	Thr	Pro	Phe	Ala	Ile	Ala	Met	Glu	Gly
			20					25					30		
Pro	Gln	Met	Trp	Ala	Ala	Gly	Trp	Gln	Lys	Ala	Leu	Ala	Glu	Val	Gly
			35				40					45			
Pro	Asn	Val	Val	Trp	Trp	Ile	Ala	Gln	Ser	Val	Phe	Tyr	His	Leu	
	50					55				60					
Tyr	Asn	Gln	Val	Ser	Tyr	Met	Ser	Leu	Asp	Gln	Ile	Ser	Pro	Leu	Thr
65				70					75					80	
Phe	Ser	Ile	Gly	Asn	Thr	Met	Lys	Arg	Ile	Ser	Val	Ile	Val	Ser	Ser
				85				90						95	
Ile	Ile	Ile	Phe	His	Thr	Pro	Val	Arg	Ala						
			100					105							

(2) INFORMATION FOR SEQ ID NO:2402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..98
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503334
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2402:

```
Met Asn Tyr Tyr Ala Cys Leu Ser Ile Met Ser Leu Val Ile Leu Thr
1           5           10           15
Pro Phe Ala Ile Ala Met Glu Gly Pro Gln Met Trp Ala Ala Gly Trp
          20           25           30
Gln Lys Ala Leu Ala Glu Val Gly Pro Asn Val Val Trp Trp Ile Ala
          35           40           45
Ala Gln Ser Val Phe Tyr His Leu Tyr Asn Gln Val Ser Tyr Met Ser
          50           55           60
Leu Asp Gln Ile Ser Pro Leu Thr Phe Ser Ile Gly Asn Thr Met Lys
65           70           75           80
Arg Ile Ser Val Ile Val Ser Ser Ile Ile Ile Phe His Thr Pro Val
          85           90           95
Arg Ala
```

- (2) INFORMATION FOR SEQ ID NO:2403:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..89
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503335
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2403:

```
Met Ser Leu Val Ile Leu Thr Pro Phe Ala Ile Ala Met Glu Gly Pro
1           5           10           15
Gln Met Trp Ala Ala Gly Trp Gln Lys Ala Leu Ala Glu Val Gly Pro
          20           25           30
Asn Val Val Trp Trp Ile Ala Ala Gln Ser Val Phe Tyr His Leu Tyr
          35           40           45
Asn Gln Val Ser Tyr Met Ser Leu Asp Gln Ile Ser Pro Leu Thr Phe
          50           55           60
Ser Ile Gly Asn Thr Met Lys Arg Ile Ser Val Ile Val Ser Ser Ile
65           70           75           80
Ile Ile Phe His Thr Pro Val Arg Ala
          85
```

- (2) INFORMATION FOR SEQ ID NO:2404:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..233
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503336
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2404:

```
aacacataga gcgctgagga cgttggtcat cagtcacac ctatctaact agctagctag      60
cttgaacaag agcgtagcta gcaagaaacg agctccgctg cgagagaaag ctaagggacc      120
tagctagcta tcatgtcttg gacctaccgt gagaacgcgc tgttcgagcg sctctggcca      180
```

cctacgaccg ggacacgccc aggcggtggg agctcgtggc cgccgcggtg ggc

(2) INFORMATION FOR SEQ ID NO:2405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..33

(D) OTHER INFORMATION: / Ceres Seq. ID 1503337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2405:

Met	Ser	Trp	Thr	Tyr	Arg	Glu	Asn	Ala	Leu	Phe	Glu	Xaa	Leu	Trp	Pro
1				5					10					15	
Pro	Thr	Thr	Gly	Thr	Arg	Pro	Gly	Gly	Gly	Ser	Ser	Trp	Pro	Pro	Arg
			20				25						30		
Trp															

(2) INFORMATION FOR SEQ ID NO:2406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1503342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2406:

actttccatt	gaggatggt	cagtattgaa	gtccttcagc	caccttctcc	atcgtaacaa	60
gaaggtagat	ttcattgaac	agttcaatga	aaagcttctg	gtcaagcagg	aaggggagaa	120
tcttcaaatt	cttgatgtaa	ggaacttcca	attgacagaa	gtgagcagaa	ctgagtttat	180
gactccatct	gcctttat	ttctgtatga	gctgcaactg	ttcctgacgt	tccggaatcg	240
atcagtagca	gtttggaact	ttcgagggtga	actggtcaca	tcatttgaag	atcacctggt	300
gtggcaccct	gactgcaaca	caaacaacat	atacattaca	agtgatcaag	atcttattat	360
ttcatactgc	aaggctgact	caactgattc	ctcttcagaa	gaaaatgctg	gctctataaa	420
cataagcagc	atactgaccg	gcaaagtctt	ggcaaaaata	aaccctggaa	attcgcgc	

(2) INFORMATION FOR SEQ ID NO:2407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1503343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2407:

Leu	Ser	Ile	Glu	Asp	Gly	Thr	Val	Leu	Lys	Ser	Phe	Ser	His	Leu	Leu
1				5					10					15	
His	Arg	Asn	Lys	Lys	Val	Asp	Phe	Ile	Glu	Gln	Phe	Asn	Glu	Lys	Leu
			20					25					30		
Leu	Val	Lys	Gln	Glu	Gly	Glu	Asn	Leu	Gln	Ile	Leu	Asp	Val	Arg	Asn
		35				40					45				
Phe	Gln	Leu	Thr	Glu	Val	Ser	Arg	Thr	Glu	Phe	Met	Thr	Pro	Ser	Ala
	50				55				60						
Phe	Ile	Phe	Leu	Tyr	Glu	Leu	Gln	Leu	Phe	Leu	Thr	Phe	Arg	Asn	Arg
65				70					75					80	

Ser Val Ala Val Trp Asn Phe Arg Gly Glu Leu Val Thr Ser Phe Glu
85 90 95
Asp His Leu Leu Trp His Pro Asp Cys Asn Thr Asn Asn Ile Tyr Ile
100 105 110
Thr Ser Asp Gln Asp Leu Ile Ile Ser Tyr Cys Lys Ala Asp Ser Thr
115 120 125
Asp Ser Ser Ser Glu Glu Asn Ala Gly Ser Ile Asn Ile Ser Ser Ile
130 135 140
Leu Thr Gly Lys Cys Leu Ala Lys Ile Asn Pro Gly Asn Ser Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1503344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2408:

Met Thr Pro Ser Ala Phe Ile Phe Leu Tyr Glu Leu Gln Leu Phe Leu
1 5 10 15
Thr Phe Arg Asn Arg Ser Val Ala Val Trp Asn Phe Arg Gly Glu Leu
20 25 30
Val Thr Ser Phe Glu Asp His Leu Leu Trp His Pro Asp Cys Asn Thr
35 40 45
Asn Asn Ile Tyr Ile Thr Ser Asp Gln Asp Leu Ile Ile Ser Tyr Cys
50 55 60
Lys Ala Asp Ser Thr Asp Ser Ser Ser Glu Glu Asn Ala Gly Ser Ile
65 70 75 80
Asn Ile Ser Ser Ile Leu Thr Gly Lys Cys Leu Ala Lys Ile Asn Pro
85 90 95
Gly Asn Ser Arg
100

(2) INFORMATION FOR SEQ ID NO:2409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..260

(D) OTHER INFORMATION: / Ceres Seq. ID 1503345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2409:

agagttgttg attgcagga aaccgccaat tggcaaggat gaagcttgat accgccttcg 60
ttgtgctgct cttttctctc ctccccgact cgtccaccgc ggaggacttc gatttcttct 120
accttggtcca acagtggccg ggctcgttct gcgacacgcg gcagggttgc tgcttccccg 180
acggcgcggg caagccggab sncgtttcgg catccacggg ctgtggccaa ctacgccaak 240
tgccgcggcc gccaccaccg

(2) INFORMATION FOR SEQ ID NO:2410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1503346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2410:

Glu Leu Leu Ile Ala Gly Lys Pro Pro Ile Gly Lys Asp Glu Ala Cys
1 5 10 15
Asp Arg Leu Arg Cys Ala Ala Leu Phe Ser Pro Pro Arg Leu Val His
20 25 30
Arg Gly Gly Leu Arg Phe Leu Leu Pro Cys Pro Thr Val Ala Gly Leu
35 40 45
Val Leu Arg His Ala Ala Gly Leu Leu Leu Pro Gly Arg Arg Gly Gln
50 55 60
Ala Gly Xaa Arg Phe Gly Ile His Gly Leu Trp Pro Thr Thr Pro Xaa
65 70 75 80
Ala Ala Ala Ala Thr Thr
85

(2) INFORMATION FOR SEQ ID NO:2411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1503347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2411:

Met Lys Leu Val Thr Ala Phe Val Val Leu Leu Phe Ser Leu Leu Pro
1 5 10 15
Asp Ser Ser Thr Ala Glu Asp Phe Asp Phe Phe Tyr Leu Val Gln Gln
20 25 30
Trp Pro Gly Ser Phe Cys Asp Thr Arg Gln Gly Cys Cys Phe Pro Asp
35 40 45
Gly Ala Gly Lys Pro Xaa Xaa Val Ser Ala Ser Thr Gly Cys Gly Gln
50 55 60
Leu Arg Gln Xaa Pro Arg Pro Pro Pro Pro
65 70

(2) INFORMATION FOR SEQ ID NO:2412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..178

(D) OTHER INFORMATION: / Ceres Seq. ID 1503351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2412:

aatctactaa aaaaactctc caactgcggc aattgccaac cgccagcacc agcgccgccc 60
ccccgnctcc cccgccggcg cctcgagaaa ttggattggc tgggcgcgtg acccgccgcc 120
gccgtccgcg agcagcagcg acccccctcg ccggccatga cctctgctca ttccaagc

(2) INFORMATION FOR SEQ ID NO:2413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..36
(D) OTHER INFORMATION: / Ceres Seq. ID 1503352
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2413:
Asn Leu Leu Lys Lys Leu Ser Asn Cys Gly Asn Cys Gln Pro Pro Ala
1 5 10 15
Pro Ala Pro Pro Pro Xaa Leu Pro Arg Arg Arg Leu Gly Glu Leu Asp
20 25 30
Trp Leu Gly Ala
35

(2) INFORMATION FOR SEQ ID NO:2414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1503353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2414:

Ser Thr Lys Lys Thr Leu Gln Leu Arg Gln Leu Pro Thr Ala Ser Thr
1 5 10 15
Ser Ala Ala Ala Pro Xaa Pro Pro Pro Ala Pro Arg Arg Ile Gly Leu
20 25 30
Ala Gly Arg Val Thr Arg Arg Arg Arg Pro Arg Ala Ala Ala Thr Pro
35 40 45
Leu Ala Gly His Asp Leu Cys Ser Phe Gln
50 55

(2) INFORMATION FOR SEQ ID NO:2415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..492

(D) OTHER INFORMATION: / Ceres Seq. ID 1503354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2415:

atacagaaat ggtagggttc ttcggcgccct ctgctgcac	tgatcactgt cgtttgctga	60
caacaaatgg atcagttcac catgaactga ttagacgaca	ccatggcaga ccaagaagt	120
cgatcaggtg ctgcagcagc acggcaagg	gaaggaccag ggactattac ataccaggtg	180
ctgggcatcg caattcaatc cacacctcag	cagatcaagg aggettacag gaaactccag	240
aagcaacacc atccagacat cgccgggtac	aaggggccacg actacacgct gctgctgaac	300
gaggcgtaga aggttctgat gcgggatgtt	tccagttcca ggcacgcga tggaaggggc	360
aggagtaggg tggggtcagg agccgggttac	accgtggacg gatacagttc ttgggaagg	420
cccgtgagaa gccaaagctct cttcgtggac	gagaacaagt gcataggatg ccgggagtg	480
gtgcaccatg cc		

(2) INFORMATION FOR SEQ ID NO:2416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1503355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2416:

Thr Glu Met Val Gly Phe Phe Gly Ala Ser Ala Ala Ser Asp His Cys
1 5 10 15
Arg Leu Leu Thr Thr Asn Gly Ser Val His His Glu Leu Ile Arg Arg
20 25 30
His His Gly Arg Pro Arg Ser Ala Ile Arg Cys Cys Ser Thr Ala
35 40 45
Arg Gly Arg Thr Arg Asp Tyr Tyr Ile Pro Gly Ala Gly His Arg Asn
50 55 60
Ser Ile His Thr Ser Ala Asp Gln Gly Gly Leu Gln Glu Thr Pro Glu
65 70 75 80
Ala Thr Pro Ser Arg His Arg Arg Leu Gln Gly Pro Arg Leu His Ala
85 90 95
Ala Ala Glu Arg Gly Val Gln Gly Ser Asp Ala Gly Cys Phe Gln Phe
100 105 110
Gln Ala Arg Arg Trp Lys Gly Gln Glu
115 120

(2) INFORMATION FOR SEQ ID NO:2417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1503356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2417:

Met Val Gly Phe Phe Gly Ala Ser Ala Ala Ser Asp His Cys Arg Leu
1 5 10 15
Leu Thr Thr Asn Gly Ser Val His His Glu Leu Ile Arg Arg His His
20 25 30
Gly Arg Pro Arg Ser Ala Ile Arg Cys Cys Ser Ser Thr Ala Arg Gly
35 40 45
Arg Thr Arg Asp Tyr Tyr Ile Pro Gly Ala Gly His Arg Asn Ser Ile
50 55 60
His Thr Ser Ala Asp Gln Gly Gly Leu Gln Glu Thr Pro Glu Ala Thr
65 70 75 80
Pro Ser Arg His Arg Arg Leu Gln Gly Pro Arg Leu His Ala Ala Ala
85 90 95
Glu Arg Gly Val Gln Gly Ser Asp Ala Gly Cys Phe Gln Phe Gln Ala
100 105 110
Arg Arg Trp Lys Gly Gln Glu
115

(2) INFORMATION FOR SEQ ID NO:2418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1503357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2418:

Met Ala Asp Gln Glu Val Arg Ser Gly Ala Ala Ala Ala Arg Gln Gly
1 5 10 15
Glu Gly Pro Gly Thr Ile Thr Tyr Gln Val Leu Gly Ile Ala Ile Gln

	20		25		30
Ser Thr Pro Gln Gln Ile Lys Glu Ala Tyr Arg Lys Leu Gln Lys Gln					
	35		40		45
His His Pro Asp Ile Ala Gly Tyr Lys Gly His Asp Tyr Thr Leu Leu					
	50		55		60
Leu Asn Glu Ala Tyr Lys Val Leu Met Arg Asp Val Ser Ser Ser Arg					
	65		70		75
His Ala Asp Gly Arg Gly Arg Ser Arg Val Gly Ser Gly Ala Gly Tyr					
	85		90		95
Thr Val Asp Gly Tyr Ser Ser Trp Glu Gly Pro Val Arg Ser Gln Ala					
	100		105		110
Leu Phe Val Asp Glu Asn Lys Cys Ile Gly Cys Arg Glu Cys Val His					
	115		120		125
His Ala					
	130				

(2) INFORMATION FOR SEQ ID NO:2419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2419:

acatgcaaag tataacacag accagatcaa acccaagttc aggcttcccg aatcattcag	60
caagccacta ttgagtgccg atccatctat catctcccgc gatcttgaac caaatgactg	120
tttcatcata ttgcgcatcag atggattgtg ggagcacctc agcaatcaag aagccgttga	180
gattgttcac agccatcaac gtgctggaag cgcaagaaga ctcattaaag ccgctctaca	240
agaagcagcg cgnaasstga gatgcgttac tcggatctta caaagatcga taagaaagtt	300
cgcaggcatt tccatgatga cattactgtc atcgtcttat ttataaacta tgacctatta	360
ttgaaagggtg ctccgcagga caaccctctt ccatcagatg tgccctagat tattgacagt	420
gagctagttc acccactggt attcaagctc ctgcgtgcag cc	

(2) INFORMATION FOR SEQ ID NO:2420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..114
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2420:

His Ala Lys Tyr Asn Thr Asp Gln Ile Lys Pro Lys Phe Arg Leu Pro	
1	5 10 15
Glu Ser Phe Ser Lys Pro Leu Leu Ser Ala Asp Pro Ser Ile Ile Ser	
	20 25 30
Arg Asp Leu Glu Pro Asn Asp Cys Phe Ile Ile Phe Ala Ser Asp Gly	
	35 40 45
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Glu Ile Val His Ser	
	50 55 60
His Gln Arg Ala Gly Ser Ala Arg Arg Leu Ile Lys Ala Ala Leu Gln	
	65 70 75 80
Glu Ala Ala Xaa Xaa Xaa Arg Cys Val Thr Arg Ile Leu Gln Arg Ser	
	85 90 95
Ile Arg Lys Phe Ala Gly Ile Ser Met Met Thr Leu Leu Ser Ser Ser	
	100 105 110

(2) INFORMATION FOR SEQ ID NO:2421:

(A) LENGTH: 346 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..346

(D) OTHER INFORMATION: / Ceres Seq. ID 1503400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2421:

Sequence description: SEQ ID NO:2421:							
tttccgtgcc	gccaccacgc	cccttaacnc	tcgttcctct	agcgcctcgc	cgcagcacag		60
cctccatttc	tcctccgacg	gcggtgcggc	tagctcaacc	atggcggact	ccaaggccac		120
ctcggcggtc	accctccgca	ctckcaagtt	catgaccaac	cggggcccn	tgctggcccg		180
cwaacaattt	gtgcttgagg	ttatccaccc	cggccgcgcc	aacgtctcca	aggcggagtt		240
gaagggaaga	ggcttgcaa	gtgtacgag	gtgaaggacc	ccaacaccat	cttcgtcttc		300
aagttccgca	cccacttcgg	tggaggcaag	tccactgqct	tcggcc			

(2) INFORMATION FOR SEQ ID NO:2422:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1503401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2422:

Phe	Arg	Ala	Ala	Thr	Gln	Pro	Leu	Asn	Xaa	Arg	Ser	Ser	Ser	Arg	Leu
1				5					10					15	
Ala	Gln	His	Ser	Leu	His	Phe	Ser	Ser	Asp	Gly	Gly	Ala	Ala	Ser	Ser
			20					25					30		
Thr	Met	Ala	Asp	Ser	Lys	Ala	Thr	Ser	Ala	Val	Thr	Leu	Arg	Thr	Xaa
			35				40					45			
Lys	Phe	Met	Thr	Asn	Arg	Gly	Pro	Xaa	Leu	Ala	Arg	Xaa	Gln	Phe	Val
	50					55					60				
Leu	Glu	Val	Ile	His	Pro	Gly	Arg	Ala	Asn	Val	Ser	Lys	Ala	Glu	Leu
65					70					75					80
Lys	Gly	Arg	Gly	Leu	Pro	Arg	Cys	Thr	Arg						
				85					90						

(2) INFORMATION FOR SEQ ID NO:2423:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

MOLECULE TYPE: peptid

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1503402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2423:

Ser	Val	Pro	Pro	Pro	Ser	Pro	Leu	Xaa	Leu	Val	Pro	Leu	Ala	Val	Ser
1				5					10					15	
Arg	Ser	Thr	Ala	Ser	Ile	Ser	Pro	Pro	Thr	Ala	Val	Arg	Leu	Ala	Gln
			20					25					30		
Pro	Trp	Arg	Thr	Pro	Arg	Pro	Pro	Arg	Arg	Ser	Pro	Ser	Ala	Leu	Xaa

35 40 45
Ser Ser
50

(2) INFORMATION FOR SEQ ID NO:2424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1503403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2424:

Met	Ala	Asp	Ser	Lys	Ala	Thr	Ser	Ala	Val	Thr	Leu	Arg	Thr	Xaa	Lys
1				5					10					15	
Phe	Met	Thr	Asn	Arg	Gly	Pro	Xaa	Leu	Ala	Arg	Xaa	Gln	Phe	Val	Leu
			20				25						30		
Glu	Val	Ile	His	Pro	Gly	Arg	Ala	Asn	Val	Ser	Lys	Ala	Glu	Leu	Lys
		35				40						45			
Gly	Arg	Gly	Leu	Pro	Arg	Cys	Thr	Arg							
	50				55										

(2) INFORMATION FOR SEQ ID NO:2425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1503422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2425:

tatgaaaaat	caagatctcc	tgggaggttc	tttgacctag	tttatcatga	aaatgcccggt	60
gttctactcc	atgatgagag	catataccga	tttgaatgtt	gctcgagtcc	gacaagggttg	120
tctattcagc	tgatggaata	tggtcacgaa	aagccagaag	tgactgcagt	atcaattgaa	180
ccaaattttt	cttcgtatct	ttttagcgag	tacttggtga	gtacgccaga	caagaaatta	240
tctgaaggcg	tctaccttgg	aaggaataag	cggaaatatt	caaataatga	tgaaccttca	300
gattctttga	aggcaatgga	tggtatcaat	gttggtgaatg	gtcttgaatg	caagatatcc	360
tgcaagacct	cgaaagtctc	atatgtcctt	gatactgaag	atttcttggt	ccggcttcgg	420
aagagaagga	aaattttgcg	gggcgggaat	gtgcccgacc	gtttgcagat	ttcatcaata	480
tctgctg						

(2) INFORMATION FOR SEQ ID NO:2426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1503423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2426:

Tyr	Glu	Lys	Ser	Arg	Ser	Pro	Gly	Arg	Phe	Phe	Asp	Leu	Val	Tyr	His
1			5					10						15	
Glu	Asn	Ala	Arg	Val	Leu	Leu	His	Asp	Glu	Ser	Ile	Tyr	Arg	Phe	Glu
		20					25					30			
Cys	Cys	Ser	Ser	Pro	Thr	Arg	Leu	Ser	Ile	Gln	Leu	Met	Glu	Tyr	Gly

35	40	45
His Glu Lys Pro Glu Val Thr Ala Val Ser Ile Glu Pro Asn Phe Ser		
50	55	60
Ser Tyr Leu Phe Ser Glu Tyr Leu Cys Ser Thr Pro Asp Lys Lys Leu		
65	70	75
Ser Glu Gly Val Tyr Leu Gly Arg Asn Lys Arg Lys Tyr Ser Asn Asn		80
	85	90
Asp Glu Pro Ser Asp Ser Leu Lys Ala Met Asp Gly Ile Asn Val Val		95
	100	105
Asn Gly Leu Glu Cys Lys Ile Ser Cys Lys Thr Ser Lys Val Ser Tyr		110
	115	120
Val Leu Asp Thr Glu Asp Phe Leu Phe Arg Leu Arg Lys Arg Arg Lys		125
	130	135
Ile Leu Arg Gly Gly Asn Val Pro Asp Arg Leu Gln Ile Ser Ser Ile		140
145	150	155
Ser Ala		160

(2) INFORMATION FOR SEQ ID NO:2427:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1503424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2427:

Met Glu Tyr Gly His Glu Lys Pro Glu Val Thr Ala Val Ser Ile Glu	
1	5
Pro Asn Phe Ser Ser Tyr Leu Phe Ser Glu Tyr Leu Cys Ser Thr Pro	10
	15
Asp Lys Lys Leu Ser Glu Gly Val Tyr Leu Gly Arg Asn Lys Arg Lys	20
	25
Tyr Ser Asn Asn Asp Glu Pro Ser Asp Ser Leu Lys Ala Met Asp Gly	30
	35
Ile Asn Val Val Asn Gly Leu Glu Cys Lys Ile Ser Cys Lys Thr Ser	40
65	45
Lys Val Ser Tyr Val Leu Asp Thr Glu Asp Phe Leu Phe Arg Leu Arg	50
	55
Lys Arg Arg Lys Ile Leu Arg Gly Gly Asn Val Pro Asp Arg Leu Gln	60
	65
Ile Ser Ser Ile Ser Ala	70
	75
	80
	85
	90
	95
	100
	105
	110
	115

(2) INFORMATION FOR SEQ ID NO:2428:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..439

(D) OTHER INFORMATION: / Ceres Seq. ID 1503429

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2428:

acacctactt cataagcctg gccttctccc cgacggccct catcggcctc aactccgacc	60
tgaaagtgcc caagtgtgag ttctgtcgac acgcgamscg tcgctgttcg attaccccaa	120
gccagtgacc cagcagacca cagccacgtc agtcaaggtg ccggcggsca tcctgtcgac	180
ctatgccaaag tccaaatcca gggcaaggaa ggacgcagag agcaaggcca aggcgaaagc	240

agaggactct tccagtgcctt ctacttcgat gcaggtggac ggcgcttctg ctgctgggtgc 300
tgctgcagag aagaaggccc cggagccaga gcctacgttc cagatcctga cgaacccggc 360
ccgggtcgtt ccagcccagg agaagttcat aaagttcctg gaagacagca ggtacaagcc 420
ggtgaaggct gccccctcg

(2) INFORMATION FOR SEQ ID NO:2429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1503430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2429:

Thr Tyr Phe Ile Ser Leu Ala Phe Ser Pro Thr Ala Leu Ile Gly Leu
1 5 10 15
Asn Ser Asp Leu Lys Val Pro Lys Phe Glu Phe Leu Ser Asn Ala Xaa
20 25 30
Arg Arg Cys Ser Ile Thr Pro Ser Gln
35 40

(2) INFORMATION FOR SEQ ID NO:2430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1503431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2430:

Met Pro Ser Pro Asn Pro Gly Gln Gly Arg Thr Gln Arg Ala Arg Pro
1 5 10 15
Arg Arg Lys Gln Arg Thr Leu Pro Val Leu Leu Leu Arg Cys Arg Trp
20 25 30
Thr Ala Leu Leu Leu Leu Val Leu Leu Gln Arg Arg Arg Pro Arg Ser
35 40 45
Gln Ser Leu Arg Ser Arg Ser
50 55

(2) INFORMATION FOR SEQ ID NO:2431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1503432

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2431:

Met Gln Val Asp Gly Ala Ser Ala Ala Gly Ala Ala Glu Lys Lys
1 5 10 15
Ala Pro Glu Pro Glu Pro Thr Phe Gln Ile Leu Thr Asn Pro Ala Arg
20 25 30
Val Val Pro Ala Gln Glu Lys Phe Ile Lys Phe Leu Glu Asp Ser Arg
35 40 45
Tyr Lys Pro Val Lys Ala Ala Pro Ser

50 55

(2) INFORMATION FOR SEQ ID NO:2432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1503443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2432:

actggcggtg	aacagcgaga	acctaaacag	gacagcgaac	acgactcgcc	taacctccgg	60
acagccacgt	ctttccccac	tctccggacg	aaccttcccg	atggcgacgc	gacctcccct	120
ccagctgccc	ccgcgtccac	cgccaccacc	tccgtctcgc	gtctccggcc	actgcgccct	180
ttccttccgc	gccttcgctt	ctggccagca	ccagtggcgg	ccgcgccgst	gtgcctttct	240
cgattgctct	gggcccaggc	tgctgtccct	tgcccggcat	acgctgtcga	gccgccgccg	300
ggccctcgcc	gccctcctca	gagccccctc	ctccatcccc	gcacggttgg	caagagaggc	360
tgtcaagttt	gcaggataga	gcaaggatct	tctttgccgt	tctgttctgg	atgtcattgt	420
ttttctgggg	aagtgcttgg	gatggaagta	acaactcggg	aggcaagaag	c	

(2) INFORMATION FOR SEQ ID NO:2433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503444

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2433:

Thr	Gly	Gly	Glu	Gln	Arg	Glu	Pro	Lys	Gln	Asp	Ser	Glu	His	Asp	Ser	
1			5						10					15		
Pro	Asn	Leu	Arg	Thr	Ala	Thr	Ser	Phe	Pro	Thr	Leu	Arg	Thr	Asn	Leu	
			20					25					30			
Pro	Asp	Gly	Asp	Ala	Thr	Ser	Pro	Pro	Ala	Ala	Pro	Ala	Ser	Thr	Ala	
		35				40					45					
Thr	Thr	Ser	Val	Ser	Arg	Leu	Arg	Pro	Leu	Arg	Pro	Phe	Leu	Pro	Arg	
	50				55				60							
Leu	Arg	Phe	Trp	Pro	Ala	Pro	Val	Ala	Ala	Pro	Xaa	Cys	Leu	Ser		
65				70					75				80			
Arg	Leu	Leu	Trp	Ala	Gln	Ala	Val	Val	Pro	Cys	Pro	Ala	Tyr	Ala	Val	
			85					90					95			
Glu	Pro	Pro	Pro	Gly	Pro	Arg	Arg	Pro	Pro	Gln	Ser	Pro	Leu	Leu	His	
		100					105					110				
Pro	Arg	Thr	Val	Gly	Lys	Arg	Gly	Cys	Gln	Val	Cys	Arg	Ile	Glu	Gln	
		115				120						125				
Gly	Ser	Ser	Leu	Pro	Phe	Cys	Ser	Gly	Cys	His	Cys	Phe	Ser	Gly	Glu	
	130				135						140					
Val	Leu	Gly	Met	Glu	Val	Thr	Thr	Arg	Glu	Ala	Arg	Ser				
145				150					155							

(2) INFORMATION FOR SEQ ID NO:2434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1503445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2434:

Leu Ala Val Asn Ser Glu Asn Leu Asn Arg Thr Ala Asn Thr Thr Arg
1 5 10 15
Leu Thr Ser Gly Gln Pro Arg Leu Ser Pro Leu Ser Gly Arg Thr Phe
20 25 30
Pro Met Ala Thr Arg Pro Pro Leu Gln Leu Pro Pro Arg Pro Pro Pro
35 40 45
Pro Pro Pro Ser Arg Val Ser Gly His Cys Ala Leu Ser Phe Arg Ala
50 55 60
Phe Ala Ser Gly Gln His Gln Trp Arg Pro Arg Xaa Cys Ala Phe Leu
65 70 75 80
Asp Cys Ser Gly Pro Arg Leu Ser Ser Leu Ala Arg His Thr Leu Ser
85 90 95
Ser Arg Arg Arg Ala Leu Ala Ala Leu Leu Arg Ala Pro Ser Ser Ile
100 105 110
Pro Ala Arg Leu Ala Arg Glu Ala Val Lys Phe Ala Gly
115 120 125

(2) INFORMATION FOR SEQ ID NO:2435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..92

(D) OTHER INFORMATION: / Ceres Seq. ID 1503446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2435:

Met Ala Thr Arg Pro Pro Leu Gln Leu Pro Pro Arg Pro Pro Pro Pro
1 5 10 15
Pro Pro Ser Arg Val Ser Gly His Cys Ala Leu Ser Phe Arg Ala Phe
20 25 30
Ala Ser Gly Gln His Gln Trp Arg Pro Arg Xaa Cys Ala Phe Leu Asp
35 40 45
Cys Ser Gly Pro Arg Leu Ser Ser Leu Ala Arg His Thr Leu Ser Ser
50 55 60
Arg Arg Arg Ala Leu Ala Leu Leu Arg Ala Pro Ser Ser Ile Pro
65 70 75 80
Ala Arg Leu Ala Arg Glu Ala Val Lys Phe Ala Gly
85 90

(2) INFORMATION FOR SEQ ID NO:2436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..445

(D) OTHER INFORMATION: / Ceres Seq. ID 1503476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2436:

gaaactcact	cgccatcgcc	gggcatcgcg	ggcatcgcac	acaaacgcaa	cctgcagcca	60
tggcacagaa	gctcgcgcca	cgcagggcgg	sggtcgctgt	cgctcgtgtg	gcgctcgccct	120
tgctggccgc	cgcgcagaaac	tgccgggtgcg	cgctcgggcct	gtgctgcagc	cggttcgggt	180
actgcgggac	gggcgaggac	tactgcggcg	ccgggtgcc	gtcggggccc	tgcgacgtgc	240
cggagaccaa	caacgcgtcc	gtggccagca	tcgtgacgcc	ggccttcttc	gacgcgcgtcc	300

tcgcgcagggc cgcgcgctcg tgcgaggcca acggcttcta caccgcgcac gccttcctcg 360
ccgcgcgcgg ctactaccgg gcgttcggcc gcaccggcac cgtcgacgac tccaagcgcg 420
agatcgccgc cttcttcggc aacgc

(2) INFORMATION FOR SEQ ID NO:2437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1503477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2437:

Lys Leu Thr Arg His Arg Arg Ala Ser Arg Ala Ser His Thr Asn Ala
1 5 10 15
Thr Cys Ser His Gly Thr Glu Ala Arg Ala Thr Asp Gly Xaa Gly Arg
20 25 30
Arg Arg Pro Ala Gly Ala Arg Leu Val Gly Arg Arg Ala Glu Leu Arg
35 40 45
Val Arg Val Gly Pro Val Leu Gln Pro Val Arg Val Leu Arg Asp Gly
50 55 60
Arg Gly Leu Leu Arg Arg Arg Val Pro Val Gly Pro Leu Arg Arg Ala
65 70 75 80
Gly Asp Gln Gln Arg Val Arg Gly Gln His Arg Asp Ala Gly Leu Leu
85 90 95
Arg Arg Ala Pro Arg Ala Gly Arg Arg Leu Val Arg Gly Gln Arg Leu
100 105 110
Leu His Pro Arg Arg Leu Pro Arg Arg Arg Arg Leu Leu Pro Gly Val
115 120 125
Arg Pro His Arg His Arg Arg Arg Leu Gln Ala Arg Asp Arg Arg Leu
130 135 140
Leu Arg Gln Arg
145

(2) INFORMATION FOR SEQ ID NO:2438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1503478

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2438:

Asn Ser Leu Ala Ile Ala Gly His Arg Gly His Arg Thr Gln Thr Gln
1 5 10 15
Pro Ala Ala Met Ala Gln Lys Leu Ala Pro Pro Thr Ala Xaa Val Val
20 25 30
Val Val Leu Leu Ala Leu Ala Leu Ser Ala Ala Ala Gln Asn Cys Gly
35 40 45
Cys Ala Ser Gly Leu Cys Cys Ser Arg Phe Gly Tyr Cys Gly Thr Gly
50 55 60
Glu Asp Tyr Cys Gly Ala Gly Cys Gln Ser Gly Pro Cys Asp Val Pro
65 70 75 80
Glu Thr Asn Asn Ala Ser Val Ala Ser Ile Val Thr Pro Ala Phe Phe
85 90 95
Asp Ala Leu Leu Ala Gln Ala Ala Ala Ser Cys Glu Ala Asn Gly Phe
100 105 110

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Tyr Thr Arg Asp Ala Phe Leu Ala Ala Ala Gly Tyr Tyr Pro Ala Phe
115 120 125
Gly Arg Thr Gly Thr Val Asp Asp Ser Lys Arg Glu Ile Ala Ala Phe
130 135 140
Phe Gly Asn
145

(2) INFORMATION FOR SEQ ID NO:2439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1503479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2439:

Met Ala Gln Lys Leu Ala Pro Pro Thr Ala Xaa Val Val Val Leu
1 5 10 15
Leu Ala Leu Ala Leu Ser Ala Ala Ala Gln Asn Cys Gly Cys Ala Ser
20 25 30
Gly Leu Cys Cys Ser Arg Phe Gly Tyr Cys Gly Thr Gly Glu Asp Tyr
35 40 45
Cys Gly Ala Gly Cys Gln Ser Gly Pro Cys Asp Val Pro Glu Thr Asn
50 55 60
Asn Ala Ser Val Ala Ser Ile Val Thr Pro Ala Phe Phe Asp Ala Leu
65 70 75 80
Leu Ala Gln Ala Ala Ala Ser Cys Glu Ala Asn Gly Phe Tyr Thr Arg
85 90 95
Asp Ala Phe Leu Ala Ala Ala Gly Tyr Tyr Pro Ala Phe Gly Arg Thr
100 105 110
Gly Thr Val Asp Asp Ser Lys Arg Glu Ile Ala Ala Phe Gly Asn
115 120 125

(2) INFORMATION FOR SEQ ID NO:2440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..511

(D) OTHER INFORMATION: / Ceres Seq. ID 1503480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2440:

caaatgcaag agcagcaact gttaagtgat gaaaaacagt gtgccgagca cataatgctt 60
gtggacttgg gaaggaatga tgttggcaag gtatccaaac caggatcagt gaaggtggag 120
aagttgatga acattgagag atactcccat gttatgcaca tcagctcaac ggtagtgga 180
cagttggatg atcatctcca gagttgggat gccttgagag ctgccttgcc cgttgaaca 240
gtcagtggtg caccaaagggt gaaggccatg gagttgattg ataagttgga agttacgagg 300
cgaggaccat atagtgggtg tctaggagga atatcgtttg atggtgacat gcaaattgca 360
ctttctctcc gcaccatcgt attctcaaca gcgccgagcc acaacacgat gtactcatatc 420
aaagacgcag ataggcgctg gggagtggtt cgctcatctt caggctggtg caggcattgt 480
tgccgacagt agcccagatg acgaacaacg t

(2) INFORMATION FOR SEQ ID NO:2441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..163
(D) OTHER INFORMATION: / Ceres Seq. ID 1503481
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2441:

Gln Met Gln Glu Gln Gln Leu Leu Ser Asp Glu Lys Gln Cys Ala Glu
1 5 10 15
His Ile Met Leu Val Asp Leu Gly Arg Asn Asp Val Gly Lys Val Ser
20 25 30
Lys Pro Gly Ser Val Lys Val Glu Lys Leu Met Asn Ile Glu Arg Tyr
35 40 45
Ser His Val Met His Ile Ser Ser Thr Val Ser Gly Gln Leu Asp Asp
50 55 60
His Leu Gln Ser Trp Asp Ala Leu Arg Ala Ala Leu Pro Val Gly Thr
65 70 75 80
Val Ser Gly Ala Pro Lys Val Lys Ala Met Glu Leu Ile Asp Lys Leu
85 90 95
Glu Val Thr Arg Arg Gly Pro Tyr Ser Gly Gly Leu Gly Gly Ile Ser
100 105 110
Phe Asp Gly Asp Met Gln Ile Ala Leu Ser Leu Arg Thr Ile Val Phe
115 120 125
Ser Thr Ala Pro Ser His Asn Thr Met Tyr Ser Tyr Lys Asp Ala Asp
130 135 140
Arg Arg Arg Gly Val Gly Arg Ser Ser Ser Gly Trp Cys Arg His Cys
145 150 155 160
Cys Arg Gln

- (2) INFORMATION FOR SEQ ID NO:2442:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..162
(D) OTHER INFORMATION: / Ceres Seq. ID 1503482
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2442:

Met Gln Glu Gln Gln Leu Leu Ser Asp Glu Lys Gln Cys Ala Glu His
1 5 10 15
Ile Met Leu Val Asp Leu Gly Arg Asn Asp Val Gly Lys Val Ser Lys
20 25 30
Pro Gly Ser Val Lys Val Glu Lys Leu Met Asn Ile Glu Arg Tyr Ser
35 40 45
His Val Met His Ile Ser Ser Thr Val Ser Gly Gln Leu Asp Asp His
50 55 60
Leu Gln Ser Trp Asp Ala Leu Arg Ala Ala Leu Pro Val Gly Thr Val
65 70 75 80
Ser Gly Ala Pro Lys Val Lys Ala Met Glu Leu Ile Asp Lys Leu Glu
85 90 95
Val Thr Arg Arg Gly Pro Tyr Ser Gly Gly Leu Gly Gly Ile Ser Phe
100 105 110
Asp Gly Asp Met Gln Ile Ala Leu Ser Leu Arg Thr Ile Val Phe Ser
115 120 125
Thr Ala Pro Ser His Asn Thr Met Tyr Ser Tyr Lys Asp Ala Asp Arg
130 135 140
Arg Arg Gly Val Gly Arg Ser Ser Ser Gly Trp Cys Arg His Cys Cys

145 150 155 160
Arg Gln

(2) INFORMATION FOR SEQ ID NO:2443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1503483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2443:

```
Met Leu Val Asp Leu Gly Arg Asn Asp Val Gly Lys Val Ser Lys Pro
1      5      10      15
Gly Ser Val Lys Val Glu Lys Leu Met Asn Ile Glu Arg Tyr Ser His
      20      25      30
Val Met His Ile Ser Ser Thr Val Ser Gly Gln Leu Asp Asp His Leu
      35      40      45
Gln Ser Trp Asp Ala Leu Arg Ala Ala Leu Pro Val Gly Thr Val Ser
      50      55      60
Gly Ala Pro Lys Val Lys Ala Met Glu Leu Ile Asp Lys Leu Glu Val
65      70      75      80
Thr Arg Arg Gly Pro Tyr Ser Gly Gly Leu Gly Gly Ile Ser Phe Asp
      85      90      95
Gly Asp Met Gln Ile Ala Leu Ser Leu Arg Thr Ile Val Phe Ser Thr
      100     105     110
Ala Pro Ser His Asn Thr Met Tyr Ser Tyr Lys Asp Ala Asp Arg Arg
      115     120     125
Arg Gly Val Gly Arg Ser Ser Ser Gly Trp Cys Arg His Cys Cys Arg
130      135      140
Gln
145
```

(2) INFORMATION FOR SEQ ID NO:2444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 1503484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2444:

```
aatcaacacc agaagctctc gatcccaccg aggaagaaga gaggaatggc gtccgaggag      60
gagggagtcg tgatcgccctg ccacaccaag gccgacttcg acgcccacat ggccaaggcc      120
aaggaggccg gcaagctggt gatcattgac ttcacggcct cctgggtgcg cccctgccgt      180
ttcatcgcg cactgttcgt cgagcacgcc aagaagttca ccaggctgt gttcctgaag      240
gtggacgtgg acgagctgaa ggaagttgcc gcggcctacg atgtcgaggc gatgccgacc      300
ttccacttcg tcaagaacgg ggtgacggtg gagaccgtcg tcggtgccag gaaggagaac      360
ctcctggccc agatcgagaa gcaactgcgc gcggccgtgt ctgctgcgtc tgcgtagaga      420
ggatggacca gcacgtacgt ggcgggtggt gtggtcttgt cgtttcagtt tgggcttgtc      480
agcgtgtgg ctgggtggtc gattgtgaac tggag
```

(2) INFORMATION FOR SEQ ID NO:2445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..138
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2445:

Asn	Gln	His	Gln	Lys	Leu	Ser	Ile	Pro	Pro	Arg	Lys	Lys	Arg	Gly	Met
1			5						10					15	
Ala	Ser	Glu	Glu	Glu	Gly	Val	Val	Ile	Ala	Cys	His	Thr	Lys	Ala	Asp
		20						25					30		
Phe	Asp	Ala	His	Met	Ala	Lys	Ala	Lys	Glu	Ala	Gly	Lys	Leu	Val	Ile
	35					40						45			
Ile	Asp	Phe	Thr	Ala	Ser	Trp	Cys	Gly	Pro	Cys	Arg	Phe	Ile	Ala	Pro
	50					55					60				
Leu	Phe	Val	Glu	His	Ala	Lys	Lys	Phe	Thr	Gln	Ala	Val	Phe	Leu	Lys
65					70					75					80
Val	Asp	Val	Asp	Glu	Leu	Lys	Glu	Val	Ala	Ala	Ala	Tyr	Asp	Val	Glu
			85						90					95	
Ala	Met	Pro	Thr	Phe	His	Phe	Val	Lys	Asn	Gly	Val	Thr	Val	Glu	Thr
			100						105					110	
Val	Val	Gly	Ala	Arg	Lys	Glu	Asn	Leu	Leu	Ala	Gln	Ile	Glu	Lys	His
		115				120							125		
Cys	Ala	Ala	Ala	Val	Ser	Ala	Ala	Ser	Ala						
	130					135									

(2) INFORMATION FOR SEQ ID NO:2446:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..123

 (D) OTHER INFORMATION: / Ceres Seq. ID 1503486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2446:

Met	Ala	Ser	Glu	Glu	Gly	Val	Val	Ile	Ala	Cys	His	Thr	Lys	Ala	
1			5					10					15		
Asp	Phe	Asp	Ala	His	Met	Ala	Lys	Ala	Lys	Glu	Ala	Gly	Lys	Leu	Val
		20					25						30		
Ile	Ile	Asp	Phe	Thr	Ala	Ser	Trp	Cys	Gly	Pro	Cys	Arg	Phe	Ile	Ala
	35					40						45			
Pro	Leu	Phe	Val	Glu	His	Ala	Lys	Lys	Phe	Thr	Gln	Ala	Val	Phe	Leu
	50					55					60				
Lys	Val	Asp	Val	Asp	Glu	Leu	Lys	Glu	Val	Ala	Ala	Tyr	Asp	Val	
65					70					75				80	
Glu	Ala	Met	Pro	Thr	Phe	His	Phe	Val	Lys	Asn	Gly	Val	Thr	Val	Glu
			85						90					95	
Thr	Val	Val	Gly	Ala	Arg	Lys	Glu	Asn	Leu	Leu	Ala	Gln	Ile	Glu	Lys
			100						105					110	
His	Cys	Ala	Ala	Ala	Val	Ser	Ala	Ala	Ser	Ala					
		115				120									

(2) INFORMATION FOR SEQ ID NO:2447:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1503487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2447:

```
Met Ala Lys Ala Lys Glu Ala Gly Lys Leu Val Ile Ile Asp Phe Thr
1          5          10          15
Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Leu Phe Val Glu
20          25          30
His Ala Lys Lys Phe Thr Gln Ala Val Phe Leu Lys Val Asp Val Asp
35          40          45
Glu Leu Lys Glu Val Ala Ala Ala Tyr Asp Val Glu Ala Met Pro Thr
50          55          60
Phe His Phe Val Lys Asn Gly Val Thr Val Glu Thr Val Val Gly Ala
65          70          75          80
Arg Lys Glu Asn Leu Leu Ala Gln Ile Glu Lys His Cys Ala Ala Ala
85          90          95
Val Ser Ala Ala Ser Ala
100
```

(2) INFORMATION FOR SEQ ID NO:2448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 522 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..522

(D) OTHER INFORMATION: / Ceres Seq. ID 1503492

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2448:

```
aacctctagc tgattgatct ctggtttacc actctttcct tccctccttc aattctaaat      60
accacaaatc aaagttgctt tgcgatggtg agcagcagca tggacacgac gagtgacaaa      120
cgtgcgtcat ccatgctggc tcctaaccct ggcaaggcca cgatcctcgc ccttggccac      180
gccttccgcg agcagntgtc atgcaggact acgtcgtcga cggcttcatt aagaacacca      240
tcgtgtacgt gctggagaac atggtggagg acacccggcg gaggaggctg ctggctgccc      300
acgacggtgg agaggactgc gaggggggtc tcctcctcdc gttcggggccg gggatcacgt      360
tcgagggcat cctcgccagg aacttgagg caaccgcgcg cgcctcagcc cagccctgat      420
cacctcttgt tgggttgctt ttctgcttgc tctgcacctc tgcttccgtg tgattgctgc      480
tttgaggag aatgctgagc atcaacattg ctcattgagca tc
```

(2) INFORMATION FOR SEQ ID NO:2449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1503493

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2449:

```
Met Gln Asp Tyr Val Val Asp Gly Phe Met Lys Asn Thr Ile Val Tyr
1          5          10          15
Val Leu Glu Asn Met Val Glu Asp Thr Arg Arg Arg Arg Leu Leu Ala
20          25          30
Ala Asp Asp Gly Gly Glu Asp Cys Glu Trp Gly Leu Ile Leu Xaa Phe
35          40          45
Gly Pro Gly Ile Thr Phe Glu Gly Ile Leu Ala Arg Asn Leu Gln Ala
50          55          60
Thr Ala Arg Ala Ser Ala Gln Pro
65          70
```

(2) INFORMATION FOR SEQ ID NO:2450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1503494

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2450:

```
Met Lys Asn Thr Ile Val Tyr Val Leu Glu Asn Met Val Glu Asp Thr
1      5      10      15
Arg Arg Arg Arg Leu Leu Ala Ala Asp Asp Gly Gly Glu Asp Cys Glu
20      25      30
Trp Gly Leu Ile Leu Xaa Phe Gly Pro Gly Ile Thr Phe Glu Gly Ile
35      40      45
Leu Ala Arg Asn Leu Gln Ala Thr Ala Arg Ala Ser Ala Gln Pro
50      55      60
```

(2) INFORMATION FOR SEQ ID NO:2451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..52

(D) OTHER INFORMATION: / Ceres Seq. ID 1503495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2451:

```
Met Val Glu Asp Thr Arg Arg Arg Arg Leu Leu Ala Ala Asp Asp Gly
1      5      10      15
Gly Glu Asp Cys Glu Trp Gly Leu Ile Leu Xaa Phe Gly Pro Gly Ile
20      25      30
Thr Phe Glu Gly Ile Leu Ala Arg Asn Leu Gln Ala Thr Ala Arg Ala
35      40      45
Ser Ala Gln Pro
50
```

(2) INFORMATION FOR SEQ ID NO:2452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..465

(D) OTHER INFORMATION: / Ceres Seq. ID 1503496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2452:

```
atgtcgacac tctacaccca ccctcctgtc gagccacggg tctccccact agtgcaaccg      60
ctttctcctc caggggtgac ccctccccc cagcgacgg cctgcgaggc tgcgacactg      120
cagcatgccc gagccatct atctcttcc cgcgtccagc tagacctccc ccgtgcctac      180
gcccatccct ggtgcggccg cgtgcccc tcatgcggcc aacatcgaca tccctcccct      240
ctcccagtac cggctgcaac tgcaggcatc aacccttcc tcacgcccag ttcattctgt      300
tgtggcgggc gcgcgcctcc tccccgcacg ctggccttgc gtcggacagc tccctccgacg      360
ccagcgtccc ctctccaaa gatgacgagt gaggcgtcyc ctccccagc tccagcgagc      420
gcaasscagg gaccataccc acgcctccct ccctcctggt cgcggg
```

(2) INFORMATION FOR SEQ ID NO:2453:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..155
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503497
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2453:
Met Ser Thr Leu Tyr Thr His Pro Pro Val Glu Pro Arg Val Ser Pro
1 5 10 15
Leu Val Gln Pro Leu Ser Pro Pro Arg Val Thr Pro Pro Pro Gln Arg
 20 25 30
Thr Ala Cys Glu Ala Ala Thr Leu Gln His Ala Arg Arg His Leu Ser
 35 40 45
Leu Pro Arg Val Gln Leu Asp Leu Pro Arg Ala Tyr Ala His Pro Trp
 50 55 60
Cys Gly Arg Ala Ala Pro Ser Cys Gly Gln His Arg His Pro Ser Pro
65 70 75 80
Leu Pro Val Pro Ala Ala Thr Ala Gly Ile Asn Pro Phe Leu Thr Pro
 85 90 95
Ser Ser Ser Ala Cys Gly Gly Gly Ala Pro Pro Pro Arg Thr Leu Ala
 100 105 110
Leu Arg Arg Thr Ala Pro Pro Thr Pro Ala Ser Pro Pro Pro Lys Met
 115 120 125
Thr Ser Glu Ala Xaa Pro Pro Ala Pro Ala Ser Ala Xaa Gln Gly
130 135 140
Pro Tyr Pro Arg Leu Pro Pro Ser Trp Ser Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2454:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..155
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503498
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2454:
Met Ser Thr Leu Tyr Thr His Pro Pro Val Glu Pro Arg Val Ser Pro
1 5 10 15
Leu Val Gln Pro Leu Ser Pro Pro Arg Val Thr Pro Pro Pro Gln Arg
 20 25 30
Thr Ala Cys Glu Ala Ala Thr Leu Gln His Ala Arg Arg His Leu Ser
 35 40 45
Leu Pro Arg Val Gln Leu Asp Leu Pro Arg Ala Tyr Ala His Pro Trp
 50 55 60
Cys Gly Arg Ala Ala Pro Ser Cys Gly Gln His Arg His Pro Ser Pro
65 70 75 80
Leu Pro Val Pro Ala Ala Thr Ala Gly Ile Asn Pro Phe Leu Thr Pro
 85 90 95
Ser Ser Ser Ala Cys Gly Gly Gly Ala Pro Pro Pro Arg Thr Leu Ala
 100 105 110
Leu Arg Arg Thr Ala Pro Pro Thr Pro Ala Ser Pro Pro Pro Lys Met
 115 120 125
Thr Ser Glu Ala Xaa Pro Pro Ala Pro Ala Ser Ala Xaa Gln Gly
130 135 140

Pro Tyr Pro Arg Leu Pro Pro Ser Trp Ser Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1503499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2455:

Val Asp Thr Leu His Pro Pro Ser Cys Arg Ala Thr Gly Leu Pro Thr
1 5 10 15
Ser Ala Thr Ala Phe Ser Ser Thr Gly Asp Pro Ser Pro Pro Ala His
20 25 30
Gly Leu Arg Gly Cys Asp Thr Ala Ala Cys Pro Thr Pro Ser Ile Ser
35 40 45
Ser Ser Arg Pro Ala Arg Pro Pro Cys Leu Arg Pro Ser Leu Val
50 55 60
Arg Pro Arg Cys Pro Leu Met Arg Pro Thr Ser Thr Ser Leu Pro Ser
65 70 75 80
Pro Ser Thr Gly Cys Asn Cys Arg His Gln Pro Leu Pro His Ala Gln
85 90 95
Phe Ile Cys Leu Trp Arg Arg Arg Ala Ser Ser Pro His Ala Gly Leu
100 105 110
Ala Ser Asp Ser Ser Ser Asp Ala Ser Val Pro Ser Ser Lys Asp Asp
115 120 125
Glu

(2) INFORMATION FOR SEQ ID NO:2456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..470

(D) OTHER INFORMATION: / Ceres Seq. ID 1503507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2456:

ttctcattga aaagcttatac gtaaagkttg ttctacctga aggggtcaaag gatatacgaag 60
tttcagctcc ctttccaaca cagcagcagc aagagggttaa gtattcacac cttgacattg 120
tcggaagacc agttgttggtc ttggagaaac ctgatgttat tccagagcat aatttgtatt 180
tccagggttta ctacagattc aacaacatat ccttgctcag agagccgttg atgctgatta 240
ctgggtttctt cctcctgttt gtggcctgta ttgtttacat gcgtactgat atgtcaatat 300
ccaagagctc tccttcctac ttggccaagc tgcaatggga tgaggtgcaa gcaactgttc 360
agaaaatcca gggtatcttt gagcaatgct tagcagttca tgataaactg gaggcctcat 420
tgcgggattt gtctaggaca ggagacattc agtcttgcaa ggcagctcgt

(2) INFORMATION FOR SEQ ID NO:2457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1503508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2457:

Leu Ile Glu Lys Leu Ile Val Lys Xaa Val Leu Pro Glu Gly Ser Lys
1 5 10 15
Asp Ile Glu Val Ser Ala Pro Leu Pro Thr Gln Gln Gln Gln Glu Val
20 25 30
Lys Tyr Ser His Leu Asp Ile Val Gly Arg Pro Val Val Val Leu Glu
35 40 45
Lys Pro Asp Val Ile Pro Glu His Asn Leu Tyr Phe Gln Val Tyr Tyr
50 55 60
Arg Phe Asn Asn Ile Ser Leu Leu Arg Glu Pro Leu Met Leu Ile Thr
65 70 75 80
Gly Phe Phe Leu Leu Phe Val Ala Cys Ile Val Tyr Met Arg Thr Asp
85 90 95
Met Ser Ile Ser Lys Ser Ser Pro Ser Tyr Leu Ala Lys Leu Gln Trp
100 105 110
Asp Glu Val Gln Ala Thr Val Gln Lys Ile Gln Gly Ile Phe Glu Gln
115 120 125
Cys Leu Ala Val His Asp Lys Leu Glu Ala Ser Leu Arg Asp Leu Ser
130 135 140
Arg Thr Gly Asp Ile Gln Ser Cys Lys Ala Ala Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1503509

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2458:

Met Leu Ile Thr Gly Phe Phe Leu Leu Phe Val Ala Cys Ile Val Tyr
1 5 10 15
Met Arg Thr Asp Met Ser Ile Ser Lys Ser Ser Pro Ser Tyr Leu Ala
20 25 30
Lys Leu Gln Trp Asp Glu Val Gln Ala Thr Val Gln Lys Ile Gln Gly
35 40 45
Ile Phe Glu Gln Cys Leu Ala Val His Asp Lys Leu Glu Ala Ser Leu
50 55 60
Arg Asp Leu Ser Arg Thr Gly Asp Ile Gln Ser Cys Lys Ala Ala Arg
65 70 75 80

(2) INFORMATION FOR SEQ ID NO:2459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..192

(D) OTHER INFORMATION: / Ceres Seq. ID 1503510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2459:

ttggatttga caaagatgcc aggagaaggc tcttcacccat gattaacaac ctgcccactg 60
tttatgaagt tgtgacgggg gttgctaaga agcaatcgaa agcccccaac ggcagcagca 120

aaagcagcaa gcctaactct aaaccatcaa aactgaccaa ttctaacagt aagcccgca 180
mscagccac cc

(2) INFORMATION FOR SEQ ID NO:2460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..63

(D) OTHER INFORMATION: / Ceres Seq. ID 1503511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2460:

Gly	Phe	Asp	Lys	Asp	Ala	Arg	Arg	Arg	Leu	Phe	Thr	Met	Ile	Asn	Asn
1			5					10					15		
Leu	Pro	Thr	Val	Tyr	Glu	Val	Val	Thr	Gly	Val	Ala	Lys	Lys	Gln	Ser
			20					25					30		
Lys	Ala	Pro	Asn	Gly	Ser	Ser	Lys	Ser	Ser	Lys	Pro	Asn	Ser	Lys	Pro
			35				40					45			
Ser	Lys	Leu	Thr	Asn	Ser	Asn	Ser	Lys	Pro	Ala	Xaa	Gln	Pro	Thr	
			50			55					60				

(2) INFORMATION FOR SEQ ID NO:2461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1503512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2461:

Met	Ile	Asn	Asn	Leu	Pro	Thr	Val	Tyr	Glu	Val	Val	Thr	Gly	Val	Ala
1			5					10				15			
Lys	Lys	Gln	Ser	Lys	Ala	Pro	Asn	Gly	Ser	Ser	Lys	Ser	Ser	Lys	Pro
			20					25				30			
Asn	Ser	Lys	Pro	Ser	Lys	Leu	Thr	Asn	Ser	Asn	Ser	Lys	Pro	Ala	Xaa
			35			40					45				
Gln	Pro	Thr													
			50												

(2) INFORMATION FOR SEQ ID NO:2462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..287

(D) OTHER INFORMATION: / Ceres Seq. ID 1503522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2462:

ctcgagcctg	acccttacgc	cttcgctcgc	gccgccgccg	ccgccgccgc	tacgccccgc	60
acctcgcttc	atttcgtgtc	gccaagatga	cgaagcgcac	taagaaggca	ggaattgttg	120
gcaaatatgg	aaccagggtat	ggtgctagct	tgcgtaassa	atcaagaaga	tgaggtatc	180
tcagcattcc	aattactttt	gcgagttctg	tgggaagttt	gctgtgaaga	ggaaagaatg	240
agcaaggttt	ttgttcgcag	ctatttttgt	ccaatgatat	tgatatt		

(2) INFORMATION FOR SEQ ID NO:2463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..46
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2463:

Met	Thr	Lys	Arg	Thr	Lys	Lys	Ala	Gly	Ile	Val	Gly	Lys	Tyr	Gly	Thr
1				5					10					15	
Arg	Tyr	Gly	Ala	Ser	Leu	Arg	Xaa	Xaa	Ser	Arg	Arg	Trp	Arg	Tyr	Leu
			20					25					30		
Ser	Ile	Pro	Ile	Thr	Phe	Ala	Ser	Ser	Val	Gly	Ser	Leu	Leu		
			35				40						45		

(2) INFORMATION FOR SEQ ID NO:2464:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..53
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2464:

Met	Glu	Pro	Gly	Met	Val	Leu	Ala	Cys	Val	Xaa	Asn	Gln	Glu	Asp	Gly
1				5					10					15	
Gly	Ile	Ser	Ala	Phe	Gln	Leu	Leu	Leu	Arg	Val	Leu	Trp	Glu	Val	Cys
			20					25					30		
Cys	Glu	Glu	Glu	Arg	Met	Ser	Lys	Val	Phe	Val	Arg	Ser	Tyr	Phe	Cys
			35				40						45		
Pro	Met	Ile	Leu	Ile											
			50												

(2) INFORMATION FOR SEQ ID NO:2465:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..49
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2465:

Met	Val	Leu	Ala	Cys	Val	Xaa	Asn	Gln	Glu	Asp	Gly	Gly	Ile	Ser	Ala
1				5					10					15	
Phe	Gln	Leu	Leu	Leu	Arg	Val	Leu	Trp	Glu	Val	Cys	Cys	Glu	Glu	Glu
			20					25					30		
Arg	Met	Ser	Lys	Val	Phe	Val	Arg	Ser	Tyr	Phe	Cys	Pro	Met	Ile	Leu
			35				40						45		
Ile															

(2) INFORMATION FOR SEQ ID NO:2466:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..498

(D) OTHER INFORMATION: / Ceres Seq. ID 1503526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2466:

ctagtagaga	gaaaggaaga	gaagggggcg	gagaagcagc	tacgtcgtac	atcgcccacc	60
gccctttgcc	tcgcctcgcc	tcgcctcgcc	tgcatatcta	acagccggag	ccggagccgg	120
agccggagcc	gacgccggcg	ccgacaatcg	ttccaactga	tatggctacg	acgccaccag	180
gattcacggg	caacctgaag	aaagcacttg	caggtctgag	agaatcagt	ttagatgggt	240
tgcgatggcg	cgtatttgat	gctaagggtc	aggtgctcgg	gcgattggct	tcccaaatag	300
ctgttgtgct	tcaaggcaag	gataaaccga	cctatgcacc	acatgtagaa	aatggagaca	360
tgtgcattgt	acttaatgca	aaggatatca	gtgtttacag	gaaggaaaat	gacagataag	420
atttactatt	ggcatacagg	gtatgtttggc	catttgaaag	aaaggaggct	caaggaccag	480
atggagaaaag	acccaact					

(2) INFORMATION FOR SEQ ID NO:2467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1503527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2467:

Leu	Val	Glu	Arg	Lys	Glu	Glu	Lys	Gly	Ala	Glu	Lys	His	Val	Arg	Arg
1				5					10					15	
Thr	Ser	Pro	Thr	Ala	Leu	Cys	Leu	Ala	Ser	Pro	Arg	Leu	Ala	Cys	Ile
			20					25					30		
Ser	Asn	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Arg	Arg	Arg	Arg
		35					40					45			
Gln	Ser	Phe	Gln	Leu	Ile	Trp	Leu	Arg	Arg	His	Gln	Asp	Ser	Arg	Ala
	50					55					60				

Thr
65

(2) INFORMATION FOR SEQ ID NO:2468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1.185

(D) OTHER INFORMATION: / Ceres Seq. ID 1503528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2468:

[illegible]

85

(2) INFORMATION FOR SEQ ID NO:2469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..49

(D) OTHER INFORMATION: / Ceres Seq. ID 1503529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2469:

```
Met Glu Thr Cys Ala Leu Tyr Leu Met Gln Arg Ile Ser Val Phe Thr
1           5           10           15
Gly Arg Lys Met Thr Asp Lys Ile Tyr Tyr Trp His Thr Gly Tyr Val
          20           25           30
Gly His Leu Lys Glu Arg Arg Leu Lys Asp Gln Met Glu Lys Asp Pro
          35           40           45
Thr
```

(2) INFORMATION FOR SEQ ID NO:2470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477

(D) OTHER INFORMATION: / Ceres Seq. ID 1503550

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2470:

```
ataaccaagg ataaccagag tgtgctggtt tattgcttct catgggttgt aattttcggt      60
gttttactcg ttatgaagac cgtatcagtg gggaggagga gggtcagtg agagttccag      120
ctagtgttcc ggctgatcaa gggctcataa tttataactt ttacagccat cgtggtaatc      180
ctaatagcaa tccctggcat gacggttctg gacatccttg tttgcatcct tgccttcatt      240
cccactggat ggggtttgct cctgattgcc caagctatca ggctgtgat tcaaaagatc      300
gggctgtggg ggtcgatcaa ggctcttgcc cggggctacg agatcctaag ggggcttctc      360
ctgttcacgc ccattgcttt ccttgccctg ttcccgttcg tgtccgagtt ccagaccagg      420
atgctgttca accaggcctt cagcagaggt tctgcagatc tcccgtatcc tggggagg
```

(2) INFORMATION FOR SEQ ID NO:2471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..159

(D) OTHER INFORMATION: / Ceres Seq. ID 1503551

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2471:

```
Ile Thr Lys Asp Asn Gln Ser Val Leu Val Tyr Cys Phe Ser Trp Val
1           5           10           15
Val Ile Phe Val Val Leu Leu Val Met Lys Thr Val Ser Val Gly Arg
          20           25           30
Arg Arg Phe Ser Ala Glu Phe Gln Leu Val Phe Arg Leu Ile Lys Gly
          35           40           45
Leu Ile Phe Ile Thr Phe Thr Ala Ile Val Val Ile Leu Ile Ala Ile
          50           55           60
```

Pro Gly Met Thr Val Leu Asp Ile Phe Val Cys Ile Leu Ala Phe Met
65 70 75 80
Pro Thr Gly Trp Gly Leu Leu Leu Ile Ala Gln Ala Ile Arg Pro Val
85 90 95
Ile Gln Lys Ile Gly Leu Trp Gly Ser Ile Lys Ala Leu Ala Arg Gly
100 105 110
Tyr Glu Ile Leu Met Gly Leu Leu Phe Thr Pro Ile Ala Phe Leu
115 120 125
Ala Trp Phe Pro Phe Val Ser Glu Phe Gln Thr Arg Met Leu Phe Asn
130 135 140
Gln Ala Phe Ser Arg Gly Ser Ala Asp Leu Pro Tyr Pro Gly Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2472:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1503552

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2472:

Met Gly Cys Asn Phe Arg Cys Phe Thr Arg Tyr Glu Asp Arg Ile Ser
1 5 10 15
Gly Glu Glu Glu Val Gln Cys Arg Val Pro Ala Ser Val Pro Ala Asp
20 25 30
Gln Gly Ser His Ile Tyr Asn Phe Tyr Ser His Arg Gly Asn Pro Asn
35 40 45
Ser Asn Pro Trp His Asp Gly Ser Gly His Leu Cys Leu His Pro Cys
50 55 60
Leu His Ala His Trp Met Gly Phe Ala Pro Asp Cys Pro Ser Tyr Gln
65 70 75 80
Ala Cys Asp Ser Lys Asp Arg Ala Val Gly Val Asp Gln Gly Ser Cys
85 90 95
Pro Gly Leu Arg Asp Pro Asn Gly Ala Ser Pro Val His Ala His Cys
100 105 110
Phe Pro Cys Leu Val Pro Val Arg Val Pro Asp Gln Asp Ala
115 120 125
Val Gln Pro Gly Leu Gln Gln Arg Phe Cys Arg Ser Pro Val Ser Trp
130 135 140
Glu
145

(2) INFORMATION FOR SEQ ID NO:2473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1503553

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2473:

Met Lys Thr Val Ser Val Gly Arg Arg Phe Ser Ala Glu Phe Gln
1 5 10 15
Leu Val Phe Arg Leu Ile Lys Gly Leu Ile Phe Ile Thr Phe Thr Ala
20 25 30
Ile Val Val Ile Leu Ile Ala Ile Pro Gly Met Thr Val Leu Asp Ile

35 40 45
Phe Val Cys Ile Leu Ala Phe Met Pro Thr Gly Trp Gly Leu Leu Leu
50 55 60
Ile Ala Gln Ala Ile Arg Pro Val Ile Gln Lys Ile Gly Leu Trp Gly
65 70 75 80
Ser Ile Lys Ala Leu Ala Arg Gly Tyr Glu Ile Leu Met Gly Leu Leu
85 90 95
Leu Phe Thr Pro Ile Ala Phe Leu Ala Trp Phe Pro Phe Val Ser Glu
100 105 110
Phe Gln Thr Arg Met Leu Phe Asn Gln Ala Phe Ser Arg Gly Ser Ala
115 120 125
Asp Leu Pro Tyr Pro Gly Arg
130 135

(2) INFORMATION FOR SEQ ID NO:2474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..420
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2474:

caggctcctag ctccggcctc cgccgccgtc tctcacctcc gctccccttc cctgccccca 60
tggcgaaggc gacgcccgtg gccgagggcg ggccgcctct cactgccccca ctcccacatg 120
ggcgcacnca cggaggccct gaccacgctc ctgaccacc cgtcccacgc gccgtcactc 180
cactgcgcagc tcttctctgc ctcccgcgtc ccgtgcccgc cgcggggcct cggctccacc 240
acgtcgtacc cgccgctcct ctgccccgny gcctcgtctc tccgctgggc tctcgcctcc 300
gtgttctctc cgccgcgcgc agcctctgcc tcccgccctc gtcctggcgc tcccggtgcc 360
ccttccaggc tccccgcgcg cggtcgtgcc ctccgcggcc atcgagccgc gcgcccgcgc 420

(2) INFORMATION FOR SEQ ID NO:2475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..139
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503555

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2475:

Gly Pro Ser Ser Gly Leu Arg Arg Arg Leu Ser Pro Pro Leu Pro Phe
1 5 10 15
Pro Ala Pro Met Ala Lys Ala Thr Pro Val Ala Glu Ala Gly Pro Pro
20 25 30
Leu Thr Ser Pro Leu Pro His Gly Arg Xaa His Gly Gly Pro Asp Pro
35 40 45
Arg Pro Asp Pro Pro Val Pro Arg Ala Val Thr Pro Leu Ala Ala Leu
50 55 60
Pro Arg Leu Pro Arg Pro Val Pro Ala Ala Gly Pro Arg Leu His His
65 70 75 80
Val Val Pro Ala Ala Pro Leu Pro Xaa Xaa Leu Ala Pro Pro Leu Gly
85 90 95
Ser Arg Leu Arg Val Pro Pro Ala Arg Ala Ser Leu Cys Leu Pro Pro
100 105 110
Ser Ser Trp Arg Ser Arg Cys Pro Phe Gln Ala Pro Arg Arg Arg Ser
115 120 125

Cys Pro Pro Arg Pro Ser Ser Arg Ala Pro Glu
130 135

(2) INFORMATION FOR SEQ ID NO:2476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1503556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2476:

Met Ala Lys Ala Thr Pro Val Ala Glu Ala Gly Pro Pro Leu Thr Ser
1 5 10 15
Pro Leu Pro His Gly Arg Xaa His Gly Gly Pro Asp Pro Arg Pro Asp
20 25 30
Pro Pro Val Pro Arg Ala Val Thr Pro Leu Ala Ala Leu Pro Arg Leu
35 40 45
Pro Arg Pro Val Pro Ala Ala Gly Pro Arg Leu His His Val Val Pro
50 55 60
Ala Ala Pro Leu Pro Xaa Xaa Leu Ala Pro Pro Leu Gly Ser Arg Leu
65 70 75 80
Arg Val Pro Pro Ala Arg Ala Ser Leu Cys Leu Pro Pro Ser Ser Trp
85 90 95
Arg Ser Arg Cys Pro Phe Gln Ala Pro Arg Arg Arg Ser Cys Pro Pro
100 105 110
Arg Pro Ser Ser Arg Ala Pro Glu
115 120

(2) INFORMATION FOR SEQ ID NO:2477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..101

(D) OTHER INFORMATION: / Ceres Seq. ID 1503557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2477:

Met Gly Ala Xaa Thr Glu Ala Leu Thr His Val Leu Thr His Pro Ser
1 5 10 15
His Ala Pro Ser Leu His Ser Gln Leu Phe Leu Ala Ser Arg Val Pro
20 25 30
Cys Pro Pro Arg Gly Leu Gly Ser Thr Thr Ser Tyr Pro Pro Leu Leu
35 40 45
Cys Pro Xaa Ala Ser Leu Leu Arg Trp Ala Leu Ala Ser Val Phe Leu
50 55 60
Pro Arg Ala Arg Ala Ser Ala Ser Arg Pro Arg Pro Gly Gly Pro Gly
65 70 75 80
Ala Pro Ser Arg Leu Pro Ala Ala Gly Arg Ala Leu Arg Gly His Arg
85 90 95
Ala Gly Arg Pro Ser
100

(2) INFORMATION FOR SEQ ID NO:2478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 418 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..418
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2478:

ttctggctcc	tcctgcttcc	tcattgatcaa	gcgtgtgtcc	tctgctccgt	ccttgctccag	60
gcaccacaag	gcaaaagaag	ctcaggtgag	aatgttgtga	tggttgatcc	actggaagct	120
aagcgcctag	ctgctaaaca	aatgcaagaa	attagggcca	aagaaaagct	gaagaggcgc	180
cgtcaagcag	aagcgatcaa	cggggcattg	gcagtgatag	gactcacggc	tggtattgcta	240
gtggaggctc	agacaggaaa	ggacatctta	gggcagctag	ctggatatct	gacggctatt	300
tctagtttat	ttggggcaata	acactggacc	atggttggag	atttattttt	cacgttccac	360
ggccaggaga	ggtcttatct	gaatcttatt	tgatggatcc	acccaatttt	tttgggag	

(2) INFORMATION FOR SEQ ID NO:2479:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..106
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2479:

Phe	Trp	Leu	Leu	Leu	Pro	His	Asp	Gln	Ala	Cys	Val	Leu	Cys	Ser	
1			5					10					15		
Val	Leu	Val	Gln	Ala	Pro	Gln	Gly	Lys	Arg	Ser	Ser	Gly	Glu	Asn	Val
			20					25					30		
Val	Met	Val	Asp	Pro	Leu	Glu	Ala	Lys	Arg	Leu	Ala	Ala	Lys	Gln	Met
			35					40					45		
Gln	Glu	Ile	Arg	Ala	Lys	Glu	Lys	Leu	Lys	Arg	Arg	Arg	Gln	Ala	Glu
			50					55					60		
Ala	Ile	Asn	Gly	Ala	Leu	Ala	Val	Ile	Gly	Leu	Thr	Ala	Gly	Leu	Leu
			65					70					75		80
Val	Glu	Ala	Gln	Thr	Gly	Lys	Asp	Ile	Leu	Gly	Gln	Leu	Ala	Gly	Tyr
			85					90							95
Leu	Thr	Ala	Ile	Ser	Ser	Leu	Phe	Gly	Gln						
			100					105							

(2) INFORMATION FOR SEQ ID NO:2480:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..73
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503571

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2480:

Met	Val	Asp	Pro	Leu	Glu	Ala	Lys	Arg	Leu	Ala	Ala	Lys	Gln	Met	Gln
1				5					10				15		
Glu	Ile	Arg	Ala	Lys	Glu	Lys	Leu	Lys	Arg	Arg	Arg	Gln	Ala	Glu	Ala
			20					25					30		
Ile	Asn	Gly	Ala	Leu	Ala	Val	Ile	Gly	Leu	Thr	Ala	Gly	Leu	Leu	Val
			35					40					45		
Glu	Ala	Gln	Thr	Gly	Lys	Asp	Ile	Leu	Gly	Gln	Leu	Ala	Gly	Tyr	Leu
			50					55					60		
Thr	Ala	Ile	Ser	Ser	Leu	Phe	Gly	Gln							

65

70

(2) INFORMATION FOR SEQ ID NO:2481:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1503572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2481:

Met Gln Glu Ile Arg Ala Lys Glu Lys Leu Lys Arg Arg Arg Gln Ala
1 5 10 15
Glu Ala Ile Asn Gly Ala Leu Ala Val Ile Gly Leu Thr Ala Gly Leu
20 25 30
Leu Val Glu Ala Gln Thr Gly Lys Asp Ile Leu Gly Gln Leu Ala Gly
35 40 45
Tyr Leu Thr Ala Ile Ser Ser Leu Phe Gly Gln
50 55

(2) INFORMATION FOR SEQ ID NO:2482:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..438

(D) OTHER INFORMATION: / Ceres Seq. ID 1503585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2482:

cagaggatat caatatttgg tgggaattc ccatcagggc atacagctga tgttcaaagt 60
gtgtccatca actcatcaat acaaatatgt ttgtctctgg ctcatgtgat acaactgtga 120
ggctgtggga tatcagaatt gcaagtcgag ctgttcgaac ctaccatgga catgaggatg 180
atgttaacag tgtgaagttt ttccctgatg gccatagggt tggtagtggc tcagattatg 240
gcacatgtag attattttgat atgagaacag ggcatacaact tcaggtgtac agtagggagc 300
ctgatatagaa tagtaatgaa ctacctactg ttacatctat tgcattttca atatcaggaa 360
ggctactttt tgctgggttac tccaatgggt actgttatgt gtggggacacm ttctcgccga 420
ggtggtactt aatttggg

(2) INFORMATION FOR SEQ ID NO:2483:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1503586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2483:

Met Phe Val Ser Gly Ser Cys Asp Thr Thr Val Arg Leu Trp Asp Ile
1 5 10 15
Arg Ile Ala Ser Arg Ala Val Arg Thr Tyr His Gly His Glu Asp Asp
20 25 30
Val Asn Ser Val Lys Phe Phe Pro Asp Gly His Arg Phe Gly Thr Gly
35 40 45
Ser Asp Tyr Gly Thr Cys Arg Leu Phe Asp Met Arg Thr Gly His Gln
50 55 60

Leu Gln Val Tyr Ser Arg Glu Pro Asp Arg Asn Ser Asn Glu Leu Pro
65 70 75 80
Thr Val Thr Ser Ile Ala Phe Ser Ile Ser Gly Arg Leu Leu Phe Ala
85 90 95
Gly Tyr Ser Asn Gly Asp Cys Tyr Val Trp Asp Xaa Phe Ser Pro Arg
100 105 110
Trp Tyr Leu Ile Trp
115

(2) INFORMATION FOR SEQ ID NO:2484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1503587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2484:

Met Arg Thr Gly His Gln Leu Gln Val Tyr Ser Arg Glu Pro Asp Arg
1 5 10 15
Asn Ser Asn Glu Leu Pro Thr Val Thr Ser Ile Ala Phe Ser Ile Ser
20 25 30
Gly Arg Leu Leu Phe Ala Gly Tyr Ser Asn Gly Asp Cys Tyr Val Trp
35 40 45
Asp Xaa Phe Ser Pro Arg Trp Tyr Leu Ile Trp
50 55

(2) INFORMATION FOR SEQ ID NO:2485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 506 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..506

(D) OTHER INFORMATION: / Ceres Seq. ID 1503588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2485:

ttcgcgcgcg	cgcgccctcg	agaagagata	gagcgcgccg	ctgcatcgac	cccgcgccac	60
ccccgcctgc	ctcccccg	accgatcg	ggtgatcgat	ggcgctgaag	aggatcctga	120
aggagttgaa	ggacctgcag	aaggaccgc	ccacctcctg	cagcgcrctc	tggttggtgag	180
gacatgttcc	attggcaagc	gaccatcatg	gggccttcg	acagcccatt	tcaggtgagg	240
gtattcttgg	tgaacattca	cttcccaccg	gattaccctt	tcaagccacc	aaaggtgtct	300
ttccgcacca	aggttttcca	cccgaacatc	aacagcaacg	gcagcatttg	ccttgacatt	360
cttaaggaac	agtggagtc	tgctttaact	atctcaaagg	ttctcctgtc	aatctgtctca	420
ctgctcacgg	acccaaaccc	tgatgatcct	cttgctccctg	agattgctca	catgtacaat	480
tcattcggtg	gaaaacctgg	aacgtg				

(2) INFORMATION FOR SEQ ID NO:2486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1503589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2486:

Met Phe His Trp Gln Ala Thr Ile Met Gly Pro Ser Asp Ser Pro Phe
1 5 10 15
Ala Gly Gly Val Phe Leu Val Asn Ile His Phe Pro Pro Asp Tyr Pro
20 25 30
Phe Lys Pro Pro Lys Val Ser Phe Arg Thr Lys Val Phe His Pro Asn
35 40 45
Ile Asn Ser Asn Gly Ser Ile Cys Leu Asp Ile Leu Lys Glu Gln Trp
50 55 60
Ser Pro Ala Leu Thr Ile Ser Lys Val Leu Leu Ser Ile Cys Ser Leu
65 70 75 80
Leu Thr Asp Pro Asn Pro Asp Asp Pro Leu Val Pro Glu Ile Ala His
85 90 95
Met Tyr Asn Ser Phe Val Gly Lys Pro Gly Thr
100 105

(2) INFORMATION FOR SEQ ID NO:2487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1503590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2487:

Met Gly Pro Ser Asp Ser Pro Phe Ala Gly Gly Val Phe Leu Val Asn
1 5 10 15
Ile His Phe Pro Pro Asp Tyr Pro Phe Lys Pro Pro Lys Val Ser Phe
20 25 30
Arg Thr Lys Val Phe His Pro Asn Ile Asn Ser Asn Gly Ser Ile Cys
35 40 45
Leu Asp Ile Leu Lys Glu Gln Trp Ser Pro Ala Leu Thr Ile Ser Lys
50 55 60
Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp Pro Asn Pro Asp Asp
65 70 75 80
Pro Leu Val Pro Glu Ile Ala His Met Tyr Asn Ser Phe Val Gly Lys
85 90 95
Pro Gly Thr

(2) INFORMATION FOR SEQ ID NO:2488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..383

(D) OTHER INFORMATION: / Ceres Seq. ID 1503591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2488:

gtacgagcgg acgcacgacg agcttgactt cgagttcctc gggaacgtgc gcggcaagga	60
gtggcgcggtg cagaccaacg tgtacggcaa cggcagcacg gcggccggcc gggaggagcg	120
ctacggcctc tggttcgacc ccacggagga cttccaccgc tacgccatcc actggacccg	180
cgacaggatc atattctaca tcgacgacac gccaatcatg gagatgggtgc ggacggagtc	240
aatgggcgcg cagttcccgt ccaagcccat gtcgctgtac gccaccatct gggacggctc	300
cagctgggcc acctcggggg gccgctacaa ggtggactac aagtacgcgc cctacgtcgc	360
cgagttcgcc gacctcgcg ccc	

(2) INFORMATION FOR SEQ ID NO:2489:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..127
(D) OTHER INFORMATION: / Ceres Seq. ID 1503592
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2489:
Tyr Glu Arg Thr His Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Val
1 5 10 15
Arg Gly Lys Glu Trp Arg Val Gln Thr Asn Val Tyr Gly Asn Gly Ser
20 25 30
Thr Ala Ala Gly Arg Glu Glu Arg Tyr Gly Leu Trp Phe Asp Pro Thr
35 40 45
Glu Asp Phe His Arg Tyr Ala Ile His Trp Thr Arg Asp Arg Ile Ile
50 55 60
Phe Tyr Ile Asp Asp Thr Pro Ile Met Glu Met Val Arg Thr Glu Ser
65 70 75 80
Met Gly Ala Gln Phe Pro Ser Lys Pro Met Ser Leu Tyr Ala Thr Ile
85 90 95
Trp Asp Gly Ser Ser Trp Ala Thr Ser Gly Gly Arg Tyr Lys Val Asp
100 105 110
Tyr Lys Tyr Ala Pro Tyr Val Ala Glu Phe Ala Asp Leu Ala Leu
115 120 125
(2) INFORMATION FOR SEQ ID NO:2490:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..127
(D) OTHER INFORMATION: / Ceres Seq. ID 1503593
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2490:
Thr Ser Gly Arg Thr Thr Ser Leu Thr Ser Ser Ser Ser Gly Thr Cys
1 5 10 15
Ala Ala Arg Ser Gly Ala Cys Arg Pro Thr Cys Thr Ala Thr Ala Ala
20 25 30
Arg Arg Pro Ala Gly Arg Ser Ala Thr Ala Ser Gly Ser Thr Pro Arg
35 40 45
Arg Thr Ser Thr Ala Thr Pro Ser Thr Gly Pro Ala Thr Gly Ser Tyr
50 55 60
Ser Thr Ser Thr Thr Arg Gln Ser Trp Arg Trp Cys Gly Arg Ser Gln
65 70 75 80
Trp Ala Arg Ser Ser Arg Pro Ser Pro Cys Arg Cys Thr Pro Pro Ser
85 90 95
Gly Thr Ala Pro Ala Gly Pro Pro Arg Gly Ala Ala Thr Arg Trp Thr
100 105 110
Thr Ser Thr Arg Pro Thr Ser Pro Ser Pro Thr Ser Arg Ser
115 120 125
(2) INFORMATION FOR SEQ ID NO:2491:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..365

(D) OTHER INFORMATION: / Ceres Seq. ID 1503594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2491:

actgaacatt	ctgcgtgaag	attggaagcc	tgttctcaac	atcaacaccg	ttatztatgg	60
cctgaatctt	ctttttacgc	aaccaaacga	cgaggatcct	ttgaaccacg	aagctgcagc	120
tgctctccgt	ggcaacccaa	agatgtttga	ggcaaattgt	aaaagagcca	tgaccggagc	180
tacgtaggcc	aacactattd	ccaaagatgc	ttggcttgat	gtgatggctt	caagccagcg	240
ggcccatgta	tcagcaccag	cgcgcccgag	tttggaggat	ttttgtggat	ttagggcgct	300
ttctggaagca	aagggtcaaat	cggctcgttg	tgataatgtg	atgtactccc	tcagttcttt	360
ttatt						

(2) INFORMATION FOR SEQ ID NO:2492:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1503595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2492:

Leu	Asn	Ile	Leu	Arg	Glu	Asp	Trp	Lys	Pro	Val	Leu	Asn	Ile	Asn	Thr
1			5					10					15		
Val	Ile	Tyr	Gly	Leu	Asn	Leu	Leu	Phe	Thr	Gln	Pro	Asn	Asp	Glu	Asp
			20					25					30		
Pro	Leu	Asn	His	Glu	Ala	Ala	Ala	Val	Leu	Arg	Gly	Asn	Pro	Lys	Met
			35					40					45		
Phe	Glu	Ala	Asn	Val	Lys	Arg	Ala	Met	Thr	Gly	Ala	Thr			
			50					55					60		

(2) INFORMATION FOR SEQ ID NO:2493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1503596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2493:

Met	Ala	Ser	Ser	Gln	Arg	Ala	His	Val	Ser	Ala	Pro	Ala	Arg	Pro	Gly
1				5				10					15		
Leu	Glu	Asp	Phe	Cys	Gly	Phe	Arg	Ala	Leu	Leu	Glu	Ala	Lys	Val	Lys
				20				25					30		
Ser	Val	Val	Val	Asp	Asn	Val	Met	Tyr	Ser	Leu	Ser	Ser	Phe	Tyr	
				35				40					45		

(2) INFORMATION FOR SEQ ID NO:2494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..31

(D) OTHER INFORMATION: / Ceres Seq. ID 1503597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2494:

Met Tyr Gln His Gln Arg Ala Gln Val Trp Arg Ile Phe Val Asp Leu
1 5 10 15
Gly Arg Phe Trp Lys Gln Arg Ser Asn Arg Ser Leu Leu Ile Met
20 25 30

(2) INFORMATION FOR SEQ ID NO:2495:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..413
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503600

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2495:

atatccgcct ccaaacccta gctcttccat tcttccccct ccggcgccgc ctcccccaga 60
cacttcgccg ccggcaagat gggccgcgtg attcgcgctc agssaagggt gcgggggtccg 120
tggtcaagtc ccatacccat caccgcaagg ccctgcgcgt tccggtccct cgacttcggc 180
gagcgcaacg ggtacctgaa gggcgtggtc accgacgtca tccacgaccc gggccgcggc 240
gcgccgctgg ccaaggtcac cttccgccat ccattccggt acaagcacca gaaggagctg 300
ttcgtggctg ctgagggcat gtacactggc cagttcggtt actgcggacg ccgtgctaca 360
ctctccattg gcaacgtcct gccgctcagg gggatccctg aggggtgccgt tgt

(2) INFORMATION FOR SEQ ID NO:2496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503601

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2496:

Ile Arg Leu Gln Thr Leu Ala Leu Pro Phe Phe Pro Leu Arg Arg Arg
1 5 10 15
Leu Pro Gln Thr Leu Arg Arg Arg Gln Asp Gly Pro Arg Asp Ser Arg
20 25 30
Ser Xaa Lys Gly Ala Gly Ser Val Phe Lys Ser His Thr His His Arg
35 40 45
Lys Ala Leu Pro Val Pro Val Pro Arg Leu Arg Arg Ala Gln Arg Val
50 55 60
Pro Glu Gly Arg Gly His Arg Arg His Pro Arg Pro Gly Pro Arg Arg
65 70 75 80
Ala Ala Gly Gln Gly His Leu Pro Pro Ser Ile Pro Val Gln Ala Pro
85 90 95
Glu Gly Ala Val Arg Gly Cys
100

(2) INFORMATION FOR SEQ ID NO:2497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..111
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2497:
Met Gly Arg Val Ile Arg Ala Gln Xaa Arg Val Arg Gly Pro Cys Ser
1 5 10 15
Ser Pro Ile Pro Ile Thr Ala Arg Pro Cys Arg Phe Arg Ser Leu Asp
20 25 30
Phe Gly Glu Arg Asn Gly Tyr Leu Lys Gly Val Val Thr Asp Val Ile
35 40 45
His Asp Pro Gly Arg Gly Ala Pro Leu Ala Lys Val Thr Phe Arg His
50 55 60
Pro Phe Arg Tyr Lys His Gln Lys Glu Leu Phe Val Ala Ala Glu Gly
65 70 75 80
Met Tyr Thr Gly Gln Phe Val Tyr Cys Gly Arg Arg Ala Thr Leu Ser
85 90 95
Ile Gly Asn Val Leu Pro Leu Arg Gly Ile Pro Glu Gly Ala Val
100 105 110

(2) INFORMATION FOR SEQ ID NO:2498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..466
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2498:

attccattcc atcgattg attgcattcc catccattc cccgctctac tcattcagat	60
ctcgctcactc gctctccaca agcagagcac cgcagcagaa cgaggatgct ggccatcttc	120
cagaagcagg tggcgacgc gtcsgcagga gcntcaacag cccccgcgc ggcgcgtgc	180
ccagcaagcc ccggaacccc gacgagatcc tgcgcgactt ccacgccgcg caccgcgcg	240
ccgccttctc cgctctcttc ggcggcgtgc gntgctcgcc ttgcgttcgg cccctccttc	300
gccaccgcca cctaccagcg ggatgtttct gcggccttgg accacatcta ctgcgtcttc	360
ctcggccgcc tcgacaacct cagcggcctc atccgccagt wacggcctgt gcggccgctc	420
ccaccaacga ggcgatgctg gtcacgagg cctaccgcac gctgcg	

(2) INFORMATION FOR SEQ ID NO:2499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..155
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2499:

Ile Pro Phe His Arg Ile Gly Leu His Ser His Pro Ile Pro Arg Ser
1 5 10 15
Thr His Ser Asp Leu Val Thr Arg Ser Pro Gln Ala Glu His Arg Ser
20 25 30
Arg Thr Arg Met Leu Ala Ile Phe Gln Lys Gln Val Ala His Ala Xaa
35 40 45
Ala Gly Xaa Ser Thr Ala Pro Ala Pro Ala Arg Arg Pro Ala Ser Pro
50 55 60
Gly Thr Pro Thr Arg Ser Cys Ala Thr Ser Thr Pro Arg Thr Arg Pro
65 70 75 80
Pro Pro Ser Pro Pro Ser Ala Ala Cys Xaa Ala Arg Leu Ala Phe
85 90 95
Gly Pro Ser Ser Ala Thr Ala Thr Tyr Gln Arg Asp Val Ser Ala Ala
100 105 110

Leu Asp His Ile Tyr Cys Val Phe Leu Gly Arg Leu Asp Asn Leu Ser
115 120 125
Gly Leu Ile Arg Gln Xaa Arg Pro Val Arg Pro Leu Pro Pro Thr Arg
130 135 140
Arg Cys Trp Ser Ser Arg Pro Thr Ala Arg Cys
145 150 155

(2) INFORMATION FOR SEQ ID NO:2500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1503617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2500:

Phe His Ser Ile Ala Leu Asp Cys Ile Pro Ile Pro Phe Pro Ala Leu
1 5 10 15
Leu Ile Gln Ile Ser Ser Leu Ala Leu His Lys Gln Ser Thr Ala Ala
20 25 30
Glu Arg Gly Cys Trp Pro Ser Ser Arg Ser Arg Trp Arg Thr Arg Xaa
35 40 45
Gln Glu Xaa Gln Gln Pro Pro Arg Arg Arg Val Ala Gln Gln Ala Pro
50 55 60
Glu Pro Arg Arg Asp Pro Ala Arg Leu Pro Arg Arg Ala Pro Gly Arg
65 70 75 80
Arg Leu Leu Arg Leu Arg Arg Arg Ala Xaa Leu Ala Leu Arg Ser
85 90 95
Ala Pro Pro Pro Pro Pro Pro Pro Thr Ser Gly Met Phe Leu Arg Pro
100 105 110
Trp Thr Thr Ser Thr Ala Ser Ser Ala Ala Ser Thr Thr Ser Ala
115 120 125
Ala Ser Ser Ala Ser Xaa Gly Leu Cys Gly Arg Ser His Gln Arg Gly
130 135 140
Asp Ala Gly His Arg Gly Leu Pro His Ala Ala
145 150 155

(2) INFORMATION FOR SEQ ID NO:2501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1503618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2501:

Ser Ile Pro Ser His Trp Ile Ala Phe Pro Ser His Ser Pro Leu Tyr
1 5 10 15
Ser Phe Arg Ser Arg His Ser Leu Ser Thr Ser Arg Ala Pro Gln Gln
20 25 30
Asn Glu Asp Ala Gly His Leu Pro Glu Ala Gly Gly Ala Arg Val Xaa
35 40 45
Arg Ser Xaa Asn Ser Pro Arg Ala Gly Ala Ser Pro Ser Lys Pro Arg
50 55 60
Asn Pro Asp Glu Ile Leu Arg Asp Phe His Ala Ala His Pro Ala Ala
65 70 75 80
Ala Phe Ser Ala Ser Phe Gly Gly Val Xaa Cys Ser Pro Cys Val Arg

85 90 95
Pro Leu Leu Arg His Arg His Leu Pro Ala Gly Cys Phe Cys Gly Leu
100 105 110
Gly Pro His Leu Leu Arg Leu Pro Arg Pro Pro Arg Gln Pro Gln Arg
115 120 125
Pro His Pro Pro Xaa Thr Ala Cys Ala Ala Ala Pro Thr Asn Glu Ala
130 135 140
Met Leu Val Ile Glu Ala Tyr Arg Thr Leu
145 150

(2) INFORMATION FOR SEQ ID NO:2502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..403
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2502:

agtgtcgggtg tggcggttg cgagtggcga ctggcgactt ctctgcctcg tccctccccg	60
ttttcccttc cgcgtccagc cckgcgcgac gccaccacgc acctagccgc ggantccgag	120
gcgcagatcc aatccagcga tggcggtccac ggcggcgagg cggttgcggg asstgcaggc	180
ccagacgggg aacaagacct gcgtggactg cgcgcrssta accgcagtg ggcgagcgtc	240
tcctacggcg tggtcatgtg cctcgagtgc tcyggcaagc accggggcct cggcgtgcac	300
atcagtttcg tgcgtcgggt caccatggac tcctggaccg aggcgcasst ccgcaagatg	360
gaggccggcg gcaacgaccg cctcaacgcc ttcctcacag cgc	

(2) INFORMATION FOR SEQ ID NO:2503:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2503:

Ser Val Gly Val Gly Val Gly Glu Trp Arg Leu Ala Thr Ser Leu Pro
1 5 10 15
Arg Pro Ser Pro Phe Ser Pro Pro Arg Pro Ala Xaa Arg Asp Ala Thr
20 25 30
Thr His Leu Ala Ala Xaa Ser Glu Ala Gln Ile Gln Ser Ser Asp Gly
35 40 45
Val His Gly Gly Glu Ala Val Ala Gly Xaa Ala Gly Pro Asp Gly Glu
50 55 60
Gln Asp Leu Arg Gly Leu Arg Xaa Xaa Asn Pro Gln Trp Ala Ser Val
65 70 75 80
Ser Tyr Gly Val Phe Met Cys Leu Glu Cys Xaa Gly Lys His Arg Gly
85 90 95
Leu Gly Val His Ile Ser Phe Val Arg Ser Val Thr Met Asp Ser Trp
100 105 110
Thr Glu Ala Xaa Xaa Arg Lys Met Glu Ala Gly Gly Asn Asp Arg Leu
115 120 125
Asn Ala Phe Leu Thr Ala
130

(2) INFORMATION FOR SEQ ID NO:2504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..72
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503623
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2504:

Cys Arg Cys Arg Arg Trp Arg Val Ala Thr Gly Asp Phe Ser Ala Ser
1 5 10 15
Ser Leu Pro Val Phe Pro Ser Ala Ser Ser Xaa Ala Arg Arg His His
20 25 30
Ala Pro Ser Arg Gly Xaa Arg Gly Ala Asp Pro Ile Gln Arg Trp Arg
35 40 45
Pro Arg Arg Arg Gly Gly Cys Gly Xaa Cys Arg Pro Arg Arg Gly Thr
50 55 60
Arg Pro Ala Trp Thr Ala Arg Xaa
65 70

(2) INFORMATION FOR SEQ ID NO:2505:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..88
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503624
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2505:

Met Ala Ser Thr Ala Ala Arg Arg Leu Arg Xaa Xaa Gln Ala Gln Thr
1 5 10 15
Gly Asn Lys Thr Cys Val Asp Cys Ala Xaa Xaa Thr Arg Ser Gly Arg
20 25 30
Ala Ser Pro Thr Ala Cys Ser Cys Ala Ser Ser Ala Xaa Ala Ser Thr
35 40 45
Gly Ala Ser Ala Cys Thr Ser Val Ser Cys Ala Arg Ser Pro Trp Thr
50 55 60
Pro Gly Pro Arg Arg Xaa Ser Ala Arg Trp Arg Pro Ala Ala Thr Thr
65 70 75 80
Ala Ser Thr Pro Ser Ser Gln Arg
85

(2) INFORMATION FOR SEQ ID NO:2506:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 389 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..389
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503662
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2506:

actcgcgcac	agsstccaat	ttcctccacc	tcccgaaccc	taccggcggc	gcmagcattc	60
acaaccacca	cccgaagatg	gtgaagtttc	tgaagcccg	caaggccgta	atcctcctcc	120
agggcagatt	cgccggccgg	aagssggtga	tcgtgcgcgt	gttcgaggag	ggcaccgcgc	180
accgtcccta	tgggcactgc	ctcgtcgccg	gcctggccaa	gtaccccaag	aaggtgatcc	240
gcaagactcc	gccaaaga	cggccaagaa	gtccgcgcgc	aagtgttca	tcaagctcat	300
caatttcact	cacctcatgc	ccaccgccta	caccctcgac	gtcgacttca	aggacgtcgc	360

ctcgggggggg cccgacgcgc tctccaccc

(2) INFORMATION FOR SEQ ID NO:2507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..129
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1503663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2507:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- ```
(A) NAME/KEY: peptide
(B) LOCATION: 1..129
```

(D) OTHER INFORMATION: / Ceres Seq. ID 1503664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2508:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503665

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2509:

Met	Val	Lys	Phe	Leu	Lys	Pro	Gly	Lys	Ala	Val	Ile	Leu	Leu	Gln	Gly
1				5					10					15	
Arg	Phe	Ala	Gly	Arg	Lys	Xaa	Val	Ile	Val	Arg	Val	Phe	Glu	Glu	Gly
		20						25				30			
Thr	Arg	Asp	Arg	Pro	Tyr	Gly	His	Cys	Leu	Val	Ala	Gly	Leu	Ala	Lys
		35				40					45				
Tyr	Pro	Lys	Lys	Val	Ile	Arg	Lys	Thr	Pro	Pro	Arg	Arg	Arg	Pro	Arg
	50					55				60					
Ser	Pro	Ala	Ser	Ser	Ala	Ser	Ser	Ser	Ser	Ser	Ile	Ser	Leu	Thr	Ser
65				70						75				80	
Cys	Pro	Pro	Ala	Thr	Pro	Ser	Thr	Ser	Thr	Ser	Arg	Thr	Ser	Pro	Arg
			85					90						95	
Gly	Gly	Pro	Thr	Arg	Ser	Pro	Pro								
			100												

(2) INFORMATION FOR SEQ ID NO:2510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..420
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503670

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2510:

atttgtgcgt	gcacacccac	tcctgagaat	gctaattgtac	gtgaccttga	actcnccatt	60
gcangtgccc	ttctgaatac	catatgatta	agtacctttc	ggcatgttaa	tttcatctcc	120
aaaagtctct	atacgaggcc	gcagcaactt	ggattatata	tccctagtcg	tcgtccacgg	180
cgggtgcggt	cgccgacgcc	gacgccgacg	ccgccacctc	ctccggcgcg	gccgcggtgg	240
tgctcttggc	cggggcgcta	ccgctcccct	cggagcttcc	cttggttttc	cggcggttgg	300
acttcttggg	aacggcgggg	aggtcctggc	atgtgcccca	ggcgtcgtcg	cggnccgact	360
tgctctgctt	cttgcggttc	tttcgggttt	gcaacaagag	gaggatgaag	atcgaagacc	420

(2) INFORMATION FOR SEQ ID NO:2511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2511:

Met	Leu	Ile	Ser	Ser	Pro	Lys	Val	Leu	Ile	Arg	Gly	Arg	Ser	Asn	Leu
1				5					10					15	
Asp	Tyr	Ile	Ser	Leu	Val	Val	Val	His	Gly	Gly	Cys	Gly	Arg	Arg	Arg

20 25 30
Arg Arg Arg Arg Arg His Leu Leu Arg Arg Gly Arg Gly Val Leu
35 40 45
Gly Arg Gly Ala Thr Ala Pro Leu Gly Ala Ser Leu Val Phe Pro Ala
50 55 60
Val Gly Leu Leu Gly Asn Gly Gly Glu Val Leu Ala Cys Ala Arg Gly
65 70 75 80
Val Val Ala Xaa Arg Leu Val Leu Leu Leu Ala Val Leu Ser Gly Leu
85 90 95
Gln Gln Glu Glu Asp Glu Asp Arg Arg
100 105

(2) INFORMATION FOR SEQ ID NO:2512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..475
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503697

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2512:

tatctattct gttgcttatg ttgatggtag ccgtgggcgt agactatagc acataggctg	60
agctttgttg agatggttgt tccttatgga gatccaagtg aaccacatta tcgcaagaat	120
gcatttgatg ctggagaaga tggacttgga aaaaatgctc attctcttaa gaagggatgc	180
gattgcttgg gctacataaa atattttgat gcacatttca caaacttcac tgggtggtg	240
gagacaattg agaactgtgt ttgtttgcat gaggaggatc atgggatcct ttggaaacat	300
caagactgga gaacdggttt agcagaagta aggcggtcaa ggaggctcac tgtttcattt	360
atctgtacag ttgcaaacta tgagtatggt ttttactggc acttctatca ggatgggaaa	420
katagaggca gaagtaaagc ttactggaat tctcagctta ggggctttga tgcct	

(2) INFORMATION FOR SEQ ID NO:2513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..134
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2513:

Met Val Val Pro Tyr Gly Asp Pro Ser Glu Pro His Tyr Arg Lys Asn	
1 5 10 15	
Ala Phe Asp Ala Gly Glu Asp Gly Leu Gly Lys Asn Ala His Ser Leu	
20 25 30	
Lys Lys Gly Cys Asp Cys Leu Gly Tyr Ile Lys Tyr Phe Asp Ala His	
35 40 45	
Phe Thr Asn Phe Thr Gly Gly Val Glu Thr Ile Glu Asn Cys Val Cys	
50 55 60	
Leu His Glu Glu Asp His Gly Ile Leu Trp Lys His Gln Asp Trp Arg	
65 70 75 80	
Xaa Gly Leu Ala Glu Val Arg Arg Ser Arg Arg Leu Thr Val Ser Phe	
85 90 95	
Ile Cys Thr Val Ala Asn Tyr Glu Tyr Gly Phe Tyr Trp His Phe Tyr	
100 105 110	
Gln Asp Gly Lys Xaa Arg Gly Arg Ser Lys Ala Tyr Trp Asn Ser Gln	
115 120 125	
Leu Arg Gly Phe Asp Ala	
130	

(2) INFORMATION FOR SEQ ID NO:2514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..495
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2514:

aaagcagagt	ctgccccctcc	ccgcgcggtt	ctttttgggtt	ccccagtc	cgccgcgcgc	60
gaaacccgca	gatggaggtc	gtcgtcgccg	cgamssagaa	ggcgaagaaa	cacatacacc	120
tcttctactg	ctcagaatgc	gaggagctcg	ccctcaagat	cgccgccagc	tccgacgcc	180
tcgagctcca	atccatcaac	tggcgasst	tcgacgacgg	gttcccgaac	ctattcatcg	240
cctcattcac	gctcgtgctg	ccattcttcc	ccacgggctc	attcgagcgc	gttgaggagg	300
agggcgatgt	cgccaccgcg	ttcaccctcg	cgcgcatctt	ctcgatgac	cccaagtcgc	360
gcggcgggcc	taccagcgtc	gtcatctacg	acatccacgc	gctccaggag	aggttttact	420
tcggggacga	tgtctgccat	gcttcgagac	agggatccc	ctcctgctgc	agcgccctcg	480
ccagctccc	gacgc					

(2) INFORMATION FOR SEQ ID NO:2515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2515:

Lys	Ala	Glu	Ser	Ala	Pro	Pro	Arg	Ala	Val	Leu	Phe	Gly	Ser	Pro	Val
1			5						10					15	
Pro	Ala	Ala	Ala	Glu	Thr	Arg	Arg	Trp	Arg	Ser	Ser	Ser	Pro	Arg	Xaa
			20					25					30		
Arg	Arg	Arg	Arg	Asn	Thr	Tyr	Thr	Ser	Ser	Thr	Ala	Gln	Asn	Ala	Arg
			35				40					45			
Ser	Ser	Pro	Ser	Arg	Ser	Pro	Pro	Ala	Pro	Thr	Pro	Ser	Ser	Ser	Asn
			50			55					60				
Pro	Ser	Thr	Gly	Gly	Xaa	Ser	Thr	Thr	Gly	Ser	Arg	Thr	Tyr	Ser	Ser
65				70					75					80	
Pro	His	Ser	Arg	Ser	Cys	Cys	His	Ser	Ser	Pro	Arg	Ala	His	Ser	Ser
			85					90					95		
Ala	Leu	Arg	Arg	Arg	Ala	Met	Ser	Pro	Pro	Arg	Ser	Pro	Ser	Arg	Ala
			100				105						110		
Phe	Ser	Arg													
			115												

(2) INFORMATION FOR SEQ ID NO:2516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..164
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2516:

Ser Arg Val Cys Pro Ser Pro Arg Arg Ser Phe Trp Phe Pro Ser Pro
1 5 10 15
Arg Arg Arg Arg Asn Pro Gln Met Glu Val Val Val Ala Ala Xaa Xaa
20 25 30
Lys Ala Lys Lys His Ile His Leu Phe Tyr Cys Ser Glu Cys Glu Glu
35 40 45
Leu Ala Leu Lys Ile Ala Ala Ser Ser Asp Ala Ile Glu Leu Gln Ser
50 55 60
Ile Asn Trp Arg Xaa Phe Asp Asp Gly Phe Pro Asn Leu Phe Ile Ala
65 70 75 80
Ser Phe Thr Leu Val Leu Pro Phe Phe Pro Thr Gly Ser Phe Glu Arg
85 90 95
Val Glu Glu Glu Gly Asp Val Ala Thr Ala Phe Thr Leu Ala Arg Ile
100 105 110
Leu Ser Met Ile Pro Lys Ser Arg Gly Gly Pro Thr Ser Val Val Ile
115 120 125
Tyr Asp Ile His Ala Leu Gln Glu Arg Phe Tyr Phe Gly Asp Asp Val
130 135 140
Cys His Ala Ser Arg Gln Gly Ser Arg Ser Cys Cys Ser Ala Ser Ala
145 150 155 160
Ser Ser Arg Thr

(2) INFORMATION FOR SEQ ID NO:2517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..141

(D) OTHER INFORMATION: / Ceres Seq. ID 1503706

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2517:

Met Glu Val Val Val Ala Ala Xaa Xaa Lys Ala Lys Lys His Ile His
1 5 10 15
Leu Phe Tyr Cys Ser Glu Cys Glu Glu Leu Ala Leu Lys Ile Ala Ala
20 25 30
Ser Ser Asp Ala Ile Glu Leu Gln Ser Ile Asn Trp Arg Xaa Phe Asp
35 40 45
Asp Gly Phe Pro Asn Leu Phe Ile Ala Ser Phe Thr Leu Val Leu Pro
50 55 60
Phe Phe Pro Thr Gly Ser Phe Glu Arg Val Glu Glu Glu Gly Asp Val
65 70 75 80
Ala Thr Ala Phe Thr Leu Ala Arg Ile Leu Ser Met Ile Pro Lys Ser
85 90 95
Arg Gly Gly Pro Thr Ser Val Val Ile Tyr Asp Ile His Ala Leu Gln
100 105 110
Glu Arg Phe Tyr Phe Gly Asp Asp Val Cys His Ala Ser Arg Gln Gly
115 120 125
Ser Arg Ser Cys Cys Ser Ala Ser Ala Ser Ser Arg Thr
130 135 140

(2) INFORMATION FOR SEQ ID NO:2518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..474

(D) OTHER INFORMATION: / Ceres Seq. ID 1503714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2518:

SEQUENCE DESCRIPTION: SEQ ID NO:2518:						
aacttcacgcg	gctctctcct	ctcttcgcgc	catcgccgct	gccggggcgc	cctacaactt	60
caaaatggcg	gctaccgcac	tcgccatggc	tatagcaact	atytcccccg	ccgctccgat	120
cccatccgcg	cccttcccat	ccctccccc	cggcctccgc	ctccgccctc	aaccctcct	180
tttcgctgct	tcccgcgcgc	gccttctctc	atgttcccaa	agccgcctcc	tgggacgaat	240
ccgtccccc	aggatggtgc	agatgcggag	gaatccggtg	ccgctgggga	cgacgaggac	300
gggacgaga	agccgcggc	cgagccggtg	tcctctcccg	agttccagtt	cgcggcgcca	360
cccgagggct	acgtcagacc	cgcggckktt	tgacgagcta	ccgcggagtt	ccccasaaga	420
cgtggcggcg	gcgtacgaat	ctctctacgg	gccggccttc	agcggcgaga	catt	

(2) INFORMATION FOR SEQ ID NO:2519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1503715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2519:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503716

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2520:

Thr	Ser	Pro	Ala	Ser	Ser	Ser	Phe	Pro	Ser	Ile	Ala	Val	Ala	Gly	Ala
1				5					10					15	
Pro	Tyr	Asn	Phe	Lys	Met	Ala	Ala	Thr	Ala	Leu	Ala	Met	Ala	Ile	Ala
			20					25					30		
Thr	Xaa	Ser	Pro	Ala	Ala	Pro	Ile	Pro	Ser	Ala	Pro	Phe	Pro	Ser	Leu
		35					40					45			
Pro	Leu	Gly	Leu	Arg	Leu	Arg	Pro	Gln	Pro	Leu	Leu	Phe	Ala	Ala	Ser
	50					55					60				

Arg Arg Arg Leu Pro Pro Cys Ser Gln Ser Arg Leu Leu Gly Arg Ile
65 70 75 80
Arg Pro Pro Arg Met Val Glu Met Arg Arg Asn Pro Leu Pro Leu Gly
85 90 95
Thr Thr Arg Thr Arg Thr Arg Ser Arg Gly Pro Ser Arg Cys Pro Pro
100 105 110
Pro Ser Ser Ser Ser Arg Arg His Pro Arg Ala Thr Ser Ser Pro Arg
115 120 125
Xaa Phe Asp Glu Leu Pro Pro Glu Ser Pro Xaa Asp Val Ala Ala Ala
130 135 140
Tyr Glu Ser Leu Tyr Gly Pro Ala Phe Ser Gly Glu Thr
145 150 155

(2) INFORMATION FOR SEQ ID NO:2521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1503717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2521:

Met Ala Ala Thr Ala Leu Ala Met Ala Ile Ala Thr Xaa Ser Pro Ala
1 5 10 15
Ala Pro Ile Pro Ser Ala Pro Phe Pro Ser Leu Pro Leu Gly Leu Arg
20 25 30
Leu Arg Pro Gln Pro Leu Leu Phe Ala Ala Ser Arg Arg Arg Leu Pro
35 40 45
Pro Cys Ser Gln Ser Arg Leu Leu Gly Arg Ile Arg Pro Pro Arg Met
50 55 60
Val Glu Met Arg Arg Asn Pro Leu Pro Leu Gly Thr Thr Arg Thr Arg
65 70 75 80
Thr Arg Ser Arg Gly Pro Ser Arg Cys Pro Pro Pro Ser Ser Ser Ser
85 90 95
Arg Arg His Pro Arg Ala Thr Ser Ser Pro Arg Xaa Phe Asp Glu Leu
100 105 110
Pro Pro Glu Ser Pro Xaa Asp Val Ala Ala Ala Tyr Glu Ser Leu Tyr
115 120 125
Gly Pro Ala Phe Ser Gly Glu Thr
130 135

(2) INFORMATION FOR SEQ ID NO:2522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

- (B) LOCATION: 1..412

(D) OTHER INFORMATION: / Ceres Seq. ID 1503718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2522:

agagcagcca agcgccacac acacgccgac gcgaaccaac caaccagctg gtagtagggt 60
cgccgcggcg cgcgctgac gatgatgcct cgccgcgccc ttctcttcgc cgcggtgctc 120
ctcgcgccct ccgcgcgcgc gtctccgggt ttcacctcgg cggggacgag agcggtctcg 180
tgagggggtg gctcgccgcg ctccgcagcg kgtccgaggc cgtggacgcc gctcgcttcg 240
ccgtcgccca ctacaacaag aaccagggcg ccgctttgga gtttactagg gtgctcaaat 300
ccaagcggca ggtggtgacc gggaccctgc atgacctgat actggaggca gctgatgctg 360
gaaaaaagag tgtgtacaga gcaaaggttt ggggtgaagcg tgggaagatt tc

(2) INFORMATION FOR SEQ ID NO:2523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..136
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2523:

```
Ser Ser Gln Ala Pro His Thr Arg Arg Arg Glu Pro Thr Asn Gln Leu
1          5          10          15
Val Val Gly Ser Pro Arg Arg Arg Ala Asp Asp Ala Ser Pro Arg
20          25          30
Pro Ser Leu Arg Arg Gly Ala Pro Arg Gly Leu Arg Arg Ala Val Ser
35          40          45
Gly Phe His Leu Gly Gly Asp Glu Ser Gly Leu Val Arg Gly Val Leu
50          55          60
Ala Ala Leu Arg Ser Xaa Ser Glu Ala Val Asp Ala Ala Arg Phe Ala
65          70          75          80
Val Ala His Tyr Asn Lys Asn Gln Gly Ala Ala Leu Glu Phe Thr Arg
85          90          95
Val Leu Lys Ser Lys Arg Gln Val Val Thr Gly Thr Leu His Asp Leu
100         105         110
Ile Leu Glu Ala Ala Asp Ala Gly Lys Lys Ser Val Tyr Arg Ala Lys
115         120         125
Val Trp Val Lys Arg Gly Lys Ile
130         135
```

(2) INFORMATION FOR SEQ ID NO:2524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..482
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2524:

```
ccccacacac tgcacgccnc cgccgggtcc tcctagggtt tcgccgcgat gtcgctccgg 60
ccgagcgagc gggagcagat gcggaagggc aactacaagc agacggtgga cgcggaggag 120
agccgccgcc gccgcgaggg ccagatgatg gacatgcgca aggccaagcg cgaggaaagt 180
ctccagaaga agcgtgcga tgggtttccc gcctccgccg ccggtgtgcc gccgatgggc 240
cactccaccg cgctccagca gaagtcccc aatcgaagag gtgatcagca caggagtggg 300
gtcgcgattc attgagtttc ttacacgtga ggaccatccc caactccagt ttgaggctgc 360
atgggcactc accaacattg catcaggcac atcagagaac actaagggtg tcgttgagag 420
tggtgctgtg cgctgtgcc catctttgtc aagctactca actccctcaa gcgaggatgt 480
tc
```

(2) INFORMATION FOR SEQ ID NO:2525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1503721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2525:

Pro His Thr Ala Arg Xaa Arg Arg Val Leu Leu Gly Phe Arg Arg Asp
1 5 10 15
Val Ala Pro Ala Glu Arg Ala Gly Ala Asp Ala Glu Gly Gln Leu Gln
20 25 30
Ala Asp Gly Gly Arg Gly Gly Glu Pro Pro Pro Pro Arg Gly Pro Asp
35 40 45
Asp Gly His Ala Gln Gly Gln Ala Arg Gly Lys Ser Pro Glu Glu Ala
50 55 60
Leu Arg Trp Val Ser Arg Leu Arg Arg Arg Cys Ala Ala Asp Gly Pro
65 70 75 80
Leu His Arg Ala Pro Ala Glu Val Pro Gln Ser Lys Arg
85 90

(2) INFORMATION FOR SEQ ID NO:2526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1503722

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2526:

Met Ser Leu Arg Pro Ser Glu Arg Glu Gln Met Arg Lys Gly Asn Tyr
1 5 10 15
Lys Gln Thr Val Asp Ala Glu Glu Ser Arg Arg Arg Arg Glu Gly Gln
20 25 30
Met Met Asp Met Arg Lys Ala Lys Arg Glu Glu Ser Leu Gln Lys Lys
35 40 45
Arg Cys Asp Gly Phe Pro Ala Ser Ala Ala Gly Val Pro Pro Met Gly
50 55 60
His Ser Thr Ala Leu Gln Gln Lys Ser Pro Asn Arg Arg Gly Asp Gln
65 70 75 80
His Arg Ser Gly Val Ala Ile His
85

(2) INFORMATION FOR SEQ ID NO:2527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1503723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2527:

Met Gly Phe Pro Pro Pro Pro Val Cys Arg Arg Trp Ala Thr Pro
1 5 10 15
Pro Arg Ser Ser Arg Ser Pro Pro Ile Glu Glu Val Ile Ser Thr Gly
20 25 30
Val Val Ser Arg Phe Ile Glu Phe Leu Thr Arg Glu Asp His Pro Gln
35 40 45
Leu Gln Phe Glu Ala Ala Trp Ala Leu Thr Asn Ile Ala Ser Gly Thr
50 55 60
Ser Glu Asn Thr Lys Val Val Val Glu Ser Gly Ala Val Arg Leu Cys
65 70 75 80
Pro Ser Leu Ser Ser Tyr Ser Thr Pro Ser Ser Glu Asp Val

85

90

(2) INFORMATION FOR SEQ ID NO:2528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1503728

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2528:

agataacagg	aaaggctctg	caacacggct	tgagttcaaa	caaaggctct	caatagctat	60
tggggcagct	aaaggtttga	atcatctgca	cagtcttgat	cctcctttga	tacacaagga	120
cttcaagaca	aacaatgtgc	tggttgatga	aaatttcatt	gcaaagggtg	ctgatgctgg	180
acttgttagg	ttaattagag	gatctgacga	tgccggccca	tcgcgtgggt	tcagtaacag	240
tgtttaccaa	gatccagagg	tacagtcgat	gactcagttc	tctgaaagca	gtgatgttta	300
cagcttgag	tttttctttt	ggagctaatt	actggcaggg	aagcagcttc	cttgatacct	360
acagagtcca	gagaatattt	ggcacactgg	atggaagcgc	atttcagttc	aaatgaactg	420
attgacccaa	gattagccgg	caacttcact	gcagaaggta	tgaaggagct	t	

(2) INFORMATION FOR SEQ ID NO:2529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1503729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2529:

Asp	Asn	Arg	Lys	Gly	Ser	Ala	Thr	Arg	Leu	Glu	Phe	Lys	Gln	Arg	Leu
1				5					10					15	
Ser	Ile	Ala	Ile	Gly	Ala	Ala	Lys	Gly	Leu	Asn	His	Leu	His	Ser	Leu
			20					25						30	
Asp	Pro	Pro	Leu	Ile	His	Lys	Asp	Phe	Lys	Thr	Asn	Asn	Val	Leu	Val
		35					40					45			
Asp	Glu	Asn	Phe	Ile	Ala	Lys	Val	Ala	Asp	Ala	Gly	Leu	Val	Arg	Leu
		50				55					60				
Ile	Arg	Gly	Ser	Asp	Asp	Ala	Gly	Pro	Ser	Arg	Gly	Phe	Ser	Asn	Ser
65				70					75					80	
Val	Tyr	Gln	Asp	Pro	Glu	Val	Gln	Ser	Met	Thr	Gln	Phe	Ser	Glu	Ser
			85					90						95	
Ser	Asp	Val	Tyr	Ser	Leu	Glu	Phe	Phe	Phe	Trp	Ser				
			100					105							

(2) INFORMATION FOR SEQ ID NO:2530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..469

(D) OTHER INFORMATION: / Ceres Seq. ID 1503734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2530:

atccttttggc	aaccgaactg	gtttgggtgtg	cccacctctc	tctcttccat	gggatatggc	60
agggacggaa	tccagatgag	gatgaactcg	tggcaggacg	gcgtcacggg	caccaactgc	120

cccatccctc cgggatggaa ctggacctac gagttccagc tcaaggacca gatcggcagc 180
ttctttctact tcccgctcgt cggcctccag cgagctgccg gcggggttcgg ccccatcacc 240
gtcaacaacc ggcgccaccgt gccnntcccc ttgcaccagc ctcatggcga catcaccctg 300
ttcatcgggg actggtacac caagggccac gttgtaagag ctttgttttt ctgtttctgt 360
caatgcaaat ctagctagat ggttcgtcct tttgtttcag atcgagatat atagccaggg 420
aaaaatatcg cgcttttccc ttgatctcag tgaactggat ttcactgag

(2) INFORMATION FOR SEQ ID NO:2531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1503735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2531:

Ile Leu Trp Gln Pro Asn Trp Phe Gly Val Pro Thr Ser Leu Ser Ser
1 5 10 15
Met Gly Tyr Gly Arg Asp Gly Ile Gln Met Arg Met Asn Ser Trp Gln
20 25 30
Asp Gly Val Thr Gly Thr Asn Cys Pro Ile Pro Pro Gly Trp Asn Trp
35 40 45
Thr Tyr Glu Phe Gln Leu Lys Asp Gln Ile Gly Ser Phe Phe Tyr Phe
50 55 60
Pro Ser Leu Gly Leu Gln Arg Ala Ala Gly Gly Phe Gly Pro Ile Thr
65 70 75 80
Val Asn Asn Arg Ala Thr Val Xaa Xaa Pro Phe Asp Gln Pro His Gly
85 90 95
Asp Ile Thr Leu Phe Ile Gly Asp Trp Tyr Thr Lys Gly His Val Val
100 105 110
Arg Ala Leu Phe Phe Cys Phe Cys Gln Cys Lys Ser Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:2532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2532:

Pro Leu Ala Thr Glu Leu Val Trp Cys Ala His Leu Ser Leu Phe His
1 5 10 15
Gly Ile Trp Gln Gly Arg Asn Pro Asp Glu Asp Glu Leu Val Ala Gly
20 25 30
Arg Arg His Gly His Gln Leu Pro His Pro Ser Arg Met Glu Leu Asp
35 40 45
Leu Arg Val Pro Ala Gln Gly Pro Asp Arg Gln Leu Leu Leu Pro
50 55 60
Val Ala Arg Pro Pro Ala Ser Cys Arg Arg Val Arg Pro His His Arg
65 70 75 80
Gln Gln Pro Arg His Arg Ala Xaa Pro Leu Arg Pro Ala Ser Trp Arg
85 90 95
His His Pro Val His Arg Gly Leu Val His Gln Gly Pro Arg Cys Lys
100 105 110
Ser Phe Val Phe Leu Phe Leu Ser Met Gln Ile

115 120
(2) INFORMATION FOR SEQ ID NO:2533:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..109
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503737
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2533:
Met Gly Tyr Gly Arg Asp Gly Ile Gln Met Arg Met Asn Ser Trp Gln
1 5 10 15
Asp Gly Val Thr Gly Thr Asn Cys Pro Ile Pro Pro Gly Trp Asn Trp
 20 25 30
Thr Tyr Glu Phe Gln Leu Lys Asp Gln Ile Gly Ser Phe Phe Tyr Phe
 35 40 45
Pro Ser Leu Gly Leu Gln Arg Ala Ala Gly Gly Phe Gly Pro Ile Thr
 50 55 60
Val Asn Asn Arg Ala Thr Val Xaa Xaa Pro Phe Asp Gln Pro His Gly
65 70 75 80
Asp Ile Thr Leu Phe Ile Gly Asp Trp Tyr Thr Lys Gly His Val Val
 85 90 95
Arg Ala Leu Phe Phe Cys Phe Cys Gln Cys Lys Ser Ser
 100 105
(2) INFORMATION FOR SEQ ID NO:2534:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..129
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503743
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2534:
aatctctttca ctcactctcc agatccgggtg cttgtgggag cctaacacgc ccccgccctc 60
cctctccgcc gtcgccgagt cctcgcccg cttaccccg cgtggcgaa ggcactccgg 120
cgtggacgc
(2) INFORMATION FOR SEQ ID NO:2535:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..42
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503744
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2535:
Ile Leu Ser Leu Thr Leu Gln Ile Arg Cys Leu Trp Glu Pro Asn Thr
1 5 10 15
Pro Pro Ala Ser Leu Ser Ala Val Ala Glu Ser Leu Ala Gly Leu Pro
 20 25 30
Arg Arg Trp Arg Arg His Ser Gly Val Asp
 35 40
(2) INFORMATION FOR SEQ ID NO:2536:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..42
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2536:

Phe Phe His Ser Leu Ser Arg Ser Gly Ala Cys Gly Ser Leu Thr Arg
1 5 10 15
Pro Pro Pro Pro Ser Pro Pro Ser Pro Ser Pro Ser Pro Ala Tyr Pro
 20 25 30
Val Ala Gly Glu Gly Thr Pro Ala Trp Thr
 35 40

(2) INFORMATION FOR SEQ ID NO:2537:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..409
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2537:

ctagccgccc ccagaccatt cgtttctcgc gagccatcct tctgtaattc tcaggcatcc 60
ggaagaaatg gccaaagtcga agaaccacac ggcgcacaac cagtcgttca aggcgcacaa 120
gaacggcatt aagaaaccca agcgcaccgc ccagacctcc accaagggga tggaccccaa 180
gttcctgagg aacctgaggt attctaggaa gggcaacaaa aagagtgggt aggcgtgaagc 240
tgaggagtag gaaggaaaagc atggctttgt ggtaatgtgc tgctgtgggg gttcattagt 300
atgaagagga agacgctgct ggcgcggagt cttttctctt ttattagtat tttgtttaaa 360
actatgtatg accgaatggt ggtatttatt tgtgtcatcc ttgactctc

(2) INFORMATION FOR SEQ ID NO:2538:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..43
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2538:

Leu Ala Ala Ala Arg Pro Phe Val Ser Arg Glu Pro Ser Phe Cys Asn
1 5 10 15
Ser Gln Ala Ser Gly Arg Asn Gly Gln Val Glu Glu Pro His Gly Ala
 20 25 30
Gln Pro Val Val Gln Gly Ala Gln Glu Arg His
 35 40

(2) INFORMATION FOR SEQ ID NO:2539:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1503748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2539:

```
Met Ala Lys Ser Lys Asn His Thr Ala His Asn Gln Ser Phe Lys Ala
1          5          10          15
His Lys Asn Gly Ile Lys Lys Pro Lys Arg His Arg Gln Thr Ser Thr
20          25          30
Lys Gly Met Asp Pro Lys Phe Leu Arg Asn Leu Arg Tyr Ser Arg Lys
35          40          45
Gly Asn Lys Lys Ser Gly Glu Ala Glu Ala Glu Glu
50          55          60
```

(2) INFORMATION FOR SEQ ID NO:2540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1503749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2540:

```
Met Lys Arg Lys Thr Leu Leu Ala Arg Ser Leu Phe Leu Phe Ile Ser
1          5          10          15
Ile Leu Phe Lys Thr Met Tyr Asp Arg Met Val Val Phe Ile Cys Val
20          25          30
Ile Leu Asp Ser
35
```

(2) INFORMATION FOR SEQ ID NO:2541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 450 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..450

(D) OTHER INFORMATION: / Ceres Seq. ID 1503769

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2541:

```
aaaatgatcg agtgggctcc catgtgattt tgtcatccta gtgacagaaa ttttctccct      60
ttttttttct caagctcaca acactcctct gctgtgattc cagatggagc gcactttcat      120
tgccatcaag cccgacggcg tccaaagagg cctgatttct gagattgtga accgattcga      180
gagaaaaggc tacaagcttg ttgccatcaa gctgattgtc ccatccaaag gattcgctga      240
gaagcactac catgatctca aggaaaggcc tttcttcaac gggttgtgtg acttcctcag      300
ctctggccct gtacttgcaa tggtttggga aggagagggt gtcatcaagt atgggagaaa      360
actaattggt gccacagacc cacagaaatc tgaaccagga accatcaggg gcgatcttgg      420
cgttgttgtg ggaagaaaca tcattcatgg
```

(2) INFORMATION FOR SEQ ID NO:2542:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1503770

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2542:

Met Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly
1 5 10 15
Leu Ile Ser Glu Ile Val Asn Arg Phe Glu Arg Lys Gly Tyr Lys Leu
20 25 30
Val Ala Ile Lys Leu Ile Val Pro Ser Lys Gly Phe Ala Glu Lys His
35 40 45
Tyr His Asp Leu Lys Glu Arg Pro Phe Phe Asn Gly Leu Cys Asp Phe
50 55 60
Leu Ser Ser Gly Pro Val Leu Ala Met Val Trp Glu Gly Glu Gly Val
65 70 75 80
Ile Lys Tyr Gly Arg Lys Leu Ile Gly Ala Thr Asp Pro Gln Lys Ser
85 90 95
Glu Pro Gly Thr Ile Arg Gly Asp Leu Gly Val Val Val Gly Arg Asn
100 105 110
Ile Ile His
115

(2) INFORMATION FOR SEQ ID NO:2543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..499

(D) OTHER INFORMATION: / Ceres Seq. ID 1503775

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2543:

tgattatttg cacaaaaagc aatctggcgg tcaaggtcag tatggacgag tttgtgggta 60
cattgagcct ctaccttcag gttctgatgg taaattcgaa tttgataaca tgattattgg 120
acaagcaatt ccttcaaact ttataccagc aatagagaag ggttttaagg aagcttgcaa 180
ttcaggctcg ttgattggtc atcctgttga aaatttaaga attgtattga ctgatggggc 240
ttcacatcag gtggattcca gtgaacttgc ttttaagcta gctgctatct atgcttttctg 300
acagtgttac acttctgcc aacctgtaat attagaacct gtgatgaagg tggaactcaa 360
atttccaact gagtttcagg gcacagtaac tgggtgatatg aacaagagaa aagggatcat 420
tgttggaaat gagcaggaag gtgacgacac cattgtagtt tgccatgtcc gctaaacaat 480
atgtttggat atgcacagc

(2) INFORMATION FOR SEQ ID NO:2544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..157

(D) OTHER INFORMATION: / Ceres Seq. ID 1503776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2544:

Asp Tyr Leu His Lys Lys Gln Ser Gly Gly Gln Gly Gln Tyr Gly Arg
1 5 10 15
Val Cys Gly Tyr Ile Glu Pro Leu Pro Ser Gly Ser Asp Gly Lys Phe
20 25 30
Glu Phe Asp Asn Met Ile Ile Gly Gln Ala Ile Pro Ser Asn Phe Ile
35 40 45
Pro Ala Ile Glu Lys Gly Phe Lys Glu Ala Cys Asn Ser Gly Ser Leu
50 55 60
Ile Gly His Pro Val Glu Asn Leu Arg Ile Val Leu Thr Asp Gly Ala
65 70 75 80

Ser His Gln Val Asp Ser Ser Glu Leu Ala Phe Lys Leu Ala Ala Ile
85 90 95
Tyr Ala Phe Arg Gln Cys Tyr Thr Ser Ala Lys Pro Val Ile Leu Glu
100 105 110
Pro Val Met Lys Val Glu Leu Lys Phe Pro Thr Glu Phe Gln Gly Thr
115 120 125
Val Thr Gly Asp Met Asn Lys Arg Lys Gly Ile Ile Val Gly Asn Glu
130 135 140
Gln Glu Gly Asp Asp Thr Ile Val Val Cys His Val Arg
145 150 155

(2) INFORMATION FOR SEQ ID NO:2545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1503777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2545:

Met Ile Ile Gly Gln Ala Ile Pro Ser Asn Phe Ile Pro Ala Ile Glu
1 5 10 15
Lys Gly Phe Lys Glu Ala Cys Asn Ser Gly Ser Leu Ile Gly His Pro
20 25 30
Val Glu Asn Leu Arg Ile Val Leu Thr Asp Gly Ala Ser His Gln Val
35 40 45
Asp Ser Ser Glu Leu Ala Phe Lys Leu Ala Ala Ile Tyr Ala Phe Arg
50 55 60
Gln Cys Tyr Thr Ser Ala Lys Pro Val Ile Leu Glu Pro Val Met Lys
65 70 75 80
Val Glu Leu Lys Phe Pro Thr Glu Phe Gln Gly Thr Val Thr Gly Asp
85 90 95
Met Asn Lys Arg Lys Gly Ile Ile Val Gly Asn Glu Gln Glu Gly Asp
100 105 110
Asp Thr Ile Val Val Cys His Val Arg
115 120

(2) INFORMATION FOR SEQ ID NO:2546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1503778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2546:

ttgattacat tattcatgga gatgacctt gtcttctacc tggatggcact gatgcatatg	60
cgctacgaag aaggtcgggc gttacaagca aatcaagcga acagaaggtg tctcgagcac	120
tgacatagtt gggaggatat tgctaacatt caggcagaaa gatgctggca ctgatttaag	180
tgttgctggt gctgagaagt ctggagagaa atcaaatgat gaagtgaata gtcagctatc	240
tcatttcctt ccaacttctc gccggatcat gcagttttca aatgggcagg ctccttcgcc	300
aggtgctcgt gttgtctatg tagatggcac atttgatctt ttccacgctg gccatgttga	360
gttcctcagg agtgccagac aacttggtga ctttcttctt gtcggtatct atgacgacga	420
gtctatcagg gatagaagag gctgccgtcc tataatgcat ctccatgagc g	

(2) INFORMATION FOR SEQ ID NO:2547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..41
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503779
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2547:
Asp Tyr Ile Ile His Gly Asp Asp Pro Cys Leu Leu Pro Asp Gly Thr
1 5 10 15
Asp Ala Tyr Ala Leu Arg Arg Arg Ser Gly Val Thr Ser Lys Ser Ser
 20 25 30
Glu Gln Lys Val Ser Arg Ala Leu Thr
 35 40
(2) INFORMATION FOR SEQ ID NO:2548:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..67
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503780
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2548:
Met Gln Phe Ser Asn Gly Gln Ala Pro Ser Pro Gly Ala Arg Val Val
1 5 10 15
Tyr Val Asp Gly Thr Phe Asp Leu Phe His Ala Gly His Val Glu Phe
 20 25 30
Leu Arg Ser Ala Arg Gln Leu Gly Asp Phe Leu Leu Val Gly Ile Tyr
 35 40 45
Asp Asp Glu Ser Ile Arg Asp Arg Arg Gly Cys Arg Pro Ile Met His
 50 55 60
Leu His Glu
65
(2) INFORMATION FOR SEQ ID NO:2549:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..43
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503781
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2549:
Met Ala His Leu Ile Phe Ser Thr Leu Ala Met Leu Ser Ser Ser Gly
1 5 10 15
Val Pro Asp Asn Leu Val Thr Phe Phe Leu Ser Val Ser Met Thr Thr
 20 25 30
Ser Leu Ser Gly Ile Glu Glu Ala Ala Val Leu
 35 40
(2) INFORMATION FOR SEQ ID NO:2550:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..395

(D) OTHER INFORMATION: / Ceres Seq. ID 1503796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2550:

cacattaatt	aaacattttt	tgtgttttctt	tttatacctt	aatttttttc	tttccctttt	60
tctctataag	tatctgactc	tacttctgct	gttgcagaat	cattcgagat	atcattcaga	120
atcatttact	gcagggtttc	tgtttggttg	caatggaaaa	gcctgtctcc	cttaagcctg	180
agcacatcag	agatkagaaa	gtcaagggtc	tgcaatctgt	gaaccctatt	aagcctgaag	240
aggtagtcct	tgggcaatac	gatgggtctac	aaggatgacc	ctacagtgcc	agatgacttg	300
aatactccaa	cttttgcatc	tgttgttctt	cgggtacaca	atgaaagatg	ggaaggtgtt	360
cctttcattc	ttaaagctgg	taaagcattg	agttc			

(2) INFORMATION FOR SEQ ID NO:2551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1503797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2551:

Thr	Leu	Ile	Lys	His	Phe	Leu	Cys	Phe	Phe	Leu	Tyr	Leu	Asn	Phe	Phe	
1			5					10					15			
Leu	Ser	Leu	Phe	Leu	Tyr	Lys	Tyr	Leu	Thr	Leu	Leu	Leu	Leu	Gln		
			20				25						30			
Asn	His	Ser	Arg	Tyr	His	Ser	Glu	Ser	Phe	Thr	Ala	Gly	Phe	Leu	Phe	
			35				40					45				
Gly	Cys	Asn	Gly	Lys	Ala	Cys	Leu	Pro								
50						55										

(2) INFORMATION FOR SEQ ID NO:2552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 1503798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2552:

Met	Glu	Lys	Pro	Val	Ser	Leu	Lys	Pro	Glu	His	Ile	Arg	Asp	Xaa	Lys	
1			5					10					15			
Val	Lys	Val	Leu	Gln	Ser	Val	Asn	Pro	Ile	Lys	Pro	Glu	Glu	Val	Val	
			20				25						30			
Leu	Gly	Gln	Tyr	Asp	Gly	Leu	Gln	Gly								
			35				40									

(2) INFORMATION FOR SEQ ID NO:2553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1503799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2553:

Met Val Tyr Lys Asp Asp Pro Thr Val Pro Asp Asp Leu Asn Thr Pro
1 5 10 15
Thr Phe Ala Ser Val Val Leu Arg Val His Asn Glu Arg Trp Glu Gly
20 25 30
Val Pro Phe Ile Leu Lys Ala Gly Lys Ala Leu Ser
35 40

(2) INFORMATION FOR SEQ ID NO:2554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..505

(D) OTHER INFORMATION: / Ceres Seq. ID 1503810

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2554:

gaagtttcgg	cggcggtcgt	ggtagcggcg	gtgtgcttgt	gatctcaatc	tcaaccccg	60
gcgagctcgg	ctccggtcac	ccgtcgatcc	acgcaaccat	gtcgaggagg	aagaccagg	120
agcccaagga	ggagaacggt	acccttggac	ccactgtccg	tgaaggagag	tttgtcttg	180
gtgttgctca	catctttgca	tccttcaatg	acaccttcat	tgtgagtgt	atatgtttt	240
ccctgtggat	gggccttttc	attatctttc	ccattgtaac	tgtgatgggtg	taatatgcag	300
catgtcactg	atttgtcttg	gagggaaact	ttgggtcgg	tcactggtgg	catgaagggt	360
aaggctgac	gtgatgagtc	gtctccttat	gctgctatgc	ttgctgcccc	agatgttgca	420
cagcggttgc	aggagctcgg	tatcacagcg	ctgcacatta	agcttcgtgc	cactggaggc	480
aacaagacca	atgacccctg	gacct				

(2) INFORMATION FOR SEQ ID NO:2555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..96

(D) OTHER INFORMATION: / Ceres Seq. ID 1503811

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2555:

Ser Phe Gly Gly Gly Val Gly Ser Gly Gly Val Leu Val Ile Ser Ile
1 5 10 15
Ser Thr Pro Gly Glu Leu Gly Ser Gly His Pro Ser Ile His Ala Thr
20 25 30
Met Ser Arg Arg Lys Thr Arg Glu Pro Lys Glu Glu Asn Val Thr Leu
35 40 45
Gly Pro Thr Val Arg Glu Gly Glu Phe Val Phe Gly Val Ala His Ile
50 55 60
Phe Ala Ser Phe Asn Asp Thr Phe Ile Val Ser Ala Ile Cys Phe Ser
65 70 75 80
Leu Trp Met Gly Leu Phe Ile Ile Phe Pro Ile Val Thr Val Met Val
85 90 95

(2) INFORMATION FOR SEQ ID NO:2556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..64

(D) OTHER INFORMATION: / Ceres Seq. ID 1503812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2556:

Met	Ser	Arg	Arg	Lys	Thr	Arg	Glu	Pro	Lys	Glu	Glu	Asn	Val	Thr	Leu
1				5				10						15	
Gly	Pro	Thr	Val	Arg	Glu	Gly	Glu	Phe	Val	Phe	Gly	Val	Ala	His	Ile
			20					25					30		
Phe	Ala	Ser	Phe	Asn	Asp	Thr	Phe	Ile	Val	Ser	Ala	Ile	Cys	Phe	Ser
		35					40					45			
Leu	Trp	Met	Gly	Leu	Phe	Ile	Ile	Phe	Pro	Ile	Val	Thr	Val	Met	Val
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:2557:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1503813

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2557:

Met	Gln	His	Val	Thr	Asp	Leu	Ser	Gly	Arg	Glu	Thr	Leu	Val	Arg	Ile
1				5				10						15	
Thr	Gly	Gly	Met	Lys	Val	Lys	Ala	Asp	Arg	Asp	Glu	Ser	Ser	Pro	Tyr
			20					25					30		
Ala	Ala	Met	Leu	Ala	Ala	Gln	Asp	Val	Ala	Gln	Arg	Cys	Lys	Glu	Leu
		35					40					45			
Gly	Ile	Thr	Ala	Leu	His	Ile	Lys	Leu	Arg	Ala	Thr	Gly	Gly	Asn	Lys
	50					55					60				
Thr	Asn	Asp	Pro	Trp	Thr										
	65				70										

(2) INFORMATION FOR SEQ ID NO:2558:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 456 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..456

(D) OTHER INFORMATION: / Ceres Seq. ID 1503822

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2558:

gcnkccgccc	cctacaacag	gtgccccagg	tcttcgctgc	gccattcgcc	agcgacgagc	60
acccaacagc	atggtcaacc	gcaatgacct	catgtactgg	attgtcgcg	cactctgatg	120
tgggtgcckc	ckckgkgcac	cagaagttga	tggggtcttt	gaacaacaac	gaggkactca	180
tgtttggggt	ggttgtggca	ckgttcaacg	aggctcgtgac	aaatttggtta	ctacagggtg	240
ccctggaaac	tttcgagcga	tactctgtta	aagcagaaaa	tataacagtt	gttagtgttc	300
ctggaagctt	tgaagttcct	ataacgkcac	aaaagcttgg	gaaatctgga	aaatttgatg	360
caattctgtg	cattggagct	gtgattagag	gtgacacaac	ccactatgat	gccgttgcaa	420
actcagctgc	atcaggtgta	ctcaatgctg	gattat			

(2) INFORMATION FOR SEQ ID NO:2559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..151
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503823
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2559:
Xaa Arg Arg Leu Gln Gln Val Pro Gln Val Phe Ala Ala Pro Phe Ala
1 5 10 15
Ser Asp Glu His Pro Thr Ala Trp Ser Thr Ala Met Thr Ser Cys Thr
 20 25 30
Gly Leu Ser Arg His Ser Asp Val Ala Xaa Xaa Xaa His Gln Lys
 35 40 45
Leu Met Gly Ser Leu Asn Asn Asn Glu Xaa Leu Met Phe Gly Val Val
 50 55 60
Val Ala Xaa Phe Asn Glu Val Val Thr Asn Leu Leu Leu Gln Gly Ala
65 70 75 80
Leu Glu Thr Phe Glu Arg Tyr Ser Val Lys Ala Glu Asn Ile Thr Val
 85 90 95
Val Ser Val Pro Gly Ser Phe Glu Val Pro Ile Thr Xaa Gln Lys Leu
 100 105 110
Gly Lys Ser Gly Lys Phe Asp Ala Ile Leu Cys Ile Gly Ala Val Ile
 115 120 125
Arg Gly Asp Thr Thr His Tyr Asp Ala Val Ala Asn Ser Ala Ala Ser
 130 135 140
Gly Val Leu Asn Ala Gly Leu
145 150
(2) INFORMATION FOR SEQ ID NO:2560:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..124
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503824
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2560:
Met Thr Ser Cys Thr Gly Leu Ser Arg His Ser Asp Val Val Ala Xaa
1 5 10 15
Xaa Xaa His Gln Lys Leu Met Gly Ser Leu Asn Asn Asn Glu Xaa Leu
 20 25 30
Met Phe Gly Val Val Val Ala Xaa Phe Asn Glu Val Val Thr Asn Leu
 35 40 45
Leu Leu Gln Gly Ala Leu Glu Thr Phe Glu Arg Tyr Ser Val Lys Ala
 50 55 60
Glu Asn Ile Thr Val Val Ser Val Pro Gly Ser Phe Glu Val Pro Ile
65 70 75 80
Thr Xaa Gln Lys Leu Gly Lys Ser Gly Lys Phe Asp Ala Ile Leu Cys
 85 90 95
Ile Gly Ala Val Ile Arg Gly Asp Thr Thr His Tyr Asp Ala Val Ala
 100 105 110
Asn Ser Ala Ala Ser Gly Val Leu Asn Ala Gly Leu
 115 120
(2) INFORMATION FOR SEQ ID NO:2561:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid

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- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..102
(D) OTHER INFORMATION: / Ceres Seq. ID 1503825
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2561:

Met Gly Ser Leu Asn Asn Asn Glu Xaa Leu Met Phe Gly Val Val Val
1 5 10 15
Ala Xaa Phe Asn Glu Val Val Thr Asn Leu Leu Leu Gln Gly Ala Leu
20 25 30
Glu Thr Phe Glu Arg Tyr Ser Val Lys Ala Glu Asn Ile Thr Val Val
35 40 45
Ser Val Pro Gly Ser Phe Glu Val Pro Ile Thr Xaa Gln Lys Leu Gly
50 55 60
Lys Ser Gly Lys Phe Asp Ala Ile Leu Cys Ile Gly Ala Val Ile Arg
65 70 75 80
Gly Asp Thr Thr His Tyr Asp Ala Val Ala Asn Ser Ala Ala Ser Gly
85 90 95
Val Leu Asn Ala Gly Leu
100

(2) INFORMATION FOR SEQ ID NO:2562:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..392
(D) OTHER INFORMATION: / Ceres Seq. ID 1503826
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2562:

gaagtgcgag tcaatgctat catgatcacc agcacagtta ttgttggttct attcagcacaca 60
atgggttttcg gcctkctgac gaagccgctg ctcagtctcc tcatcccacc aaggactgga 120
ctgaacacagt cgtctctgct ctcaagccag tctatgctgg acccactcct tactagcatg 180
atgggggtctg acttttgatgt agggcagatc aactcccctc aataacaacct ccagtttcatt 240
ctcaccgcgc casstcgctc cgtccatcgc ctttgkycaa gtttgacgat cggtttcatg 300
cgccccggtgt tcggggggcg aggtttcgtc ccctttgtgc ctggttcgcc kktkkagagk 360
agtgtccctg aatctcacct gggcactgtg ac

(2) INFORMATION FOR SEQ ID NO:2563:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..130
(D) OTHER INFORMATION: / Ceres Seq. ID 1503827
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2563:

Glu Val Arg Val Asn Ala Ile Met Ile Thr Ser Thr Val Ile Val Val
1 5 10 15
Leu Phe Ser Thr Met Val Phe Gly Xaa Leu Thr Lys Pro Leu Leu Ser
20 25 30
Leu Leu Ile Pro Pro Arg Thr Gly Leu Asn Thr Ser Ser Leu Leu Ser
35 40 45
Ser Gln Ser Met Leu Asp Pro Leu Leu Thr Ser Met Met Gly Ser Asp
50 55 60

Phe Asp Val Gly Gln Ile Asn Ser Pro Gln Tyr Asn Leu Gln Phe Ile
65 70 75 80
Leu Thr Ala Pro Xaa Arg Ser Val His Arg Leu Xaa Xaa Ser Leu Thr
85 90 95
Ile Gly Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe
100 105 110
Val Pro Gly Ser Xaa Xaa Xaa Xaa Ser Val Pro Glu Ser His Leu Gly
115 120 125
Thr Val
130

(2) INFORMATION FOR SEQ ID NO:2564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..123

(D) OTHER INFORMATION: / Ceres Seq. ID 1503828

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2564:

Met Ile Thr Ser Thr Val Ile Val Val Leu Phe Ser Thr Met Val Phe
1 5 10 15
Gly Xaa Leu Thr Lys Pro Leu Leu Ser Leu Leu Ile Pro Pro Arg Thr
20 25 30
Gly Leu Asn Thr Ser Ser Leu Leu Ser Ser Gln Ser Met Leu Asp Pro
35 40 45
Leu Leu Thr Ser Met Met Gly Ser Asp Phe Asp Val Gly Gln Ile Asn
50 55 60
Ser Pro Gln Tyr Asn Leu Gln Phe Ile Leu Thr Ala Pro Xaa Arg Ser
65 70 75 80
Val His Arg Leu Xaa Xaa Ser Leu Thr Ile Gly Phe Met Arg Pro Val
85 90 95
Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser Xaa Xaa Xaa
100 105 110
Xaa Ser Val Pro Glu Ser His Leu Gly Thr Val
115 120

(2) INFORMATION FOR SEQ ID NO:2565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1503829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2565:

Met Val Phe Gly Xaa Leu Thr Lys Pro Leu Leu Ser Leu Leu Ile Pro
1 5 10 15
Pro Arg Thr Gly Leu Asn Thr Ser Ser Leu Leu Ser Ser Gln Ser Met
20 25 30
Leu Asp Pro Leu Leu Thr Ser Met Gly Ser Asp Phe Asp Val Gly
35 40 45
Gln Ile Asn Ser Pro Gln Tyr Asn Leu Gln Phe Ile Leu Thr Ala Pro
50 55 60
Xaa Arg Ser Val His Arg Leu Xaa Xaa Ser Leu Thr Ile Gly Phe Met
65 70 75 80
Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro Gly Ser

85 90 95
Xaa Xaa Xaa Xaa Ser Val Pro Glu Ser His Leu Gly Thr Val
100 105 110

(2) INFORMATION FOR SEQ ID NO:2566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2566:

gtagtgaggaa	ggggtacgtt	agcktttgck	gcgcgtmrac	tccccacgca	aagccgcccgc	60
cggtccctct	cggtcttccc	agttccccta	cgccggtaat	cccacgtcct	atcagccgnc	120
gatccagcct	tgcttccatc	catccatcca	tccatccatc	catctcgtcg	cttctctctg	180
ttccgcgtgc	gatcgagtag	atcaaaagga	ggaggaggat	ggcgaggagt	tcgttcaagt	240
tggagcaccc	cttcgaaagg	aggcaagctg	aggctaaccg	catcagggag	aaataccctg	300
acagaatccc	tgctattgtt	gagaaggccg	agaggagtga	catcccagac	attgacaaga	360
aaaagtacct	tggtcctgcc	gacctcacag	tcggacagtt	tgtgtatgtg	gtacggaagc	420
ggatcaagct	aagcgctgag	aaggcaatct	tcattctcgt	aaag		

(2) INFORMATION FOR SEQ ID NO:2567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..65
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2567:

Ser	Gly	Lys	Gly	Tyr	Val	Ser	Xaa	Cys	Xaa	Ala	Xaa	Thr	Pro	His	Ala
1				5				10						15	
Lys	Pro	Pro	Pro	Phe	Pro	Leu	Val	Phe	Pro	Ser	Ser	Pro	Thr	Pro	Val
			20					25					30		
Ile	Pro	Arg	Pro	Ile	Ser	Xaa	Arg	Ser	Ser	Leu	Ala	Ser	Ile	His	Pro
		35				40						45			
Ser	Ile	His	Pro	Ser	Ile	Ser	Ser	Leu	Leu	Ser	Val	Pro	Arg	Ala	Ile
	50					55					60				
Glu															
65															

(2) INFORMATION FOR SEQ ID NO:2568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503871

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2568:

Met	Ala	Arg	Ser	Ser	Phe	Lys	Leu	Glu	His	Pro	Phe	Glu	Arg	Arg	Gln
1					5				10					15	
Ala	Glu	Ala	Asn	Arg	Ile	Arg	Glu	Lys	Tyr	Pro	Asp	Arg	Ile	Pro	Val
		20						25					30		

Ile Val Glu Lys Ala Glu Arg Ser Asp Ile Pro Asp Ile Asp Lys Lys
35 40 45
Lys Tyr Leu Val Pro Ala Asp Leu Thr Val Gly Gln Phe Val Tyr Val
50 55 60
Val Arg Lys Arg Ile Lys Leu Ser Ala Glu Lys Ala Ile Phe Ile Phe
65 70 75 80
Val Lys

(2) INFORMATION FOR SEQ ID NO:2569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..479
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503873

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2569:

cccagtcattg atgcacccga tccatgagat cgtcgagaca aggttcagat ccaacagatg	60
ctttcggaag ctcagccaca acgatggcgg cgcggagtg ataggttgc acgcwagggc	120
tgctctcgtg gtggcggtcc tcaactgtgtt ggcgtccttc atccccttct ttgggtcctt	180
catctcgttc gtcgggagca ccatgtggcg cttctctcct ttgtgctgcc ggctctcttc	240
catctcagca ttgtaggctc gtcaataccc ttgtggaggc gggttgctgg actacggcat	300
ccttctcttt ggtctggctt tcgctggata tggctcttgc actgctctct cctcgcttgc	360
aacaatggcc caaacagtca aaaaagtgc gagatcagga tatcttgtga tgacakgagt	420
caaatggatg ctaggagcac catatatcag atagcacgc tcggattagt gcgtgattg	

(2) INFORMATION FOR SEQ ID NO:2570:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..84
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2570:

Pro Val Met Met His Pro Ile His Glu Ile Val Glu Thr Arg Phe Arg
1 5 10 15
Ser Asn Arg Cys Phe Arg Lys Leu Ser His Asn Asp Gly Gly Ala Glu
20 25 30
Trp Ile Gly Leu His Xaa Xaa Ala Val Leu Val Val Ala Val Leu Thr
35 40 45
Val Val Ala Ser Phe Ile Pro Phe Phe Gly Ser Phe Ile Ser Phe Val
50 55 60
Gly Ser Thr Met Trp Arg Phe Ser Pro Leu Cys Cys Arg Leu Ser Ser
65 70 75 80
Ile Ser Ala Leu

(2) INFORMATION FOR SEQ ID NO:2571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1503875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2571:

```
Met Met His Pro Ile His Glu Ile Val Glu Thr Arg Phe Arg Ser Asn
1          5          10          15
Arg Cys Phe Arg Lys Leu Ser His Asn Asp Gly Gly Ala Glu Trp Ile
          20          25          30
Gly Leu His Xaa Xaa Ala Val Leu Val Val Ala Val Leu Thr Val Val
          35          40          45
Ala Ser Phe Ile Pro Phe Phe Gly Ser Phe Ile Ser Phe Val Gly Ser
          50          55          60
Thr Met Trp Arg Phe Ser Pro Leu Cys Cys Arg Leu Ser Ser Ile Ser
65          70          75          80
Ala Leu
```

(2) INFORMATION FOR SEQ ID NO:2572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1503876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2572:

```
Met Leu Ser Glu Ala Gln Pro Gln Arg Trp Arg Arg Gly Val Asp Arg
1          5          10          15
Leu Ala Arg Xaa Xaa Cys Pro Arg Gly Gly Gly Pro His Cys Gly Gly
          20          25          30
Val Leu His Pro Leu Leu Trp Val Leu His Leu Val Arg Arg Glu His
          35          40          45
His Val Ala Leu Leu Ser Phe Val Leu Pro Ala Leu Phe His Leu Ser
          50          55          60
Ile Val Gly Ser Ser Ile Pro Leu Trp Arg Arg Val Ala Gly Leu Arg
65          70          75          80
His Pro Ser Leu Trp Ser Gly Phe Arg Trp Ile Trp Ser Cys His Cys
          85          90          95
Ser Leu Leu Ala Leu Asn Asn Gly Pro Asn Ser Gln Lys Ser Ala Glu
          100          105          110
Ile Arg Ile Ser Cys Asp Asp Xaa Ser Gln Met Asp Ala Arg Ser Thr
          115          120          125
Ile Tyr Gln Ile Ala Arg Leu Gly Leu Val Arg Asp
          130          135          140
```

(2) INFORMATION FOR SEQ ID NO:2573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1503886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2573:

```
aaaccttccc accacctcct cccctcctc ccaacagtca ccacgtcgca ctaccgagcc      60
atgtcctccg ctaccaacct cgtttattg tcgtgggact gcgccgagga cccgctggat      120
ttcggtgctg tcgccgacac cgcgtttctc ccgctccagc
```

(2) INFORMATION FOR SEQ ID NO:2574:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..53
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503887
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2574:
Lys Pro Ser His His Leu Leu Pro Leu Leu Pro Thr Val Thr Thr Ser
1 5 10 15
His Tyr Arg Ala Met Ser Ser Ala Thr Asn Leu Arg Leu Leu Ser Trp
 20 25 30
Asp Cys Ala Glu Asp Pro Leu Asp Phe Gly Ala Phe Ala Asp Thr Ala
 35 40 45
Phe Leu Pro Leu Gln
50
(2) INFORMATION FOR SEQ ID NO:2575:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..53
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503888
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2575:
Asn Leu Pro Thr Thr Ser Ser Pro Ser Ser Gln Gln Ser Pro Arg Arg
1 5 10 15
Thr Thr Glu Pro Cys Pro Pro Leu Pro Thr Ser Val Tyr Cys Arg Gly
 20 25 30
Thr Ala Pro Arg Thr Arg Trp Ile Ser Val Arg Ser Pro Thr Pro Arg
 35 40 45
Phe Ser Arg Ser Ser
50
(2) INFORMATION FOR SEQ ID NO:2576:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..52
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503889
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2576:
Thr Phe Pro Pro Pro Pro Pro Pro Pro Asn Ser His His Val Ala
1 5 10 15
Leu Pro Ser His Val Leu Arg Tyr Gln Pro Pro Phe Ile Val Val Gly
 20 25 30
Leu Arg Arg Gly Pro Ala Gly Phe Arg Cys Val Arg Arg His Arg Val
 35 40 45
Ser Pro Ala Pro
50
(2) INFORMATION FOR SEQ ID NO:2577:
 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..338
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2577:

agctcgctct	gggagaggtt	aatggcgcca	agtctccagc	tcgccatttt	catgtccgcc	60
gccatcgcg	tcgggttcgg	cggcgccag	gccggcgcg	cgcasstgtg	cagcgagtac	120
tacgaccgga	cgtgccccgt	cgtgcaccgg	gtcgtgcggc	gggtgctgaa	gaaggcgcac	180
gagtccgacg	tccgcatcta	cgccagcctc	acccgcctcc	acttccacga	ctgcttcgtg	240
caaggctgcg	acgggtccat	cctgctggac	aacagctcca	gcacgtgtgc	ggagaagttc	300
gccacgcccc	acaacaactc	ggcgcgcg	ggg	taccccg		

(2) INFORMATION FOR SEQ ID NO:2578:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2578:

Ser	Ser	Leu	Trp	Glu	Arg	Leu	Met	Ala	Ala	Ser	Leu	Gln	Leu	Ala	Ile	
1				5					10					15		
Phe	Met	Ser	Ala	Ala	Ile	Ala	Leu	Gly	Phe	Gly	Gly	Val	Gln	Ala	Gly	
			20					25					30			
Ala	Ala	Xaa	Xaa	Cys	Ser	Glu	Tyr	Tyr	Asp	Arg	Thr	Cys	Pro	Val	Val	
			35				40					45				
His	Arg	Val	Val	Arg	Arg	Val	Leu	Lys	Lys	Ala	His	Glu	Ser	Asp	Val	
			50			55				60						
Arg	Ile	Tyr	Ala	Ser	Leu	Thr	Arg	Leu	His	Phe	His	Asp	Cys	Phe	Val	
65					70				75					80		
Gln	Gly	Cys	Asp	Gly	Ser	Ile	Leu	Leu	Asp	Asn	Ser	Ser	Ser	Ile	Val	
			85						90					95		
Ser	Glu	Lys	Phe	Ala	Thr	Pro	Asn	Asn	Asn	Ser	Ala	Arg	Gly	Tyr	Pro	
			100					105						110		

(2) INFORMATION FOR SEQ ID NO:2579:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..112
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503892

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2579:

Leu	Ala	Leu	Gly	Glu	Val	Asn	Gly	Gly	Lys	Ser	Pro	Ala	Arg	His	Phe	
1				5					10					15		
His	Val	Arg	Arg	His	Arg	Ala	Arg	Val	Arg	Arg	Arg	Pro	Gly	Arg	Arg	
			20				25						30			
Gly	Ala	Xaa	Val	Gln	Arg	Val	Leu	Arg	Pro	Asp	Val	Pro	Arg	Arg	Ala	

35 40 45
Pro Gly Arg Ala Ala Gly Ala Glu Glu Gly Ala Arg Val Arg Arg Pro
50 55 60
His Leu Arg Gln Pro His Pro Pro Pro Leu Pro Arg Leu Leu Arg Ala
65 70 75 80
Arg Leu Arg Arg Leu His Pro Ala Gly Gln Leu Gln His Arg Val
85 90 95
Gly Glu Val Arg His Ala Gln Gln Gln Leu Gly Ala Arg Val Pro Arg
100 105 110

(2) INFORMATION FOR SEQ ID NO:2580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..105
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2580:

Met Ala Ala Ser Leu Gln Leu Ala Ile Phe Met Ser Ala Ala Ile Ala
1 5 10 15
Leu Gly Phe Gly Gly Val Gln Ala Gly Ala Ala Xaa Xaa Cys Ser Glu
20 25 30
Tyr Tyr Asp Arg Thr Cys Pro Val Val His Arg Val Val Arg Arg Val
35 40 45
Leu Lys Lys Ala His Glu Ser Asp Val Arg Ile Tyr Ala Ser Leu Thr
50 55 60
Arg Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp Gly Ser Ile
65 70 75 80
Leu Leu Asp Asn Ser Ser Ser Ile Val Ser Glu Lys Phe Ala Thr Pro
85 90 95
Asn Asn Asn Ser Ala Arg Gly Tyr Pro
100 105

(2) INFORMATION FOR SEQ ID NO:2581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503894

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2581:

agggtttttt gccaaagtcgc cgccgctcgt ctgcccgcac tcccttccac aacaccgaga 60
cgccaggatg acggcgacaga ctgcggagga gtcgcccacc cagatcgagc agcagaagct 120
cgaggagcag aagaccgagg cagaggaggt tgtggtggag gatgaggagg acgacgacga 180
tgaggacgat gaggatgatg atgaacttga cggacaagaa ggggatgccca gcggcaagtc 240
aaagcaaagc aggagtgaga agaagagccg caaagccatg ctgaagcttg gcatgaagcc 300
catcactggt gtcagccgtg tcaactgtgaa gaaaagcaag aatatactgt ttgtcatctc 360
gaagccagat gtgttcaaga gcccgaactc agacacatac gtcatatctg gcgaggccaa 420
gatcgaggac ctcagctccc agctgcagac ccaggccgca gaacagttca aggcccttgc 480
acttgagcca gatcacgagt ccagagactt

(2) INFORMATION FOR SEQ ID NO:2582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..159
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503895
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2582:

Gly	Phe	Phe	Ala	Lys	Ser	Pro	Pro	Ser	Leu	Cys	Pro	His	Ser	Leu	Pro
1			5						10					15	
Gln	His	Arg	Asp	Ala	Arg	Met	Thr	Ala	Gln	Thr	Ala	Glu	Glu	Leu	Ala
			20					25					30		
Thr	Gln	Ile	Glu	Gln	Gln	Lys	Leu	Glu	Glu	Gln	Lys	Thr	Glu	Ala	Glu
		35				40					45				
Glu	Val	Val	Val	Glu	Asp	Glu	Glu	Asp	Asp	Asp	Asp	Glu	Asp	Asp	Glu
	50				55				60						
Asp	Asp	Asp	Glu	Leu	Asp	Gly	Gln	Glu	Gly	Asp	Ala	Ser	Gly	Lys	Ser
65				70					75					80	
Lys	Gln	Ser	Arg	Ser	Glu	Lys	Lys	Ser	Arg	Lys	Ala	Met	Leu	Lys	Leu
			85					90					95		
Gly	Met	Lys	Pro	Ile	Thr	Gly	Val	Ser	Arg	Val	Thr	Val	Lys	Lys	Ser
			100					105					110		
Lys	Asn	Ile	Leu	Phe	Val	Ile	Ser	Lys	Pro	Asp	Val	Phe	Lys	Ser	Pro
	115					120						125			
Asn	Ser	Asp	Thr	Tyr	Val	Ile	Phe	Gly	Glu	Ala	Lys	Ile	Glu	Asp	Leu
	130					135					140				
Ser	Ser	Gln	Leu	Gln	Thr	Gln	Ala	Ala	Glu	Gln	Phe	Lys	Ala	Pro	
145				150						155					

- (2) INFORMATION FOR SEQ ID NO:2583:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..137
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503896
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2583:

Met	Thr	Ala	Gln	Thr	Ala	Glu	Glu	Leu	Ala	Thr	Gln	Ile	Glu	Gln	Gln
1			5					10					15		
Lys	Leu	Glu	Glu	Gln	Lys	Thr	Glu	Ala	Glu	Glu	Val	Val	Val	Glu	Asp
		20					25					30			
Glu	Glu	Asp	Asp	Asp	Asp	Glu	Asp	Glu	Asp	Asp	Asp	Asp	Glu	Leu	Asp
		35				40					45				
Gly	Gln	Glu	Gly	Asp	Ala	Ser	Gly	Lys	Ser	Lys	Gln	Ser	Arg	Ser	Glu
	50				55				60						
Lys	Lys	Ser	Arg	Lys	Ala	Met	Leu	Lys	Leu	Gly	Met	Lys	Pro	Ile	Thr
65			70						75				80		
Gly	Val	Ser	Arg	Val	Thr	Val	Lys	Lys	Ser	Lys	Asn	Ile	Leu	Phe	Val
			85				90					95			
Ile	Ser	Lys	Pro	Asp	Val	Phe	Lys	Ser	Pro	Asn	Ser	Asp	Thr	Tyr	Val
		100				105						110			
Ile	Phe	Gly	Glu	Ala	Lys	Ile	Glu	Asp	Leu	Ser	Ser	Gln	Leu	Gln	Thr
	115					120						125			
Gln	Ala	Ala	Glu	Gln	Phe	Lys	Ala	Pro							
	130					135									

- (2) INFORMATION FOR SEQ ID NO:2584:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 459 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..459
(D) OTHER INFORMATION: / Ceres Seq. ID 1503899
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2584:
acaactttac agctaacatg gagacagagc tagataatgt ctctgctggg tcaactgaat 60
ggaagggtct tctgaaagac tactgggaac gattcagcaa atattgtgca gatgtgagta 120
aactggatgg cagaaaggta gagagaatgc ttgaagaaaa atttggtcct atcctctttt 180
ccgatgttta caaggattgt agaatttgcc ctagtgtgtc tgaaggaacc ttgagattca 240
aagttagtag gtacggtgaa ggctattttg taggttgtga tcgacatcca aaatgcaagt 300
acattgctcg ctactgtca cagcaagaag atgaaactga acccatagaa gaaaatgcaa 360
aatcttttga acccagggtta cttggtgtca tgcctgattc tgatcaaaag gtgtttttga 420
aacaagggcc atatggctac tatgttcaag ttggagagg
(2) INFORMATION FOR SEQ ID NO:2585:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..152
(D) OTHER INFORMATION: / Ceres Seq. ID 1503900
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2585:
Asn Phe Thr Ala Asn Met Glu Thr Glu Leu Asp Asn Val Ser Ala Gly
1 5 10 15
Ser Thr Glu Trp Lys Gly Leu Leu Lys Asp Tyr Trp Glu Arg Phe Ser
20 25 30
Lys Tyr Cys Ala Asp Val Ser Lys Leu Asp Gly Arg Lys Val Glu Arg
35 40 45
Met Leu Glu Glu Lys Phe Gly Pro Ile Leu Phe Ser Asp Val Tyr Lys
50 55 60
Asp Cys Arg Ile Cys Pro Ser Cys Ser Glu Gly Thr Leu Arg Phe Lys
65 70 75 80
Val Ser Arg Tyr Gly Glu Gly Tyr Phe Val Gly Cys Asp Arg His Pro
85 90 95
Lys Cys Lys Tyr Ile Ala Arg Ser Leu Ser Gln Gln Glu Asp Glu Thr
100 105 110
Glu Pro Ile Glu Glu Asn Ala Lys Ser Phe Glu Pro Arg Leu Leu Gly
115 120 125
Val Met Pro Asp Ser Asp Gln Lys Val Phe Leu Lys Gln Gly Pro Tyr
130 135 140
Gly Tyr Tyr Val Gln Val Gly Glu
145 150
(2) INFORMATION FOR SEQ ID NO:2586:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..147
(D) OTHER INFORMATION: / Ceres Seq. ID 1503901

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2586:
Met Glu Thr Glu Leu Asp Asn Val Ser Ala Gly Ser Thr Glu Trp Lys
1 5 10 15
Gly Leu Leu Lys Asp Tyr Trp Glu Arg Phe Ser Lys Tyr Cys Ala Asp
20 25 30
Val Ser Lys Leu Asp Gly Arg Lys Val Glu Arg Met Leu Glu Glu Lys
35 40 45
Phe Gly Pro Ile Leu Phe Ser Asp Val Tyr Lys Asp Cys Arg Ile Cys
50 55 60
Pro Ser Cys Ser Glu Gly Thr Leu Arg Phe Lys Val Ser Arg Tyr Gly
65 70 75 80
Glu Gly Tyr Phe Val Gly Cys Asp Arg His Pro Lys Cys Lys Tyr Ile
85 90 95
Ala Arg Ser Leu Ser Gln Gln Glu Asp Glu Thr Glu Pro Ile Glu Glu
100 105 110
Asn Ala Lys Ser Phe Glu Pro Arg Leu Leu Gly Val Met Pro Asp Ser
115 120 125
Asp Gln Lys Val Phe Leu Lys Gln Gly Pro Tyr Gly Tyr Tyr Val Gln
130 135 140
Val Gly Glu
145

(2) INFORMATION FOR SEQ ID NO:2587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1503902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2587:

Met Leu Glu Glu Lys Phe Gly Pro Ile Leu Phe Ser Asp Val Tyr Lys
1 5 10 15
Asp Cys Arg Ile Cys Pro Ser Cys Ser Glu Gly Thr Leu Arg Phe Lys
20 25 30
Val Ser Arg Tyr Gly Glu Gly Tyr Phe Val Gly Cys Asp Arg His Pro
35 40 45
Lys Cys Lys Tyr Ile Ala Arg Ser Leu Ser Gln Gln Glu Asp Glu Thr
50 55 60
Glu Pro Ile Glu Glu Asn Ala Lys Ser Phe Glu Pro Arg Leu Leu Gly
65 70 75 80
Val Met Pro Asp Ser Asp Gln Lys Val Phe Leu Lys Gln Gly Pro Tyr
85 90 95
Gly Tyr Tyr Val Gln Val Gly Glu
100

(2) INFORMATION FOR SEQ ID NO:2588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..444

(D) OTHER INFORMATION: / Ceres Seq. ID 1503924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2588:

cggaagaatt ttgatatttg gcggtctcagt ggcaggtctt cactcagcgt cacagcttta 60
tctgttggat ccaactgaag aaaakccgac ctggagaata ttgaatattc ctggtcgtcc 120

tccccgtttc gcctggggcc acagcacctg tgttggttga ggaacaaagg cgatagtgtc 180
tgggtggacaa actggagaag agtggatgct tacagaaata catgagcttt ctttggtcag 240
ccgctcagtt tgagttcttg aatggtttgt agtcatgttc cttgcaaatt agatgctggc 300
tcttatgcaa cctgaagttt gattgccgtc ttcagaagaa ctagaagaat gaatgctggg 360
catactgaat cttctggcag ctacctggcg gacttggaag atgaaatggc atcgactggt 420
ttgctcgctt tgtgtagaaa aggg

(2) INFORMATION FOR SEQ ID NO:2589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..83
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2589:

Gly Arg Ile Leu Ile Phe Gly Gly Ser Val Ala Gly Leu His Ser Ala
1 5 10 15
Ser Gln Leu Tyr Leu Leu Asp Pro Thr Glu Glu Xaa Pro Thr Trp Arg
20 25 30
Ile Leu Asn Ile Pro Gly Arg Pro Pro Arg Phe Ala Trp Gly His Ser
35 40 45
Thr Cys Val Val Gly Gly Thr Lys Ala Ile Val Leu Gly Gly Gln Thr
50 55 60
Gly Glu Glu Trp Met Leu Thr Glu Ile His Glu Leu Ser Leu Val Ser
65 70 75 80
Arg Ser Val

(2) INFORMATION FOR SEQ ID NO:2590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..510
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503926

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2590:

tctgtgcac ttaaatatgg gggacagtag agctgtgctt gcttccatgc catatgtaga 60
aaatgggtgct ttgaaggcta ctcaactgac agagacccac tcgcttgaaa atccttttga 120
gtaccaaaaa ctttttagctg aacatcccaa tgattcttca gttgtcaggg gtaacaaaat 180
aaaaggaaaag ctgaagggtta ctctgtgcttt tggagttggc tatctgaagc agaggaagtt 240
caacgatgca ctcatgggca ttctgcgagt ccgcgatttg agcagccctc catatgttta 300
cacaaatcca cacacattga gccacaaagt tacagaagat gatttatattg ttgtgcttgg 360
tagtgatggc ttatttgatt tcttcagcaa tgatgaagtt gttcggtttg tttatcaatt 420
tatgcatgat aatccaatgg gggatcctgc aaaatatcct attgagcaac tttatactca 480
aagcagccaa gggagcagct ctaacagccg

(2) INFORMATION FOR SEQ ID NO:2591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1503927

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2591:

Leu Cys Ile Leu Asn Met Gly Asp Ser Arg Ala Val Leu Ala Ser Met
1 5 10 15
Pro Tyr Val Glu Asn Gly Ala Leu Lys Ala Thr Gln Leu Thr Glu Thr
20 25 30
His Ser Leu Glu Asn Pro Leu Glu Tyr Gln Lys Leu Leu Ala Glu His
35 40 45
Pro Asn Asp Ser Ser Val Val Arg Gly Asn Lys Ile Lys Gly Lys Leu
50 55 60
Lys Val Thr Arg Ala Phe Gly Val Gly Tyr Leu Lys Gln Arg Lys Phe
65 70 75 80
Asn Asp Ala Leu Met Gly Ile Leu Arg Val Arg Asp Leu Ser Ser Pro
85 90 95
Pro Tyr Val Tyr Thr Asn Pro His Thr Leu Ser His Lys Val Thr Glu
100 105 110
Asp Asp Leu Phe Val Val Leu Gly Ser Asp Gly Leu Phe Asp Phe Phe
115 120 125
Ser Asn Asp Glu Val Val Arg Leu Val Tyr Gln Phe Met His Asp Asn
130 135 140
Pro Met Gly Asp Pro Ala Lys Tyr Leu Ile Glu Gln Leu Tyr Thr Gln
145 150 155 160
Ser Ser Gln Gly Ser Ser Ser Asn Ser
165

(2) INFORMATION FOR SEQ ID NO:2592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 1503928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2592:

Met Gly Asp Ser Arg Ala Val Leu Ala Ser Met Pro Tyr Val Glu Asn
1 5 10 15
Gly Ala Leu Lys Ala Thr Gln Leu Thr Glu Thr His Ser Leu Glu Asn
20 25 30
Pro Leu Glu Tyr Gln Lys Leu Leu Ala Glu His Pro Asn Asp Ser Ser
35 40 45
Val Val Arg Gly Asn Lys Ile Lys Gly Lys Leu Lys Val Thr Arg Ala
50 55 60
Phe Gly Val Gly Tyr Leu Lys Gln Arg Lys Phe Asn Asp Ala Leu Met
65 70 75 80
Gly Ile Leu Arg Val Arg Asp Leu Ser Ser Pro Pro Tyr Val Tyr Thr
85 90 95
Asn Pro His Thr Leu Ser His Lys Val Thr Glu Asp Asp Leu Phe Val
100 105 110
Val Leu Gly Ser Asp Gly Leu Phe Asp Phe Phe Ser Asn Asp Glu Val
115 120 125
Val Arg Leu Val Tyr Gln Phe Met His Asp Asn Pro Met Gly Asp Pro
130 135 140
Ala Lys Tyr Leu Ile Glu Gln Leu Tyr Thr Gln Ser Ser Gln Gly Ser
145 150 155 160
Ser Ser Asn Ser

(2) INFORMATION FOR SEQ ID NO:2593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..154
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2593:

```
Met Pro Tyr Val Glu Asn Gly Ala Leu Lys Ala Thr Gln Leu Thr Glu
1          5          10          15
Thr His Ser Leu Glu Asn Pro Leu Glu Tyr Gln Lys Leu Leu Ala Glu
          20          25          30
His Pro Asn Asp Ser Ser Val Val Arg Gly Asn Lys Ile Lys Gly Lys
          35          40          45
Leu Lys Val Thr Arg Ala Phe Gly Val Gly Tyr Leu Lys Gln Arg Lys
          50          55          60
Phe Asn Asp Ala Leu Met Gly Ile Leu Arg Val Arg Asp Leu Ser Ser
65          70          75          80
Pro Pro Tyr Val Tyr Thr Asn Pro His Thr Leu Ser His Lys Val Thr
          85          90          95
Glu Asp Asp Leu Phe Val Val Leu Gly Ser Asp Gly Leu Phe Asp Phe
          100         105         110
Phe Ser Asn Asp Glu Val Val Arg Leu Val Tyr Gln Phe Met His Asp
          115         120         125
Asn Pro Met Gly Asp Pro Ala Lys Tyr Leu Ile Glu Gln Leu Tyr Thr
          130         135         140
Gln Ser Ser Gln Gly Ser Ser Ser Asn Ser
145         150
```

(2) INFORMATION FOR SEQ ID NO:2594:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..161
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2594:

```
accgcaccca gaggaggcaa ggagcccatc cacatccacc tggctcctgct ctcaccacac      60
cgccgcgcca attggggctc gcggcagcac cgccgcggct tcccgcctggt cccgctcctg      120
ctctccctcc tggcgcgcgc cgcgtacggc cgctcatct c
```

(2) INFORMATION FOR SEQ ID NO:2595:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..53
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1503935

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2595:

```
Thr Ala Pro Arg Gly Gly Lys Glu Pro Ile His Ile His Leu Val Leu
1          5          10          15
Leu Ser Pro His Arg Arg Ala Asn Trp Gly Ser Arg Gln His Arg Arg
          20          25          30
Gly Phe Pro Leu Val Pro Leu Leu Leu Ser Leu Leu Ala Ala Ala Ala
```

35 40 45
Tyr Gly Arg Leu Ile
50
(2) INFORMATION FOR SEQ ID NO:2596:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1503936
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2596:
Pro His Pro Glu Glu Ala Arg Ser Pro Ser Thr Ser Thr Trp Ser Cys
1 5 10 15
Ser His His Thr Ala Ala Pro Ile Gly Ala Arg Gly Ser Thr Ala Ala
20 25 30
Ala Ser Arg Trp Ser Arg Ser Cys Ser Pro Ser Trp Pro Pro Pro Arg
35 40 45
Thr Ala Ala Ser Ser
50

(2) INFORMATION FOR SEQ ID NO:2597:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..53
(D) OTHER INFORMATION: / Ceres Seq. ID 1503937
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2597:
Arg Thr Gln Arg Arg Gln Gly Ala His Pro His Pro Pro Gly Pro Ala
1 5 10 15
Leu Thr Thr Pro Pro Arg Gln Leu Gly Leu Ala Ala Ala Pro Pro Arg
20 25 30
Leu Pro Ala Gly Pro Ala Pro Ala Leu Pro Pro Gly Arg Arg Arg Val
35 40 45
Arg Pro Pro His Leu
50

(2) INFORMATION FOR SEQ ID NO:2598:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..435
(D) OTHER INFORMATION: / Ceres Seq. ID 1503942
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2598:
gaaccacttc acagaagaag tgctttaccc tcacccgccc cacgcgcggt agttcgttcg 60
acacagtcac agtcacagac cagtcgtttc tcccttctct cccccgggccc cggagaggag 120
aggatggccc gccggagcag cctctccatg gtcgcgtcgc accggctctt cacgccgggc 180
aaccagtggc gcggcgccga ccacggcgtg ggagctcgac gaggccgacg tcactctggg 240
cggcggcggc ggatacccg cgctcgtctc accgctcgtc tcgcggttc tgctctccgc 300
ggtcgaccgc tacgcgcggt cgccgcccgt ggccgcgcgc tccaagcaga agccgcgtgg 360

ggtgggtggcc ggcgctccgg ggccggcgta cgggtgcccg caacatcccg gactgggtcca 420
agatcctggg cgccg

(2) INFORMATION FOR SEQ ID NO:2599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503943

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2599:

Glu Pro Leu His Arg Arg Ser Ala Leu Pro Ser Pro Ala Pro Arg Ala
1 5 10 15
Val Val Arg Ser Thr Gln Ser Gln Ser Gln Thr Ser Arg Phe Ser Leu
20 25 30
Leu Ser Pro Gly Pro Gly Glu Glu Arg Met Ala Gly Arg Ser Ser Leu
35 40 45
Ser Met Val Ala Ser His Arg Leu Phe Thr Pro Val Asn Pro Val Gly
50 55 60
Gly Ala Asp His Gly Val Gly Ala Arg Arg Gly Arg Arg His Leu Gly
65 70 75 80
Arg Arg Arg Arg Ile Pro Gly Val Val Leu Thr Val Val Val Ala Val
85 90 95
Pro Val Leu Arg Gly Arg Pro Val Arg Ala Val Ala Ala Gly Gly Arg
100 105 110
Ala Val Gln Ala Glu Ala Ala Trp Gly Gly Gly Arg Arg Ser Gly Ala
115 120 125
Gly Val Arg Cys Pro Ser Thr Ser Arg Thr Gly Pro Arg Ser Trp Ala
130 135 140
Pro
145

(2) INFORMATION FOR SEQ ID NO:2600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..144
- (D) OTHER INFORMATION: / Ceres Seq. ID 1503944

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2600:

Thr Thr Ser Gln Lys Lys Cys Phe Thr Leu Thr Arg Pro Thr Arg Gly
1 5 10 15
Ser Ser Phe Asp Thr Val Thr Val Thr Asp Gln Ser Phe Leu Pro Ser
20 25 30
Leu Pro Arg Ala Arg Arg Gly Glu Asp Gly Arg Pro Glu Gln Pro Leu
35 40 45
His Gly Arg Val Ala Pro Ala Leu His Ala Gly Gln Pro Ser Gly Arg
50 55 60
Arg Arg Pro Arg Arg Gly Ser Ser Thr Arg Pro Thr Ser Ser Gly Ala
65 70 75 80
Ala Ala Ala Asp Thr Arg Arg Arg Pro His Arg Arg Arg Arg Ser
85 90 95
Cys Pro Pro Arg Ser Thr Arg Thr Arg Gly Arg Arg Arg Trp Pro Arg
100 105 110
Arg Pro Ser Arg Ser Arg Val Gly Trp Trp Pro Ala Leu Arg Gly Arg

115 120 125
Arg Thr Val Pro Val Asn Ile Pro Asp Trp Ser Lys Ile Leu Gly Ala
130 135 140

(2) INFORMATION FOR SEQ ID NO:2601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1503945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2601:

Met Ala Gly Arg Ser Ser Leu Ser Met Val Ala Ser His Arg Leu Phe
1 5 10 15
Thr Pro Val Asn Pro Val Gly Gly Ala Asp His Gly Val Gly Ala Arg
20 25 30
Arg Gly Arg Arg His Leu Gly Arg Arg Arg Arg Ile Pro Gly Val Val
35 40 45
Leu Thr Val Val Val Ala Val Pro Val Leu Arg Gly Arg Pro Val Arg
50 55 60
Ala Val Ala Ala Gly Gly Arg Ala Val Gln Ala Glu Ala Ala Trp Gly
65 70 75 80
Gly Gly Arg Arg Ser Gly Ala Gly Val Arg Cys Pro Ser Thr Ser Arg
85 90 95
Thr Gly Pro Arg Ser Trp Ala Pro
100

(2) INFORMATION FOR SEQ ID NO:2602:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 494 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..494

(D) OTHER INFORMATION: / Ceres Seq. ID 1503946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2602:

tggtcagttg caagaaagtg tacggggctg tgatgttttc cttgtgcaac cgtcgtgtcc 60
tccagcaaat gaaaatctta tggagcttct gatcatgatt gatgcctgta ggagagcatc 120
tgctaagaat atcactgcag ttatccctta ttttggttat gcaagggctg acaggaagtc 180
ccagggcagg gaatctatag ctgcaaaact tgtagctaata atgattaccg aagctggtgc 240
caacgtgtcc ttgtttgtga tcttcattct agtcaagcaa tgggatactt tgacatccca 300
gtagatcacg tttatggcca gcctgttatt cttgattatc tcgccagcaa gacaatatgt 360
tcagatgact tggtagttgt atctcctgat gttggagggtg ttgccagggc acgtgccttt 420
gccaaaaagc tgtcagatgc acctctagct attgtagata aaagaaggca aggacataat 480
gtcgtgagg tgat

(2) INFORMATION FOR SEQ ID NO:2603:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1503947

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2603:

Val Gln Leu Gln Glu Ser Val Arg Gly Cys Asp Val Phe Leu Val Gln
1 5 10 15
Pro Ser Cys Pro Pro Ala Asn Glu Asn Leu Met Glu Leu Leu Ile Met
20 25 30
Ile Asp Ala Cys Arg Arg Ala Ser Ala Lys Asn Ile Thr Ala Val Ile
35 40 45
Pro Tyr Phe Gly Tyr Ala Arg Ala Asp Arg Lys Ser Gln Gly Arg Glu
50 55 60
Ser Ile Ala Ala Lys Leu Val Ala Asn Met Ile Thr Glu Ala Gly Ala
65 70 75 80
Asn Val Ser Leu Phe Val Ile Phe Ile Leu Val Lys Gln Trp Asp Thr
85 90 95
Leu Thr Ser Gln
100

(2) INFORMATION FOR SEQ ID NO:2604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1503948

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2604:

Met Glu Leu Leu Ile Met Ile Asp Ala Cys Arg Arg Ala Ser Ala Lys
1 5 10 15
Asn Ile Thr Ala Val Ile Pro Tyr Phe Gly Tyr Ala Arg Ala Asp Arg
20 25 30
Lys Ser Gln Gly Arg Glu Ser Ile Ala Ala Lys Leu Val Ala Asn Met
35 40 45
Ile Thr Glu Ala Gly Ala Asn Val Ser Leu Phe Val Ile Phe Ile Leu
50 55 60
Val Lys Gln Trp Asp Thr Leu Thr Ser Gln
65 70

(2) INFORMATION FOR SEQ ID NO:2605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 1503949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2605:

Met Gly Tyr Phe Asp Ile Pro Val Asp His Val Tyr Gly Gln Pro Val
1 5 10 15
Ile Leu Asp Tyr Leu Ala Ser Lys Thr Ile Cys Ser Asp Asp Leu Val
20 25 30
Val Val Ser Pro Asp Val Gly Gly Val Ala Arg Ala Arg Ala Phe Ala
35 40 45
Lys Lys Leu Ser Asp Ala Pro Leu Ala Ile Val Asp Lys Arg Arg Gln
50 55 60
Gly His Asn Val Ala Glu Val
65 70

(2) INFORMATION FOR SEQ ID NO:2606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..435
(D) OTHER INFORMATION: / Ceres Seq. ID 1503969

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2606:

gattttgaaa	ggggtttcat	atgcgctgag	gtaatgaagt	ttgaagatct	gaaagaactg	60
ggcagtgaat	ctgctgtaaa	ggctgctgga	aaatacaagc	aggaggggaa	aacctatgtg	120
gtccaggacg	gggacatcat	ctttttcaaa	ttcaacgtgt	ctgggtggcg	gaagaagtga	180
ataatgtatg	aagatggtag	catcaacagt	gttttacgtc	ttaccccgaa	tttctcattc	240
aacagtgttt	acaccttgcc	ccgtattttc	acatttttga	ggtcgcttcc	cagtagctct	300
aggttccggt	atcgaaaact	tgtacaacaa	ggctccagac	cgttgaagga	tttgtattaa	360
taacatgcac	aattgtatgg	cttgtgcttg	agctctcgct	gttaccagaa	gcttagaatc	420
gtttgaqtcc	tttgg					

(2) INFORMATION FOR SEQ ID NO:2607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..59
(D) OTHER INFORMATION: / Ceres Seq. ID 1503970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2607:

Asp	Phe	Glu	Arg	Gly	Phe	Ile	Cys	Ala	Glu	Val	Met	Lys	Phe	Glu	Asp
1				5					10					15	
Leu	Lys	Glu	Leu	Gly	Ser	Glu	Ser	Ala	Val	Lys	Ala	Ala	Gly	Lys	Tyr
			20					25					30		
Lys	Gln	Glu	Gly	Lys	Thr	Tyr	Val	Val	Gln	Asp	Gly	Asp	Ile	Ile	Phe
		35					40					45			
Phe	Lys	Phe	Asn	Val	Ser	Gly	Gly	Gly	Lys	Lys					
	50					55									

(2) INFORMATION FOR SEQ ID NO:2608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..48
(D) OTHER INFORMATION: / Ceres Seq. ID 1503971

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2608:

Met	Lys	Phe	Glu	Asp	Leu	Lys	Glu	Leu	Gly	Ser	Glu	Ser	Ala	Val	Lys
1				5					10					15	
Ala	Ala	Gly	Lys	Tyr	Lys	Gln	Glu	Gly	Lys	Thr	Tyr	Val	Val	Gln	Asp
			20					25					30		
Gly	Asp	Ile	Ile	Phe	Phe	Lys	Phe	Asn	Val	Ser	Gly	Gly	Gly	Lys	Lys
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:2609:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..58
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503972
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2609:

Met Tyr Glu Asp Gly Ser Ile Asn Ser Val Leu Arg Leu Thr Pro Asn
1 5 10 15
Phe Ser Phe Asn Ser Val Tyr Thr Leu Pro Arg Ile Ser Thr Phe Leu
 20 25 30
Arg Ser Leu Pro Ser Ser Ser Arg Phe Arg Tyr Arg Lys Leu Val Gln
 35 40 45
Gln Gly Ser Arg Pro Leu Lys Asp Leu Tyr
50 55

(2) INFORMATION FOR SEQ ID NO:2610:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..506
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503989
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2610:

accgcgccct gatccactct ccgcttcccg ctccgatcga cctgctccct cccaccacc 60
gagcccatgg cggaccagct caccgacgac cagatcgccg agttcaagga ggccttcagc 120
ctcttcgaca aggacgggga tgggtgcatc acgaccaagg agctgggcac tgtcatgcgc 180
tcgctggggc aaaatcctac agaggctgag ctccaggaca tgatcaacga ggtcgatgct 240
gatggcaacg gcaccatcga tttcccagag tttctcaacc ttatggctcg caagatgaag 300
gacaccgact ctgaggaaga gctcaaggag gccttcogtg tgtttgacaa ggaccagaac 360
ggcttcatct cggccgccga gctccgccat gtcatgacaa atcttggtga gaagctaact 420
gatgaggagg tggacgagat gatccgtgag gctgatgtcg atggtgatgg ccagatcaac 480
tacgaggagt ttgtcaaggt catgat

(2) INFORMATION FOR SEQ ID NO:2611:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..146
 (D) OTHER INFORMATION: / Ceres Seq. ID 1503990
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2611:

Met Ala Asp Gln Leu Thr Asp Asp Gln Ile Ala Glu Phe Lys Glu Ala
1 5 10 15
Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Cys Ile Thr Thr Lys Glu
 20 25 30
Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu
 35 40 45
Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile
50 55 60
Asp Phe Pro Glu Phe Leu Asn Leu Met Ala Arg Lys Met Lys Asp Thr

65					70					75					80
Asp	Ser	Glu	Glu	Glu	Leu	Lys	Glu	Ala	Phe	Arg	Val	Phe	Asp	Lys	Asp
				85					90					95	
Gln	Asn	Gly	Phe	Ile	Ser	Ala	Ala	Glu	Leu	Arg	His	Val	Met	Thr	Asn
			100					105					110		
Leu	Gly	Glu	Lys	Leu	Thr	Asp	Glu	Glu	Val	Asp	Glu	Met	Ile	Arg	Glu
		115					120					125			
Ala	Asp	Val	Asp	Gly	Asp	Gly	Gln	Ile	Asn	Tyr	Glu	Glu	Phe	Val	Lys
	130					135					140				
Val	Met														

145

(2) INFORMATION FOR SEQ ID NO:2612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1503991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2612:

Met	Arg	Ser	Leu	Gly	Gln	Asn	Pro	Thr	Glu	Ala	Glu	Leu	Gln	Asp	Met
1			5						10				15		
Ile	Asn	Glu	Val	Asp	Ala	Asp	Gly	Asn	Gly	Thr	Ile	Asp	Phe	Pro	Glu
			20				25					30			
Phe	Leu	Asn	Leu	Met	Ala	Arg	Lys	Met	Lys	Asp	Thr	Asp	Ser	Glu	Glu
	35					40					45				
Glu	Leu	Lys	Glu	Ala	Phe	Arg	Val	Phe	Asp	Lys	Asp	Gln	Asn	Gly	Phe
	50				55				60						
Ile	Ser	Ala	Ala	Glu	Leu	Arg	His	Val	Met	Thr	Asn	Leu	Gly	Glu	Lys
65				70				75					80		
Leu	Thr	Asp	Glu	Glu	Val	Asp	Glu	Met	Ile	Arg	Glu	Ala	Asp	Val	Asp
			85					90					95		
Cly	Asp	Gly	Gln	Ile	Asn	Tyr	Glu	Glu	Phe	Val	Lys	Val	Met		
		100					105					110			

(2) INFORMATION FOR SEQ ID NO:2613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1503992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2613:

Met	Ile	Asn	Glu	Val	Asp	Ala	Asp	Gly	Asn	Gly	Thr	Ile	Asp	Phe	Pro
1			5					10					15		
Glu	Phe	Leu	Asn	Leu	Met	Ala	Arg	Lys	Met	Lys	Asp	Thr	Asp	Ser	Glu
		20					25					30			
Glu	Glu	Leu	Lys	Glu	Ala	Phe	Arg	Val	Phe	Asp	Lys	Asp	Gln	Asn	Gly
	35				40					45					
Phe	Ile	Ser	Ala	Ala	Glu	Leu	Arg	His	Val	Met	Thr	Asn	Leu	Gly	Glu
	50				55				60						
Lys	Leu	Thr	Asp	Glu	Glu	Val	Asp	Glu	Met	Ile	Arg	Glu	Ala	Asp	Val
65			70					75					80		
Asp	Gly	Asp	Gly	Gln	Ile	Asn	Tyr	Glu	Glu	Phe	Val	Lys	Val	Met	
			85					90					95		

(2) INFORMATION FOR SEQ ID NO:2614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..479
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2614:

tcaacgcaca tctccaccgt cgccgcgcgc cgccgaagac ggaaggagaa gaggggtacgg	60
ccgtctcctc gcccccatgg cccacgagaa gaagctgtcc aaccgatgc gggagatcaa	120
ggtgcagaag ctgctcctca atatctcgt cggggagagc ggcgaccgtc tcaccgcgc	180
cgcaaagggtg ctgagcagc tcagcggcca gaccccgctc ttctccaagg gtgagtactg	240
agttctcgcg gctccgtttc atgccttcog ctgacggggg gcttccttct gcctgctggc	300
ggtgttggtt cgtcttgacg cgaggtacac ggtgcggtcg ttcggcatcc ggcgtaacga	360
gaagatcgcc tgctacgtca cggtgagggg cgagaaggcc atgcagctgc ttgagagcgg	420
cctcaaggtc aaggagtacg agctgctcag gaggaacttc agcgacaccg ggtgctttg	

(2) INFORMATION FOR SEQ ID NO:2615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504002

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2615:

Ser Thr His Ile Ser Thr Val Val Arg Arg Arg Arg Arg Lys Glu	
1 5 10 15	
Lys Arg Val Arg Pro Ser Pro Arg Pro His Gly Pro Arg Glu Glu Ala	
20 25 30	
Val Gln Pro Asp Ala Gly Asp Gln Gly Ala Glu Ala Arg Pro Gln Tyr	
35 40 45	
Leu Arg Arg Gly Glu Arg Arg Pro Ser His Pro Arg Arg Lys Gly Ala	
50 55 60	
Arg Ala Ala Gln Arg Pro Asp Pro Arg Leu Leu Gln Gly	
65 70 75	

(2) INFORMATION FOR SEQ ID NO:2616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2616:

Gln Arg Thr Ser Pro Pro Ser Ser Ala Ala Glu Asp Gly Arg Arg	
1 5 10 15	
Arg Gly Tyr Gly Arg Leu Leu Ala Pro Met Ala His Glu Lys Lys Leu	
20 25 30	
Ser Asn Pro Met Arg Glu Ile Lys Val Gln Lys Leu Val Leu Asn Ile	
35 40 45	
Ser Val Gly Glu Ser Gly Asp Arg Leu Thr Arg Ala Ala Lys Val Leu	

50 55 60
Glu Gln Leu Ser Gly Gln Thr Pro Val Phe Ser Lys Gly Glu Tyr
65 70 75

(2) INFORMATION FOR SEQ ID NO:2617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..127
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2617:

Asn Ala His Leu His Arg Arg Pro Pro Pro Pro Lys Thr Glu Gly Glu
1 5 10 15
Glu Gly Thr Ala Val Ser Ser Pro Pro Trp Pro Thr Arg Arg Ser Cys
20 25 30
Pro Thr Arg Cys Gly Arg Ser Arg Cys Arg Ser Ser Ser Ser Ile Ser
35 40 45
Pro Ser Gly Arg Ala Ala Thr Val Ser Pro Ala Pro Gln Arg Cys Ser
50 55 60
Ser Ser Ser Ala Ala Arg Pro Pro Ser Ser Pro Arg Val Ser Thr Glu
65 70 75 80
Phe Ser Arg Leu Arg Phe Met Pro Ser Ala Asp Gly Val Leu Pro Ser
85 90 95
Ala Cys Trp Arg Cys Trp Phe Val Leu Gln Arg Gly Thr Arg Cys Gly
100 105 110
Arg Ser Ala Ser Gly Val Thr Arg Arg Ser Pro Ala Thr Ser Arg
115 120 125

(2) INFORMATION FOR SEQ ID NO:2618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..477
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504016

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2618:

atcgagacac acacagaact tctcctgtcg gctactaat acagctagct agctgccctc 60
ttaggtatac tgtgatggcc acaaccttgt cctccacagt agtagttgca cttggtgacc 120
tctcttcttg ctcttgtaa cgtgtggctc gtgcgcgagg ccggtgagct ttaacgcctc 180
cgacctcacc gccgatccc gctgggatgc tgccagggcc acctgttacg gtgcgcccac 240
cggcgcggcc ctgatgacga cgggtgtgcc tgtggattca agaactgaa tctgccgcgc 300
ttctcgga tgacgtcgtg cggcaacgag cccctgttca aggacggcaa gggctgcggc 360
tcctgctacc agatacgatg ccaaaaccac ccggcctgct ccggcaaccc agagacgggtg 420
atcatcactg acatgaacta ctaccccggtg gccaaagtacc acttcgacct yagcggc

(2) INFORMATION FOR SEQ ID NO:2619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1504017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2619:

Arg Asp Thr His Arg Thr Ser Pro Val Gly Leu Leu Ile Gln Leu Ala
1 5 10 15
Ser Cys Pro Leu Arg Tyr Thr Val Met Ala Thr Thr Leu Ser Ser Thr
20 25 30
Val Val Val Ala Leu Gly Asp Leu Ser Ser Cys Ser Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:2620:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1504018

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2620:

Met Thr Ser Cys Gly Asn Glu Pro Leu Phe Lys Asp Gly Lys Gly Cys
1 5 10 15
Gly Ser Cys Tyr Gln Ile Arg Cys Gln Asn His Pro Ala Cys Ser Gly
20 25 30
Asn Pro Glu Thr Val Ile Ile Thr Asp Met Asn Tyr Tyr Pro Val Ala
35 40 45
Lys Tyr His Phe Asp Xaa Ser Gly
50 55

(2) INFORMATION FOR SEQ ID NO:2621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..430

(D) OTHER INFORMATION: / Ceres Seq. ID 1504025

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2621:

catgtggttg tgggcactgt gaaagctctt tggccactca cagaagccct agaataagaa 60
tattgctaatt gatgagaagt aactaaaaca atatcataca attgcagtgc tctctccaat 120
agtttgagg gtatgctcct tggaagattt ttggtaggaa cagggatggg attgggtcca 180
ccagtagctt cactttatat aacggagggt tctccttcta cagtggaggg tacatatggt 240
agctttgttc agattgcaac ctgccttgga attatagtat cactactcat tggtagacct 300
gtcaaagata ttgatagatg gtggagagtg tgtttctggg ttgccgttat ccagcaact 360
ttacaagctc tcggtatgga gttttgtgct gagagccctc agtggcttta taagtgtgga 420
aaaataagtg

(2) INFORMATION FOR SEQ ID NO:2622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1504026

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2622:

Met Leu Leu Gly Arg Phe Leu Val Gly Thr Gly Met Gly Leu Gly Pro

1 5 10 15
Pro Val Ala Ser Leu Tyr Ile Thr Glu Val Ser Pro Ser Thr Val Arg
20 25 30
Gly Thr Tyr Gly Ser Phe Val Gln Ile Ala Thr Cys Leu Gly Ile Ile
35 40 45
Val Ser Leu Leu Ile Gly Thr Pro Val Lys Asp Ile Asp Arg Trp Trp
50 55 60
Arg Val Cys Phe Trp Val Ala Val Ile Pro Ala Thr Leu Gln Ala Leu
65 70 75 80
Gly Met Glu Phe Cys Ala Glu Ser Pro Gln Trp Leu Tyr Lys Cys Gly
85 90 95
Lys Ile Ser

(2) INFORMATION FOR SEQ ID NO:2623:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..88
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2623:

Met Gly Leu Gly Pro Pro Val Ala Ser Leu Tyr Ile Thr Glu Val Ser
1 5 10 15
Pro Ser Thr Val Arg Gly Thr Tyr Gly Ser Phe Val Gln Ile Ala Thr
20 25 30
Cys Leu Gly Ile Ile Val Ser Leu Leu Ile Gly Thr Pro Val Lys Asp
35 40 45
Ile Asp Arg Trp Trp Arg Val Cys Phe Trp Val Ala Val Ile Pro Ala
50 55 60
Thr Leu Gln Ala Leu Gly Met Glu Phe Cys Ala Glu Ser Pro Gln Trp
65 70 75 80
Leu Tyr Lys Cys Gly Lys Ile Ser
85

(2) INFORMATION FOR SEQ ID NO:2624:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..462
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2624:

tattatcaga gaaacaagag ctgtgcttct ctgttgctctc attgctctgg cagaagctca 60
tagcttctcc tgaatgcag atgtctgcag aaagtacatc agctcaccaa ggatggagga 120
aggttgttga tgcactttgt gatgtcgttt cagcctcacc aaccaaggca tcagctgcta 180
tcgttctcca ggccgagaag gacttgccagc cttggattgc tagagatgac gaacaaggtc 240
agaagatgtg gagagtcaac cagcgtatag tgaagcttat agctgagctt atgaggaacc 300
atgacagccc tgaagcgttg gtgatactcg ctagtgccctc cgaccttcta cttcgtgcta 360
ccgatggaat gctcgtcgat ggtgaagctt gtactttgcc acagcttgag cttctggaag 420
tgaccgctcg ggctgtccat cttatcatcg aatggggaga tc

(2) INFORMATION FOR SEQ ID NO:2625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..153
(D) OTHER INFORMATION: / Ceres Seq. ID 1504037
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2625:

Leu Ser Glu Lys Gln Glu Leu Cys Phe Ser Val Val Ser Leu Leu Trp
1 5 10 15
Gln Lys Leu Ile Ala Ser Pro Glu Met Gln Met Ser Ala Glu Ser Thr
20 25 30
Ser Ala His Gln Gly Trp Arg Lys Val Val Asp Ala Leu Cys Asp Val
35 40 45
Val Ser Ala Ser Pro Thr Lys Ala Ser Ala Ala Ile Val Leu Gln Ala
50 55 60
Glu Lys Asp Leu Gln Pro Trp Ile Ala Arg Asp Glu Gln Gly Gln
65 70 75 80
Lys Met Trp Arg Val Asn Gln Arg Ile Val Lys Leu Ile Ala Glu Leu
85 90 95
Met Arg Asn His Asp Ser Pro Glu Ala Leu Val Ile Leu Ala Ser Ala
100 105 110
Ser Asp Leu Leu Arg Ala Thr Asp Gly Met Leu Val Asp Gly Glu
115 120 125
Ala Cys Thr Leu Pro Gln Leu Glu Leu Leu Glu Val Thr Ala Arg Ala
130 135 140
Val His Leu Ile Ile Glu Trp Gly Asp
145 150

(2) INFORMATION FOR SEQ ID NO:2626:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..129

(D) OTHER INFORMATION: / Ceres Seq. ID 1504038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2626:

Met Gln Met Ser Ala Glu Ser Thr Ser Ala His Gln Gly Trp Arg Lys
1 5 10 15
Val Val Asp Ala Leu Cys Asp Val Val Ser Ala Ser Pro Thr Lys Ala
20 25 30
Ser Ala Ala Ile Val Leu Gln Ala Glu Lys Asp Leu Gln Pro Trp Ile
35 40 45
Ala Arg Asp Asp Glu Gln Gly Gln Lys Met Trp Arg Val Asn Gln Arg
50 55 60
Ile Val Lys Leu Ile Ala Glu Leu Met Arg Asn His Asp Ser Pro Glu
65 70 75 80
Ala Leu Val Ile Leu Ala Ser Ala Ser Asp Leu Leu Leu Arg Ala Thr
85 90 95
Asp Gly Met Leu Val Asp Gly Glu Ala Cys Thr Leu Pro Gln Leu Glu
100 105 110
Leu Leu Glu Val Thr Ala Arg Ala Val His Leu Ile Ile Glu Trp Gly
115 120 125
Asp

(2) INFORMATION FOR SEQ ID NO:2627:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..127
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504039
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2627:

```
Met Ser Ala Glu Ser Thr Ser Ala His Gln Gly Trp Arg Lys Val Val
1          5          10          15
Asp Ala Leu Cys Asp Val Val Ser Ala Ser Pro Thr Lys Ala Ser Ala
20          25          30
Ala Ile Val Leu Gln Ala Glu Lys Asp Leu Gln Pro Trp Ile Ala Arg
35          40          45
Asp Asp Glu Gln Gly Gln Lys Met Trp Arg Val Asn Gln Arg Ile Val
50          55          60
Lys Leu Ile Ala Glu Leu Met Arg Asn His Asp Ser Pro Glu Ala Leu
65          70          75          80
Val Ile Leu Ala Ser Ala Ser Asp Leu Leu Leu Arg Ala Thr Asp Gly
85          90          95
Met Leu Val Asp Gly Glu Ala Cys Thr Leu Pro Gln Leu Glu Leu Leu
100         105         110
Glu Val Thr Ala Arg Ala Val His Leu Ile Ile Glu Trp Gly Asp
115         120         125
```

- (2) INFORMATION FOR SEQ ID NO:2628:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..463
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504044

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2628:

```
aaatctctct cttctcctcg cctcgcccttg gtgttcacgc cgctcgctagc gcctgckcct      60
gccssggcka asttcctgcc ctccccggcg ccgggctcgg gtcgtcgtcg gccaggaaga      120
tggttgccgg cttcagggtg ctgcatctgg tcaggccttt tctggctttc ttgccatakk      180
ttgcagagcg cggatagkaa gataccgttc agagaaaaag ttatctacac tgttatttcc      240
ctcttcattt tcctggtctg cagccagctc ccactctatg gcattcattc aacaactgga      300
gctgacccct tctactggat gcgtgttatc ctgcacatcaa accgtggcac tgtgatggag      360
ttgggtatta ctccaattgt gacatctggg atggtaatgc aacttcttgt tggatcgaag      420
atcatttgaa gttgacaaca gtgtgagaka ggatcgtgct ctg
```

- (2) INFORMATION FOR SEQ ID NO:2629:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..142
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504045
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2629:

```
Lys Ser Leu Ser Ser Pro Arg Leu Ala Leu Val Phe Thr Pro Ser Leu
1          5          10          15
Ala Pro Xaa Pro Ala Xaa Xaa Xaa Phe Leu Pro Ser Pro Ala Pro Gly
20          25          30
```

Ser Gly Arg Arg Arg Pro Gly Arg Trp Leu Ala Ala Ser Gly Tyr Cys
35 40 45
Ile Trp Ser Gly Leu Phe Trp Leu Ser Cys His Xaa Leu Gln Ser Ala
50 55 60
Asp Xaa Lys Ile Pro Phe Arg Glu Lys Val Ile Tyr Thr Val Ile Ser
65 70 75 80
Leu Phe Ile Phe Leu Val Cys Ser Gln Leu Pro Leu Tyr Gly Ile His
85 90 95
Ser Thr Thr Gly Ala Asp Pro Phe Tyr Trp Met Arg Val Ile Leu Ala
100 105 110
Ser Asn Arg Gly Thr Val Met Glu Leu Gly Ile Thr Pro Ile Val Thr
115 120 125
Ser Gly Met Val Met Gln Leu Val Gly Ser Lys Ile Ile
130 135 140

(2) INFORMATION FOR SEQ ID NO:2630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..502
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504050

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2630:

atctgaagga	tatggcttat	catggagtat	ttttaagag	ggacatttgt	taagtgggtc	60
tgacgatgct	caaatttgct	tgtgggacat	taaagcaaat	agtagaaaca	aaagtcttga	120
cgccttgacg	atttttaagc	atcatgatgg	tgtcgttgaa	gatgttgctt	ggcacttgag	180
gcatgagtac	ttatttgggt	cagttgggtga	cgattatcat	cttttgattt	gggacctgcg	240
gtctcccgcc	cctactaaac	ctgttcagtc	agtgggtggcg	caccaggggtg	aggtgaactg	300
cctggctttt	aacccggttca	acgaatgggt	tgttgcaact	ggttctactg	acaagactgt	360
caaattattt	gatcttagga	agattgatac	ttctctgcac	acctttgact	gtcacaaaga	420
ggaagttttt	caagttggat	ggagtccaaa	gaatgaaact	gtacttgcat	cctgttgtct	480
gggcagaagg	ctcatgggtct	gg				

(2) INFORMATION FOR SEQ ID NO:2631:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..167
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2631:

Ser Glu Gly Tyr Gly Leu Ser Trp Ser Ile Phe Lys Glu Gly His Leu
1 5 10 15
Leu Ser Gly Ser Asp Asp Ala Gln Ile Cys Leu Trp Asp Ile Lys Ala
20 25 30
Asn Ser Arg Asn Lys Ser Leu Asp Ala Leu Gln Ile Phe Lys His His
35 40 45
Asp Gly Val Val Glu Asp Val Ala Trp His Leu Arg His Glu Tyr Leu
50 55 60
Phe Gly Ser Val Gly Asp Asp Tyr His Leu Leu Ile Trp Asp Leu Arg
65 70 75 80
Ser Pro Ala Pro Thr Lys Pro Val Gln Ser Val Val Ala His Gln Gly
85 90 95
Glu Val Asn Cys Leu Ala Phe Asn Pro Phe Asn Glu Trp Val Val Ala
100 105 110

Thr Gly Ser Thr Asp Lys Thr Val Lys Leu Phe Asp Leu Arg Lys Ile
115 120 125
Asp Thr Ser Leu His Thr Phe Asp Cys His Lys Glu Glu Val Phe Gln
130 135 140
Val Gly Trp Ser Pro Lys Asn Glu Thr Val Leu Ala Ser Cys Cys Leu
145 150 155 160
Gly Arg Arg Leu Met Val Trp
165

(2) INFORMATION FOR SEQ ID NO:2632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..514
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2632:

attccggttcc	gagagccaaa	aactccactg	ctttcatcaa	ctccggcgac	ttggagaaga	60
cgaaktccag	aatccgatcg	gaagtttggt	gctcgcgcct	tgacggattg	atttcggtgc	120
gccgatgggg	caggcggtcc	gcaagctgtt	cgattccttc	ttcggcacca	gcgagatgag	180
ggttgatgatg	cttggtctgg	atgctgccgg	taaaaccacc	atattgtaca	agctgcatat	240
cggggagggtt	ttgtcgactg	ttcccacgat	tggtttcaac	gtcgagaaag	ttcaatacaa	300
gaatgtgatg	tttactgtgt	gggatgttgg	tggccaagaa	aagttgaggg	tgactacgtc	360
cgcaaaggag	atgagtttgg	gtatttcttc	tttggaggga	gtacagtgat	atgcgtcttc	420
gagaaggacg	ccatccaatt	tgacgctgat	ctcgtggcaa	acagcgaaag	gtcactggag	480
accaagtccc	ggatctgcag	aaagtttcgc	tcgg			

(2) INFORMATION FOR SEQ ID NO:2633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..94
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504099

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2633:

Met Gly Gln Ala Phe Arg Lys Leu Phe Asp Ser Phe Phe Gly Thr Ser	
1 5 10 15	
Glu Met Arg Val Val Met Leu Gly Leu Asp Ala Ala Gly Lys Thr Thr	
20 25 30	
Ile Leu Tyr Lys Leu His Ile Gly Glu Val Leu Ser Thr Val Pro Thr	
35 40 45	
Ile Gly Phe Asn Val Glu Lys Val Gln Tyr Lys Asn Val Met Phe Thr	
50 55 60	
Val Trp Asp Val Gly Gly Gln Glu Lys Leu Arg Val Thr Thr Ser Ala	
65 70 75 80	
Lys Glu Met Ser Leu Gly Ile Ser Pro Leu Glu Gly Val Gln	
85 90	

(2) INFORMATION FOR SEQ ID NO:2634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..77
(D) OTHER INFORMATION: / Ceres Seq. ID 1504100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2634:

```
Met Arg Val Val Met Leu Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile
1          5          10          15
Leu Tyr Lys Leu His Ile Gly Glu Val Leu Ser Thr Val Pro Thr Ile
          20          25          30
Gly Phe Asn Val Glu Lys Val Gln Tyr Lys Asn Val Met Phe Thr Val
          35          40          45
Trp Asp Val Gly Gly Gln Glu Lys Leu Arg Val Thr Thr Ser Ala Lys
          50          55          60
Glu Met Ser Leu Gly Ile Ser Pro Leu Glu Gly Val Gln
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:2635:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..73
(D) OTHER INFORMATION: / Ceres Seq. ID 1504101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2635:

```
Met Leu Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile Leu Tyr Lys Leu
1          5          10          15
His Ile Gly Glu Val Leu Ser Thr Val Pro Thr Ile Gly Phe Asn Val
          20          25          30
Glu Lys Val Gln Tyr Lys Asn Val Met Phe Thr Val Trp Asp Val Gly
          35          40          45
Gly Gln Glu Lys Leu Arg Val Thr Thr Ser Ala Lys Glu Met Ser Leu
          50          55          60
Gly Ile Ser Pro Leu Glu Gly Val Gln
65          70
```

(2) INFORMATION FOR SEQ ID NO:2636:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 460 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..460
(D) OTHER INFORMATION: / Ceres Seq. ID 1504102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2636:

```
atatatactc ctgttgcgta gaatcggcac aagggtgcac gttcaggagg agctctcgtg      60
gcgtcctagt ctgtggaagg tccaaagaag aagatggacg gcgagatgga cgaggacgtt      120
ctcacggaga tcctcgcgag gctgccgtgc aggtcgtctg cgcggttcca gtgcgtgtcc      180
acgtcgtgcg gcgcattcat tccagcgact acctccgccg ccggtgtgcc ctcattcacgt      240
cgggcgtgct ctaccacgat ggtggcagga ggcagcagtc gtacacgtac gcgtgcgcgt      300
caggcggcgg cggcggcggc ggcgcattgg cggaggccgc ggacatgcgc ttcttcccgc      360
gccacgagac gtccaccatc atcgacggct gcaacggcct gctgctctac tacgcgtccc      420
gcccggcgcg ttccacgtcg tgagcccgcac cagcggcgcg
```

(2) INFORMATION FOR SEQ ID NO:2637:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..153
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2637:

Tyr	Ile	Leu	Leu	Leu	Arg	Arg	Ile	Gly	Thr	Arg	Val	His	Val	Gln	Glu
1			5						10					15	
Glu	Leu	Ser	Trp	Arg	Pro	Ser	Leu	Trp	Lys	Val	Gln	Arg	Arg	Arg	Trp
		20						25					30		
Thr	Ala	Arg	Trp	Thr	Arg	Thr	Phe	Ser	Arg	Arg	Ser	Ser	Arg	Gly	Cys
		35					40					45			
Arg	Ala	Gly	Arg	Trp	Arg	Gly	Ser	Ser	Ala	Cys	Pro	Arg	Arg	Ala	Ala
	50					55					60				
His	His	Leu	Gln	Arg	Leu	Pro	Pro	Pro	Pro	Ala	Ala	Ala	His	His	Val
65					70					75					80
Gly	Arg	Ala	Leu	Pro	Arg	Trp	Trp	Gln	Glu	Ala	Ala	Val	Val	His	Val
			85						90					95	
Arg	Val	Arg	Val	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Arg	Ile	Gly	Gly	Gly
			100					105					110		
Arg	Gly	His	Ala	Leu	Leu	Pro	Ala	Pro	Arg	Asp	Val	His	His	His	Arg
		115					120					125			
Arg	Leu	Gln	Arg	Pro	Ala	Ala	Leu	Leu	Arg	Val	Pro	Pro	Gly	Ala	Phe
	130					135					140				
His	Val	Val	Ser	Pro	Thr	Thr	Arg	Arg							
145					150										

(2) INFORMATION FOR SEQ ID NO:2638:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..146
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2638:

Ile	Tyr	Ser	Cys	Cys	Val	Glu	Ser	Ala	Gln	Gly	Cys	Thr	Phe	Arg	Arg
1			5						10					15	
Ser	Ser	Arg	Gly	Val	Leu	Val	Cys	Gly	Arg	Ser	Lys	Glu	Glu	Asp	Gly
		20						25				30			
Arg	Arg	Asp	Gly	Arg	Gly	Arg	Ser	His	Gly	Asp	Pro	Arg	Glu	Ala	Ala
		35					40				45				
Val	Gln	Val	Ala	Gly	Ala	Val	Pro	Val	Arg	Val	His	Val	Val	Arg	Arg
	50					55					60				
Ile	Ile	Ser	Ser	Asp	Tyr	Leu	Arg	Arg	Arg	Leu	Pro	Leu	Ile	Thr	Ser
65					70					75					80
Gly	Val	Leu	Tyr	His	Asp	Gly	Gly	Arg	Arg	Gln	Gln	Ser	Tyr	Thr	Tyr
			85					90					95		
Ala	Cys	Ala	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Leu	Ala	Glu	Ala
		100						105					110		
Ala	Asp	Met	Arg	Phe	Phe	Pro	Arg	His	Glu	Thr	Ser	Thr	Ile	Ile	Asp
		115					120					125			
Gly	Cys	Asn	Gly	Leu	Leu	Leu	Tyr	Tyr	Ala	Ser	Arg	Pro	Ala	Arg	Ser
	130					135					140				
Thr	Ser														
145															

(2) INFORMATION FOR SEQ ID NO:2639:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..122
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2639:

Met	Asp	Gly	Glu	Met	Asp	Glu	Asp	Val	Leu	Thr	Glu	Ile	Leu	Ala	Arg
1			5						10					15	
Leu	Pro	Cys	Arg	Ser	Leu	Ala	Arg	Phe	Gln	Cys	Val	Ser	Thr	Ser	Cys
		20					25						30		
Gly	Ala	Ser	Ser	Pro	Ala	Thr	Thr	Ser	Ala	Ala	Gly	Cys	Arg	Ser	Ser
		35				40					45				
Arg	Arg	Ala	Cys	Ser	Thr	Thr	Met	Val	Ala	Gly	Gly	Ser	Ser	Arg	Thr
	50				55					60					
Arg	Thr	Arg	Ala	Arg	Gln	Ala	Ala	Ala	Ala	Ala	Ala	Ala	His	Trp	Arg
65				70					75					80	
Arg	Pro	Arg	Thr	Cys	Ala	Ser	Ser	Arg	Ala	Thr	Arg	Arg	Pro	Pro	Ser
			85					90					95		
Ser	Thr	Ala	Ala	Thr	Ala	Cys	Cys	Ser	Thr	Thr	Arg	Pro	Ala	Arg	Arg
		100					105						110		
Val	Pro	Arg	Arg	Glu	Pro	Asp	His	Ala	Ala						
		115				120									

(2) INFORMATION FOR SEQ ID NO:2640:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 469 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: -
 - (B) LOCATION: 1..469
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2640:

aactg	cggt	gtgc	gcttc	gttc	agttc	ag	ttcat	ccgtg	ttctt	gtttg	cgagg	tcgag		60
agagac	tgag	agagg	atgtc	gtgct	gcgga	ggcaac	tgcg	gggtc	cggtc	gcaag			120	
tgcgga	caacg	gctgc	ggagg	gtgcag	caag	atgtac	ccgc	agaat	gggta	tcgac	ctcgt		180	
cgccg	gtggg	aggaata	aga	agcaag	c	actgc	gcgc	aagtct	gacg	atgtc	tacct		240	
caagtc	cctc	gtcaag	ctct	accgtt	tctt	ggtcag	gagg	accaag	agca	atttca	acgc		300	
tgtcat	tctc	aagagg	cttt	tcatg	agtaa	aacca	accga	ccacca	aatct	ccatg	cgccg		360	
ccttgt	caag	tttatg	gaag	gaaag	gagaa	gaacat	tgtc	gtcatt	gttg	gcacag	tcac		420	
agatga	caaaa	aggatc	cagg	aggtt	ccagc	aatga	agggt	actgc	ccctg					

(2) INFORMATION FOR SEQ ID NO:2641:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: peptide
 - (B) LOCATION: 1..156
 - (D) OTHER INFORMATION: / Ceres Seq. ID 1504108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2641:

Thr	Ala	Ala	Val	Arg	Phe	Val	Gln	Phe	Ser	Ser	Ser	Val	Phe	Leu	Phe
1			5				10					15			
Ala	Arg	Ser	Arg	Glu	Thr	Glu	Arg	Gly	Cys	Arg	Ala	Ala	Glu	Ala	Thr

	20		25		30
Ala Gly	Ala Ala Pro Ala Ala Ser	Ala Ala Thr Ala Ala Glu Gly	Ala		
	35		40		45
Ala Arg	Cys Thr Arg Arg Met Gly	Ile Asp Leu Val Ala Gly Gly	Arg		
	50		55		60
Asn Lys	Lys Thr Lys Arg Thr Ala Pro	Lys Ser Asp Asp Val Tyr Leu			
65		70		75	80
Lys Leu	Leu Val Lys Leu Tyr Arg Phe	Leu Val Arg Arg Thr Lys Ser			
		85		90	95
Asn Phe	Asn Ala Val Ile Leu Lys Arg	Leu Phe Met Ser Lys Thr Asn			
	100		105		110
Arg Pro	Pro Ile Ser Met Arg Arg Leu	Val Lys Phe Met Glu Gly Lys			
	115		120		125
Glu Lys	Asn Ile Ala Val Ile Val Gly	Thr Val Thr Asp Asp Lys Arg			
	130		135		140
Ile Gln	Glu Val Pro Ala Met Lys Val	Thr Ala Leu			
145		150		155	

(2) INFORMATION FOR SEQ ID NO:2642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1504109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2642:

Leu Arg	Leu Cys Ala Ser Phe Ser Ser	Val His Pro Cys Ser Cys Leu		
1		5		10
Arg Gly	Arg Glu Arg Leu Arg Glu Asp	Val Val Leu Arg Arg Gln Leu		
	20		25	30
Arg Val	Arg Leu Arg Leu Gln Val Arg	Gln Arg Leu Arg Arg Val Gln		
	35		40	45
Gln Asp	Val Pro Ala Glu Trp Val Ser	Thr Ser Ser Pro Val Gly Gly		
	50		55	60
Ile Arg	Arg Pro Ser Ala Leu Arg Pro	Ser Leu Thr Met Ser Thr Ser		
65		70		75
Ser Ser	Ser Ser Ser Thr Val Ser Trp	Ser Gly Gly Pro Arg Ala		
	85		90	95
Ile Ser	Thr Leu Ser Phe Ser Arg Gly	Phe Ser		
	100		105	

(2) INFORMATION FOR SEQ ID NO:2643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1504110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2643:

Met Gly	Ile Asp Leu Val Ala Gly Gly	Arg Asn Lys Lys Thr Lys Arg		
1		5		10
Thr Ala	Pro Lys Ser Asp Asp Val Tyr	Leu Lys Leu Leu Val Lys Leu		
	20		25	30
Tyr Arg	Phe Leu Val Arg Arg Thr	Lys Ser Asn Phe Asn Ala Val Ile		
	35		40	45

Leu Lys Arg Leu Phe Met Ser Lys Thr Asn Arg Pro Pro Ile Ser Met
50 55 60
Arg Arg Leu Val Lys Phe Met Glu Gly Lys Glu Lys Asn Ile Ala Val
65 70 75 80
Ile Val Gly Thr Val Thr Asp Asp Lys Arg Ile Gln Glu Val Pro Ala
85 90 95
Met Lys Val Thr Ala Leu
100

(2) INFORMATION FOR SEQ ID NO:2644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..437
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2644:

acatcaccag cgcacagctt tcctcatcga ggcccagagtc ctgctctgat ggcgaccgac	60
gtggctgaga ctcccgcgcc gttggtggat gcggcccctg aggcgcccgc ggacaccccgc	120
gcggcgctgc tgttgacgcg amscggccaa ggccaagaag gccacagcgc cgaagaagcg	180
cgccassccg acccatccgc cgtacgccga gatggtctcg gaggcgatcg cgtcgctcaa	240
ggagaggacg gggtcacgca gctttgctat tgccaagtgc ttggaggaca agcacaagga	300
caagctcccc cccaacttcc gcaagcttct gaacgttcag ctcaagaagc tcgtcgccgcg	360
cggcaagctg accaaggtga agaactcgta caagctgtcg tccgccacca agccaaaag	420
ccgccccgaa gaagacc	

(2) INFORMATION FOR SEQ ID NO:2645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..145
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2645:

Thr Ser Pro Ala His Ser Phe Pro His Arg Gly Pro Ser Pro Ala Leu	
1 5 10 15	
Met Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala	
20 25 30	
Pro Glu Ala Pro Ala Asp Thr Pro Ala Ala Leu Leu Leu Thr Arg Xaa	
35 40 45	
Gly Gln Gly Gln Glu Gly His Ser Ala Glu Glu Ala Arg Xaa Xaa Asp	
50 55 60	
Pro Ser Ala Val Arg Arg Asp Gly Leu Gly Gly Asp Arg Val Ala Gln	
65 70 75 80	
Gly Glu Asp Gly Val Gln Gln Leu Cys Tyr Cys Gln Val Leu Gly Gly	
85 90 95	
Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu Arg	
100 105 110	
Ser Ala Gln Glu Ala Arg Arg Arg Gln Ala Asp Gln Gly Glu Glu	
115 120 125	
Leu Val Gln Ala Val Val Arg His Gln Ala Lys Arg Pro Pro Arg Arg	
130 135 140	

Arg
145

(2) INFORMATION FOR SEQ ID NO:2646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..129
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2646:

Met Ala Thr Asp Val Ala Glu Thr Pro Ala Pro Leu Val Asp Ala Ala
1 5 10 15
Pro Glu Ala Pro Ala Asp Thr Pro Ala Ala Leu Leu Leu Thr Arg Xaa
20 25 30
Gly Gln Gly Gln Glu Gly His Ser Ala Glu Glu Ala Arg Xaa Xaa Asp
35 40 45
Pro Ser Ala Val Arg Arg Asp Gly Leu Gly Gly Asp Arg Val Ala Gln
50 55 60
Gly Glu Asp Gly Val Gln Gln Leu Cys Tyr Cys Gln Val Leu Gly Gly
65 70 75 80
Gln Ala Gln Gly Gln Ala Pro Ala Gln Leu Pro Gln Ala Ser Glu Arg
85 90 95
Ser Ala Gln Glu Ala Arg Arg Arg Arg Gln Ala Asp Gln Gly Glu Glu
100 105 110
Leu Val Gln Ala Val Val Arg His Gln Ala Lys Arg Pro Pro Arg Arg
115 120 125
Arg

(2) INFORMATION FOR SEQ ID NO:2647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2647:

Met Val Ser Glu Ala Ile Ala Ser Leu Lys Glu Arg Thr Gly Ser Ser
1 5 10 15
Ser Phe Ala Ile Ala Lys Phe Leu Glu Asp Lys His Lys Asp Lys Leu
20 25 30
Pro Pro Asn Phe Arg Lys Leu Leu Asn Val Gln Leu Lys Lys Leu Val
35 40 45
Ala Gly Gly Lys Leu Thr Lys Val Lys Asn Ser Tyr Lys Leu Ser Ser
50 55 60
Ala Thr Lys Pro Lys Gly Arg Pro Glu Glu Asp
65 70 75

(2) INFORMATION FOR SEQ ID NO:2648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..257

(D) OTHER INFORMATION: / Ceres Seq. ID 1504119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2648:

cacccaaaag	cgagagscgn	gggctggtgg	ctgctgacca	aaacgaatcc	ctcgccgccc	60
cttcccga	ttccccaaat	ccggagccaa	tgccgcccgc	ccctcccacc	ccggcgccac	120
ncaaaaactat	cgccgacttc	ttcgcgcgcc	ccgccaagcg	cctgtgctg	ccccggccgc	180
ctccctctcc	tccaactcct	ctccctcctc	gctgtcgccg	gagcagcgcc	gtcgcgscga	240
caccaacctg	gcgctcg					

(2) INFORMATION FOR SEQ ID NO:2649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1504120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2649:

His	Pro	Lys	Ala	Arg	Xaa	Xaa	Gly	Trp	Trp	Leu	Leu	Thr	Lys	Thr	Asn
1					5				10					15	
Pro	Ser	Pro	Pro	Leu	Pro	Glu	Ile	Pro	Gln	Ile	Arg	Ser	Gln	Cys	Arg
			20					25					30		
Arg	Pro	Leu	Pro	Pro	Arg	Arg	His	Xaa	Lys	Leu	Ser	Pro	Thr	Ser	Ser
		35					40					45			
Arg	Ala	Pro	Pro	Ser	Ala	Cys	Ala	Cys	Pro	Gly	Arg	Leu	Pro	Leu	Leu
	50					55				60					
Gln	Leu	Leu	Ser	Leu	Leu	Ala	Val	Ala	Gly	Ala	Ala	Pro	Ser	Xaa	Arg
65					70				75						80
His	Gln	Pro	Gly	Ala											
															85

(2) INFORMATION FOR SEQ ID NO:2650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85

(D) OTHER INFORMATION: / Ceres Seq. ID 1504121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2650:

Pro	Lys	Ser	Glu	Xaa	Xaa	Gly	Leu	Val	Ala	Ala	Asp	Gln	Asn	Glu	Ser
1				5					10					15	
Leu	Ala	Ala	Ala	Ser	Arg	Asn	Pro	Pro	Asn	Pro	Glu	Pro	Met	Pro	Pro
			20					25					30		
Ser	Pro	Pro	Thr	Pro	Ala	Ala	Xaa	Lys	Thr	Ile	Ala	Asp	Phe	Phe	Ala
		35					40				45				
Arg	Pro	Ala	Lys	Arg	Leu	Cys	Val	Pro	Arg	Pro	Pro	Pro	Ser	Pro	Pro
	50					55				60					
Thr	Pro	Leu	Pro	Pro	Arg	Cys	Arg	Arg	Ser	Ser	Ala	Val	Ala	Xaa	Thr
65					70				75						80
Pro	Thr	Trp	Arg	Ser											
															85

(2) INFORMATION FOR SEQ ID NO:2651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1504122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2651:

```
Met Pro Pro Ser Pro Pro Thr Pro Ala Ala Xaa Lys Thr Ile Ala Asp
1          5          10          15
Phe Phe Ala Arg Pro Ala Lys Arg Leu Cys Val Pro Arg Pro Pro Pro
20          25          30
Ser Pro Pro Thr Pro Leu Pro Pro Arg Cys Arg Arg Ser Ser Ala Val
35          40          45
Ala Xaa Thr Pro Thr Trp Arg Ser
50          55
```

(2) INFORMATION FOR SEQ ID NO:2652:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..426

(D) OTHER INFORMATION: / Ceres Seq. ID 1504161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2652:

```
acgcgcctcc tctcgccctc gtcgcgcgc gcgcgcgcgc gccgcatcaw gcacccgccc      60
cgccgctgcc tgaggtagac accaatccgc cgccatgdgg sstatgcaca gccgcgggaa      120
ctggagggaac tgagcggtgg ggcccncgcg gccaaagttat cctgttcgct accgtgttgt      180
ttaccctagt ccagagtgtt tatcttcgtt cgtctcgtgt ttgttggtgc ccatctgtgt      240
ttttgattga aggtcgtctt gtgtcagttg ttagtgctgt gttcatcctc ggctccagca      300
gacccatgca tcaaccagca tggactgcgg atcgatgggt gctgttaccc ccgtcagctt      360
tattctaagt taaatcctaa ggaaaaaaat ggtgcttctt ggtgctgcaa aatggttgtg      420
ctcatg
```

(2) INFORMATION FOR SEQ ID NO:2653:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1504162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2653:

```
Ala Pro Pro Leu Ala Leu Ala Pro Pro Pro Pro Pro Pro Pro His Xaa
1          5          10          15
Ala Pro Ala Pro Pro Ser Pro Glu Val Asp Thr Asn Pro Pro Pro Xaa
20          25          30
Xaa Xaa Cys Thr Ala Ala Gly Thr Gly Gly Thr Glu Arg Trp Gly Xaa
35          40          45
Arg Gly Gln Val Ile Leu Phe Ala Thr Val Leu Phe Thr Leu Val Gln
50          55          60
Ser Val Tyr Leu Arg Ser Ser Arg Val Cys Cys Cys Pro Ser Val Phe
65          70          75          80
Leu Ile Glu Gly Arg Ser Val Ser Val Val Ser Ala Val Phe Ile Leu
85          90          95
Gly Ser Ser Arg Pro Met His Gln Pro Ala Trp Thr Ala Asp Arg Trp
100          105          110
Val Leu Leu Pro Pro Ser Ala Leu Phe
```

115 120
(2) INFORMATION FOR SEQ ID NO:2654:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 194 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..194
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504170
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2654:
acccacccca tccaaggccc tcccaaagtc ccaaaggccg ccgcccggcg ccagcccacc 60
atggcgcgcg agtccttctt cctcgccgcc actgcccggc ccagtccccc gcggtcttcg 120
ccgctcccta ttctctccgca cgccctttcc actcggtcca cttcgtcgcc ggcccgtggg 180
gcgcccggcg cgcc

(2) INFORMATION FOR SEQ ID NO:2655:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..64
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504171
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2655:
Thr His Pro Ile Gln Gly Pro Pro Lys Val Pro Lys Ala Ala Ala Ala
1 5 10 15
Arg Gln Pro Thr Met Ala Ala Gln Ser Phe Leu Leu Ala Ala Thr Ala
20 25 30
Ala Ala Ser Pro Pro Arg Ser Ser Pro Leu Pro Ile Pro Pro His Ala
35 40 45
Leu Ser Thr Arg Ser Thr Ser Ser Pro Ala Arg Gly Ala Pro Pro Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:2656:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..64
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504172
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2656:
Pro Thr Pro Ser Lys Ala Leu Pro Lys Ser Gln Arg Pro Pro Pro Pro
1 5 10 15
Ala Ser Pro Pro Trp Pro Arg Ser Pro Ser Ser Ser Pro Pro Leu Pro
20 25 30
Pro Pro Val Pro Arg Gly Leu Arg Arg Ser Leu Phe Leu Arg Thr Pro
35 40 45
Phe Pro Leu Gly Pro Leu Arg Arg Arg Pro Val Gly Arg Arg Arg Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO:2657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2657:

```
Pro Pro His Pro Arg Pro Ser Gln Ser Pro Lys Gly Arg Arg Pro
1           5           10           15
Pro Ala His His Gly Arg Ala Val Leu Pro Pro Arg Arg His Cys Arg
                20           25           30
Arg Gln Ser Pro Ala Val Phe Ala Ala Pro Tyr Ser Ser Ala Arg Pro
        35           40           45
Phe His Ser Val His Phe Val Ala Gly Pro Trp Gly Ala Ala Ala Ala
50           55           60
```

(2) INFORMATION FOR SEQ ID NO:2658:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..185
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2658:

```
tagcaaaata tggtttaagt gatgatacag tggatttcat tggacatgca cttgctcttc      60
atagagatga tcgctatctt gatgaaccgg cacttgatac agtgaaaagg atgaaactat      120
attcagagtc tcttgcgcg cttcaaggag gctcgccata tatctatcca wtgtatggtc      180
ygggt
```

(2) INFORMATION FOR SEQ ID NO:2659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..61
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2659:

```
Ala Lys Tyr Gly Leu Ser Asp Asp Thr Val Asp Phe Ile Gly His Ala
1           5           10           15
Leu Ala Leu His Arg Asp Asp Arg Tyr Leu Asp Glu Pro Ala Leu Asp
        20           25           30
Thr Val Lys Arg Met Lys Leu Tyr Ser Glu Ser Leu Ala Arg Phe Gln
        35           40           45
Gly Gly Ser Pro Tyr Ile Tyr Pro Xaa Tyr Gly Xaa Gly
50           55           60
```

(2) INFORMATION FOR SEQ ID NO:2660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..509
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2660:

caattccaat cccaatccca ccagtgtcca gtgctcgggg aacgacacag ctctcagca	60
gagaagccag cagcacaagc cggatcagca gacagcaggc atggcgctcg cggaggccga	120
cgacggcgcg gtggtcttcg gcgaggagca ggaggcgctg gtgctcaagt cgtgggccgt	180
catgaagaag gacgccgcca acctgggcct ccgcttcttc ctcaaggtct tcgagatcgc	240
gccgtcggaa gcagatgttc tegtccctgc gcgactccga cgtgccgctg gagaagaacc	300
ccaagctcaa gacgcacgcc atgtccgtct tcgtcatgac ctgcgaggcg gcggcgcast	360
tccgcaaggc cgggaaggtc accgtgagga gaccacgctc aagaggctgg gcgccacgca	420
cttgaggtac ggcgtcgcag atggacactt cgaggtgacg gggttcgcgc tgcttgagac	480
gatcaaggag gcgctccccg ctgacatgt	

(2) INFORMATION FOR SEQ ID NO:2661:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..112
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2661:

Gln	Phe	Gln	Ser	Gln	Ser	His	Gln	Cys	Pro	Val	Leu	Gly	Glu	Arg	His
1			5					10						15	
Ser	Ser	Ser	Ala	Glu	Lys	Pro	Ala	Arg	Gln	Ala	Arg	Ser	Ala	Asp	Ser
			20					25					30		
Arg	His	Gly	Ala	Arg	Gly	Gly	Arg	Arg	Arg	Arg	Gly	Gly	Leu	Arg	Arg
		35					40					45			
Gly	Ala	Gly	Gly	Ala	Gly	Ala	Gln	Val	Val	Gly	Arg	His	Glu	Glu	Gly
	50					55				60					
Arg	Arg	Gln	Pro	Gly	Pro	Pro	Leu	Leu	Pro	Gln	Gly	Leu	Arg	Asp	Arg
65					70					75				80	
Ala	Val	Gly	Ser	Arg	Cys	Ser	Arg	Ser	Cys	Ala	Thr	Pro	Thr	Cys	Arg
			85						90					95	
Trp	Arg	Arg	Thr	Pro	Ser	Ser	Arg	Arg	Thr	Pro	Cys	Pro	Ser	Ser	Ser
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:2662:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 169 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..169
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504182

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2662:

Asn	Ser	Asn	Pro	Asn	Pro	Thr	Ser	Val	Gln	Cys	Ser	Gly	Asn	Asp	Thr
1				5					10				15		
Ala	Pro	Gln	Gln	Arg	Ser	Gln	His	Asp	Lys	Pro	Asp	Gln	Gln	Thr	Ala

	20		25		30
Gly Met Ala Leu Ala Glu Ala Asp Asp Gly Ala Val Val Phe Gly Glu					
	35		40		45
Glu Gln Glu Ala Leu Val Leu Lys Ser Trp Ala Val Met Lys Lys Asp					
	50		55		60
Ala Ala Asn Leu Gly Leu Arg Phe Phe Leu Lys Val Phe Glu Ile Ala					
65		70		75	80
Pro Ser Glu Ala Asp Val Leu Val Pro Ala Arg Leu Arg Arg Ala Ala					
	85		90		95
Gly Glu Glu Pro Gln Ala Gln Asp Ala Arg His Val Arg Leu Arg His					
	100		105		110
Asp Leu Arg Gly Gly Gly Ala Xaa Pro Gln Gly Arg Glu Gly His Arg					
	115		120		125
Glu Glu Thr Thr Leu Lys Arg Leu Gly Ala Thr His Leu Arg Tyr Gly					
	130		135		140
Val Ala Asp Gly His Phe Glu Val Thr Gly Phe Ala Leu Leu Glu Thr					
145		150		155	160
Ile Lys Glu Ala Leu Pro Ala Asp Met					
	165				

(2) INFORMATION FOR SEQ ID NO:2663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1504183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2663:

Met Ala Leu Ala Glu Ala Asp Asp Gly Ala Val Val Phe Gly Glu Glu					
1		5		10	15
Gln Glu Ala Leu Val Leu Lys Ser Trp Ala Val Met Lys Lys Asp Ala					
	20		25		30
Ala Asn Leu Gly Leu Arg Phe Phe Leu Lys Val Phe Glu Ile Ala Pro					
	35		40		45
Ser Glu Ala Asp Val Leu Val Pro Ala Arg Leu Arg Arg Ala Ala Gly					
	50		55		60
Glu Glu Pro Gln Ala Gln Asp Ala Arg His Val Arg Leu Arg His Asp					
65		70		75	80
Leu Arg Gly Gly Gly Ala Xaa Pro Gln Gly Arg Glu Gly His Arg Glu					
	85		90		95
Glu Thr Thr Leu Lys Arg Leu Gly Ala Thr His Leu Arg Tyr Gly Val					
	100		105		110
Ala Asp Gly His Phe Glu Val Thr Gly Phe Ala Leu Leu Glu Thr Ile					
	115		120		125
Lys Glu Ala Leu Pro Ala Asp Met					
	130		135		

(2) INFORMATION FOR SEQ ID NO:2664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 491 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..491

(D) OTHER INFORMATION: / Ceres Seq. ID 1504184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2664:

ttagcatgcc	tacaattgtt	catcgagatc	tgaaatctcc	aaacttgctg	gttgacaata	60
attggaatgt	taaggtttgt	gactttggac	tttcgcggtt	gaagcacagt	acatttttgt	120
catccaaatc	tacagctggw	acacctgagt	ggatggcacc	tgaggttctg	cggaatgaac	180
aatcgaatga	aaagtgtgat	gtttatagct	ttggtgtcat	cttatgggaa	ctggcaacac	240
ttagaatgcc	atggagtggg	atgaatccaa	tgcaagttgt	gggggcagtt	ggtttccagg	300
atagacggct	tgatattccc	aaggaagttg	atcctctggt	cgcaaggata	atatttgaat	360
gctggcgaaa	ggatccaaat	ttgcgcccg	catttgcaca	gttaacaagt	gccctgaaga	420
ctgttcaaag	actagtgacc	ctttgtcacc	aggagaacca	gagcccatg	ttcaacaaga	480
aatctcagtg	c					

(2) INFORMATION FOR SEQ ID NO:2665:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 1504185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2665:

Ser	Met	Pro	Thr	Ile	Val	His	Arg	Asp	Leu	Lys	Ser	Pro	Asn	Leu	Leu	
1				5					10					15		
Val	Asp	Asn	Asn	Trp	Asn	Val	Lys	Val	Cys	Asp	Phe	Gly	Leu	Ser	Arg	
		20						25					30			
Leu	Lys	His	Ser	Thr	Phe	Leu	Ser	Ser	Lys	Ser	Thr	Ala	Xaa	Thr	Pro	
		35					40					45				
Glu	Trp	Met	Ala	Pro	Glu	Val	Leu	Arg	Asn	Glu	Gln	Ser	Asn	Glu	Lys	
	50					55				60						
Cys	Asp	Val	Tyr	Ser	Phe	Gly	Val	Ile	Leu	Trp	Glu	Leu	Ala	Thr	Leu	
65					70					75				80		
Arg	Met	Pro	Trp	Ser	Gly	Met	Asn	Pro	Met	Gln	Val	Val	Gly	Ala	Val	
			85						90					95		
Gly	Phe	Gln	Asp	Arg	Arg	Leu	Asp	Ile	Pro	Lys	Glu	Val	Asp	Pro	Leu	
		100					105						110			
Val	Ala	Arg	Ile	Ile	Phe	Glu	Cys	Trp	Gln	Lys	Asp	Pro	Asn	Leu	Arg	
	115						120					125				
Pro	Ser	Phe	Ala	Gln	Leu	Thr	Ser	Ala	Leu	Lys	Thr	Val	Gln	Arg	Leu	
	130					135					140					
Val	Thr	Leu	Cys	His	Gln	Glu	Asn	Gln	Ser	Pro	Met	Phe	Asn	Lys	Lys	
145					150					155					160	
Ser	Gln	Cys														

(2) INFORMATION FOR SEQ ID NO:2666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..162

(D) OTHER INFORMATION: / Ceres Seq. ID 1504186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2666:

Met	Pro	Thr	Ile	Val	His	Arg	Asp	Leu	Lys	Ser	Pro	Asn	Leu	Leu	Val	
1				5					10					15		
Asp	Asn	Asn	Trp	Asn	Val	Lys	Val	Cys	Asp	Phe	Gly	Leu	Ser	Arg	Leu	
		20						25					30			
Lys	His	Ser	Thr	Phe	Leu	Ser	Ser	Lys	Ser	Thr	Ala	Xaa	Thr	Pro	Glu	
		35					40					45				

Trp Met Ala Pro Glu Val Leu Arg Asn Glu Gln Ser Asn Glu Lys Cys
50 55 60
Asp Val Tyr Ser Phe Gly Val Ile Leu Trp Glu Leu Ala Thr Leu Arg
65 70 75 80
Met Pro Trp Ser Gly Met Asn Pro Met Gln Val Val Gly Ala Val Gly
85 90 95
Phe Gln Asp Arg Arg Leu Asp Ile Pro Lys Glu Val Asp Pro Leu Val
100 105 110
Ala Arg Ile Ile Phe Glu Cys Trp Gln Lys Asp Pro Asn Leu Arg Pro
115 120 125
Ser Phe Ala Gln Leu Thr Ser Ala Leu Lys Thr Val Gln Arg Leu Val
130 135 140
Thr Leu Cys His Gln Glu Asn Gln Ser Pro Met Phe Asn Lys Lys Ser
145 150 155 160
Gln Cys

(2) INFORMATION FOR SEQ ID NO:2667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..113

(D) OTHER INFORMATION: / Ceres Seq. ID 1504187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2667:

Met Ala Pro Glu Val Leu Arg Asn Glu Gln Ser Asn Glu Lys Cys Asp
1 5 10 15
Val Tyr Ser Phe Gly Val Ile Leu Trp Glu Leu Ala Thr Leu Arg Met
20 25 30
Pro Trp Ser Gly Met Asn Pro Met Gln Val Val Gly Ala Val Gly Phe
35 40 45
Gln Asp Arg Arg Leu Asp Ile Pro Lys Glu Val Asp Pro Leu Val Ala
50 55 60
Arg Ile Ile Phe Glu Cys Trp Gln Lys Asp Pro Asn Leu Arg Pro Ser
65 70 75 80
Phe Ala Gln Leu Thr Ser Ala Leu Lys Thr Val Gln Arg Leu Val Thr
85 90 95
Leu Cys His Gln Glu Asn Gln Ser Pro Met Phe Asn Lys Lys Ser Gln
100 105 110
Cys

(2) INFORMATION FOR SEQ ID NO:2668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..482

(D) OTHER INFORMATION: / Ceres Seq. ID 1504192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2668:

aaagctggag tgaatccagc aggctgcttc tgaaaaaaaaa agtagcagat gcaacgagtg	60
cactocaatg ctgcagttac aatgcaatga ccgggtttgt tagtgagcta gcacgcgtcg	120
sggctccttg agggacaata atcatcgtga catggtgcc a taggaacctg gatccatccg	180
aaacctcgct aaagcccgat gaactgagcc tcctgaggag gatatgcgac gcgtactacc	240
tcccggactg gtgctcacct tcagactatg tgaacattgc caagtcactg tctctcgagg	300

atatcaagac agctgactgg tcggagaacg tggccccgtt ttggcccgcc gtgataaaat 360
cagcgctaac atggaagggc ttcacctctc tgctgacgac cggatggaag acgatcagag 420
gcgcgatggt gatgccgcta atgatccagg gctacaagaa ggggctcatc aaattcacca 480
tc

(2) INFORMATION FOR SEQ ID NO:2669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1504193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2669:

Ser	Trp	Ser	Glu	Ser	Ser	Arg	Leu	Leu	Leu	Lys	Lys	Lys	Val	Ala	Asp
1			5						10					15	
Ala	Thr	Ser	Ala	Leu	Gln	Cys	Cys	Ser	Tyr	Asn	Ala	Met	Thr	Gly	Phe
			20					25					30		
Val	Ser	Glu	Leu	Ala	Arg	Val	Xaa	Ala	Pro	Gly	Gly	Thr	Ile	Ile	Ile
			35				40					45			
Val	Thr	Trp	Cys	His	Arg	Asn	Leu	Asp	Pro	Ser	Glu	Thr	Ser	Leu	Lys
			50			55					60				
Pro	Asp	Glu	Leu	Ser	Leu	Arg	Arg	Ile	Cys	Asp	Ala	Tyr	Tyr	Leu	
65					70				75					80	
Pro	Asp	Trp	Cys	Ser	Pro	Ser	Asp	Tyr	Val	Asn	Ile	Ala	Lys	Ser	Leu
			85					90						95	
Ser	Leu	Glu	Asp	Ile	Lys	Thr	Ala	Asp	Trp	Ser	Glu	Asn	Val	Ala	Pro
			100				105						110		
Phe	Trp	Pro	Ala	Val	Ile	Lys	Ser	Ala	Leu	Thr	Trp	Lys	Gly	Phe	Thr
			115				120					125			
Ser	Leu	Leu	Thr	Thr	Gly	Trp	Lys	Thr	Ile	Arg	Gly	Ala	Met	Val	Met
			130				135				140				
Pro	Leu	Met	Ile	Gln	Gly	Tyr	Lys	Lys	Gly	Leu	Ile	Lys	Phe	Thr	Ile
145				150						155					160

(2) INFORMATION FOR SEQ ID NO:2670:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..132

(D) OTHER INFORMATION: / Ceres Seq. ID 1504194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2670:

Met	Thr	Gly	Phe	Val	Ser	Glu	Leu	Ala	Arg	Val	Xaa	Ala	Pro	Gly	Gly
1				5					10					15	
Thr	Ile	Ile	Ile	Val	Thr	Trp	Cys	His	Arg	Asn	Leu	Asp	Pro	Ser	Glu
				20				25					30		
Thr	Ser	Leu	Lys	Pro	Asp	Glu	Leu	Ser	Leu	Leu	Arg	Arg	Ile	Cys	Asp
			35				40					45			
Ala	Tyr	Tyr	Leu	Pro	Asp	Trp	Cys	Ser	Pro	Ser	Asp	Tyr	Val	Asn	Ile
			50				55				60				
Ala	Lys	Ser	Leu	Ser	Leu	Glu	Asp	Ile	Lys	Thr	Ala	Asp	Trp	Ser	Glu
65				70					75					80	
Asn	Val	Ala	Pro	Phe	Trp	Pro	Ala	Val	Ile	Lys	Ser	Ala	Leu	Thr	Trp

85 90 95
Lys Gly Phe Thr Ser Leu Leu Thr Thr Gly Trp Lys Thr Ile Arg Gly
100 105 110
Ala Met Val Met Pro Leu Met Ile Gln Gly Tyr Lys Lys Gly Leu Ile
115 120 125
Lys Phe Thr Ile
130

(2) INFORMATION FOR SEQ ID NO:2671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..511
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2671:

agcggttaga	gagagagaag	acagggagaa	ggaggaagag	ccgccgcgnt	ggaccgggtg	60
atttgtcagg	gttgtcaggg	gagtcgtcag	gacacgggca	agctttgtac	gctaccaatt	120
cagcgaataa	ccgacggggg	tgcgtggaat	tgctcaccgg	agcaaaccct	ccgccgccga	180
accaccatcc	ttctgagcag	cgcacgctag	cgtccggttc	ctggacgcac	gccgtgaact	240
cgaagtccac	cgctctgtga	gcatcaagcg	ccggcatcgc	tagggtttca	cgcccccatc	300
cccccagggc	gccgtcgatc	ccggtcggcc	atctcccggg	gcctggtaac	tgatcgttaa	360
tttcatcgat	gggtgccatg	gaggaccgca	gctccaagca	ggcaggcgcg	ggcttggtgg	420
cccacctcca	cgacgacctc	cttgtggaga	tcctctcccc	cgtccccgcc	aagtcctgtc	480
gccggttcaa	gtgcgtgtcc	aaggcctggc	t			

(2) INFORMATION FOR SEQ ID NO:2672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2672:

Arg	Leu	Glu	Arg	Glu	Lys	Thr	Gly	Arg	Arg	Arg	Lys	Ser	Arg	Arg	Xaa
1				5				10						15	
Gly	Pro	Gly	Asp	Leu	Ser	Gly	Leu	Ser	Gly	Glu	Ser	Ser	Gly	His	Gly
			20				25						30		
Gln	Ala	Leu	Tyr	Ala	Thr	Asn	Ser	Ala	Asn	Asn	Arg	Arg	Gly	Cys	Val
		35				40					45				
Glu	Leu	Leu	Thr	Gly	Ala	Asn	Pro	Pro	Pro	Pro	Asn	His	His	Pro	Ser
	50				55						60				
Glu	Gln	Arg	Thr	Leu	Ala	Ser	Gly	Ser	Trp	Thr	His	Ala	Val	Asn	Ser
65				70						75				80	
Lys	Ser	Thr	Ala	Leu											
				85											

(2) INFORMATION FOR SEQ ID NO:2673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1504203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2673:

Met Gly Ala Met Glu Asp Arg Ser Ser Lys Gln Ala Gly Ala Gly Leu
1 5 10 15
Val Ala His Leu His Asp Asp Leu Leu Val Glu Ile Leu Ser Arg Val
20 25 30
Pro Ala Lys Ser Val Cys Arg Phe Lys Cys Val Ser Lys Ala Trp
35 40 45

(2) INFORMATION FOR SEQ ID NO:2674:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1504204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2674:

Met Glu Asp Arg Ser Ser Lys Gln Ala Gly Ala Gly Leu Val Ala His
1 5 10 15
Leu His Asp Asp Leu Leu Val Glu Ile Leu Ser Arg Val Pro Ala Lys
20 25 30
Ser Val Cys Arg Phe Lys Cys Val Ser Lys Ala Trp
35 40

(2) INFORMATION FOR SEQ ID NO:2675:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..436

(D) OTHER INFORMATION: / Ceres Seq. ID 1504231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2675:

cattgtcaat ttctcccagg ataaatcatg gcgtgttcgt tatatggtcg ccaatcagtt 60
atatgagctc tgtgaggctg ttggccctga gccacaaga gctgatttgg tgccctgcata 120
tgttcgtctc cttcgcgata atgaggctga agtgccaata gcggctgctg gaaaagtaac 180
taagttctgc cgcataattaa atccacagct ttcaatccaa catattcttc cgtgcgttaa 240
ggaattgtca tcatattcat cccagcatgt tcgttcagct ttagcctcag tcattatggg 300
aatggctcct gtactgggaa aggatgctac catggaacag cttcttccaa tttttctctc 360
tttgctgaag gatgaatttc cagatgttcg gcttaacata atcagcaagc ttgatcaggt 420
taatcaggtt attggc

(2) INFORMATION FOR SEQ ID NO:2676:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1504232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2676:

Ile Val Asn Phe Ser Gln Asp Lys Ser Trp Arg Val Arg Tyr Met Val
1 5 10 15

Ala Asn Gln Leu Tyr Glu Leu Cys Glu Ala Val Gly Pro Glu Pro Thr
20 25 30
Arg Ala Asp Leu Val Pro Ala Tyr Val Arg Leu Leu Arg Asp Asn Glu
35 40 45
Ala Glu Val Arg Ile Ala Ala Ala Gly Lys Val Thr Lys Phe Cys Arg
50 55 60
Ile Leu Asn Pro Gln Leu Ser Ile Gln His Ile Leu Pro Cys Val Lys
65 70 75 80
Glu Leu Ser Ser Tyr Ser Ser Gln His Val Arg Ser Ala Leu Ala Ser
85 90 95
Val Ile Met Gly Met Ala Pro Val Leu Gly Lys Asp Ala Thr Met Glu
100 105 110
Gln Leu Leu Pro Ile Phe Leu Ser Leu Leu Lys Asp Glu Phe Pro Asp
115 120 125
Val Arg Leu Asn Ile Ile Ser Lys Leu Asp Gln Val Asn Gln Val Ile
130 135 140
Gly
145

(2) INFORMATION FOR SEQ ID NO:2677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..131
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2677:

Met Val Ala Asn Gln Leu Tyr Glu Leu Cys Glu Ala Val Gly Pro Glu
1 5 10 15
Pro Thr Arg Ala Asp Leu Val Pro Ala Tyr Val Arg Leu Leu Arg Asp
20 25 30
Asn Glu Ala Glu Val Arg Ile Ala Ala Ala Gly Lys Val Thr Lys Phe
35 40 45
Cys Arg Ile Leu Asn Pro Gln Leu Ser Ile Gln His Ile Leu Pro Cys
50 55 60
Val Lys Glu Leu Ser Ser Tyr Ser Ser Gln His Val Arg Ser Ala Leu
65 70 75 80
Ala Ser Val Ile Met Gly Met Ala Pro Val Leu Gly Lys Asp Ala Thr
85 90 95
Met Glu Gln Leu Leu Pro Ile Phe Leu Ser Leu Leu Lys Asp Glu Phe
100 105 110
Pro Asp Val Arg Leu Asn Ile Ile Ser Lys Leu Asp Gln Val Asn Gln
115 120 125
Val Ile Gly
130

(2) INFORMATION FOR SEQ ID NO:2678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..446
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504239

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2678:

cgatcctttt atccgtaact atattgagga cttattgaag aacatcagaa cccaagtgtc

gctcaagctt attaaacat atactcgaat caggatacca ttcatttcac aggaactcaa 120
ttttccagaa aaggatgtcg agcagctggt ggtgtcactc attctggaca accgtatcca 180
aggccacata gatcaggtta acaagctgct agaacgtgga gaaaggtcca aggggatgag 240
gaagtacaat gctatcgaca agtggataac tcagctgaag tccatttacc aaacattgtc 300
caacagagtt tgatgaggag gatcgtgctgct gctgctgcgt gcattgcaca cctagaattg 360
ttgatagcct gttttgtgga tttgaggga actgcaaaga actgtctggt gacgcttgcg 420
atagaatcct ggatctgggt aaagtt

(2) INFORMATION FOR SEQ ID NO:2679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..103
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2679:

Asp Pro Phe Ile Arg Asn Tyr Ile Glu Asp Leu Leu Lys Asn Ile Arg
1 5 10 15
Thr Gln Val Leu Leu Lys Leu Ile Lys Pro Tyr Thr Arg Ile Arg Ile
20 25 30
Pro Phe Ile Ser Gln Glu Leu Asn Phe Pro Glu Lys Asp Val Glu Gln
35 40 45
Leu Leu Val Ser Leu Ile Leu Asp Asn Arg Ile Gln Gly His Ile Asp
50 55 60
Gln Val Asn Lys Leu Leu Glu Arg Gly Glu Arg Ser Lys Gly Met Arg
65 70 75 80
Lys Tyr Asn Ala Ile Asp Lys Trp Asn Thr Gln Leu Lys Ser Ile Tyr
85 90 95
Gln Thr Leu Ser Asn Arg Val
100

(2) INFORMATION FOR SEQ ID NO:2680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..326
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2680:

gtttttctctt gatcgctttg tcaacttgaat ccgtgcctgc tctaacagag agcggagacg 60
accacgacga cggcgaggcc aggctctgct atggagcagg agccgcaccg gcccatggag 120
ctgcccccg gcttccgctt ccacccgacc gacgaggagn tcatcacgca ctacctggcc 180
cgcaaggcgc cgacgcccgc ttcgccgcgc ttgccgtcgc cgaggccgac ctcaacaagt 240
gcgagccctg ggacctgcca tcgctggcga ggatggggga gaaggagtgg tacttcttct 300
gcctcaagga ccgcaagtac ccgacg

(2) INFORMATION FOR SEQ ID NO:2681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1504255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2681:

Phe Leu Leu Ile Ala Leu Ser Leu Glu Ser Val Pro Ala Leu Thr Glu
1 5 10 15
Ser Gly Asp Asp His Asp Asp Gly Glu Ala Arg Leu Cys Asp Gly Ala
20 25 30
Gly Ala Ala Pro Ala His Gly Ala Ala Pro Gly Leu Pro Leu Pro Pro
35 40 45
Asp Arg Arg Gly Xaa His His Ala Leu Pro Gly Pro Gln Gly Ala Asp
50 55 60
Ala Arg Phe Ala Ala Leu Ala Val Ala Glu Ala Asp Leu Asn Lys Cys
65 70 75 80
Glu Pro Trp Asp Leu Pro Ser Leu Ala Arg Met Gly Glu Lys Glu Trp
85 90 95
Tyr Phe Phe Cys Leu Lys Asp Arg Lys Tyr Pro Thr
100 105

(2) INFORMATION FOR SEQ ID NO:2682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1504256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2682:

Met Glu Gln Glu Pro His Arg Pro Met Glu Leu Pro Pro Gly Phe Arg
1 5 10 15
Phe His Pro Thr Asp Glu Glu Xaa Ile Thr His Tyr Leu Ala Arg Lys
20 25 30
Ala Pro Thr Pro Ala Ser Pro Arg Leu Pro Ser Pro Arg Pro Thr Ser
35 40 45
Thr Ser Ala Ser Pro Gly Thr Cys His Arg Trp Arg Gly Trp Gly Arg
50 55 60
Arg Ser Gly Thr Ser Ser Ala Ser Arg Thr Ala Ser Thr Arg
65 70 75

(2) INFORMATION FOR SEQ ID NO:2683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1504257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2683:

Met Glu Leu Pro Pro Gly Phe Arg Phe His Pro Thr Asp Glu Glu Xaa
1 5 10 15
Ile Thr His Tyr Leu Ala Arg Lys Ala Pro Thr Pro Ala Ser Pro Arg
20 25 30
Leu Pro Ser Pro Arg Pro Thr Ser Thr Ser Ala Ser Gly Thr Cys
35 40 45
His Arg Trp Arg Gly Trp Gly Arg Arg Ser Gly Thr Ser Ser Ala Ser
50 55 60
Arg Thr Ala Ser Thr Arg
65 70

(2) INFORMATION FOR SEQ ID NO:2684:

2025 RELEASE UNDER E.O. 14176

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..307
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504258
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2684:
aattccctc cctgtcgtc gtctccctc acccgaagcc ccgdttcgaa accggcggcg 60
ttcgatttgg ggatttcggc gtctcgctcc ccggaatttc ttggatctga gtctgtccgc 120
cgtcttcgat ttgcggctgc agtgagcctg cgagttttcc ggctctgatt tggwcggggh 180
cttcgatttc ggggatggcg tcgtctcccg tgcctactg gtgctacagc tgcagccgct 240
tcgtgagggt atctccgtcc accgtygtct gcccggagtg cgatggcggc ttcctggagc 300
agtttac
(2) INFORMATION FOR SEQ ID NO:2685:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..55
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504259
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2685:
Asn Ser Pro Pro Leu Ser Ser Ser Pro Leu Thr Arg Ser Pro Xaa Ser
1 5 10 15
Lys Pro Ala Ala Phe Asp Leu Gly Ile Ser Ala Ser Arg Ser Pro Glu
20 25 30
Phe Leu Gly Ser Glu Ser Val Arg Arg Leu Arg Phe Ala Ala Val
35 40 45
Ser Leu Arg Val Phe Arg Leu
50 55
(2) INFORMATION FOR SEQ ID NO:2686:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..47
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504260
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2686:
Ile Pro Leu Pro Cys Arg Arg Leu Pro Ser Pro Glu Ala Pro Xaa Arg
1 5 10 15
Asn Arg Arg Arg Ser Ile Trp Gly Phe Arg Arg Leu Ala Pro Arg Asn
20 25 30
Phe Leu Asp Leu Ser Leu Ser Ala Val Phe Asp Leu Arg Leu Gln
35 40 45
(2) INFORMATION FOR SEQ ID NO:2687:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..37

(D) OTHER INFORMATION: / Ceres Seq. ID 1504261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2687:

Met Ala Ser Ser Pro Val Ser Tyr Trp Cys Tyr Ser Cys Ser Arg Phe
1 5 10 15
Val Arg Val Ser Pro Ser Thr Xaa Val Cys Pro Glu Cys Asp Gly Gly
20 25 30
Phe Leu Glu Gln Phe
35

(2) INFORMATION FOR SEQ ID NO:2688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..234

(D) OTHER INFORMATION: / Ceres Seq. ID 1504270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2688:

actcgcgtcg ssccccctcca ctgcaccagc gtcattggcgg tggcctcgac ctgcgcgtcg 60
tccgccaagc cgcacacggc cccctcgccg cccgctcccg gatccgggct cctcgtctc 120
ggcgttcgcs cggccccgc cactgccgcg tggaggaggc tccgcgtgga ggcgatcagg 180
acgcagcggg agaagcagcg ggcggaggtg cccgctcgagg agtccgcccc cgcc

(2) INFORMATION FOR SEQ ID NO:2689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1504271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2689:

Thr Arg Val Xaa Pro Leu His Cys Thr Ser Val Met Ala Val Ala Ser
1 5 10 15
Thr Ser Pro Leu Ser Ala Lys Pro Ala Thr Ala Pro Ser Pro Pro Ala
20 25 30
Pro Gly Ser Gly Leu Leu Ala Leu Gly Val Arg Xaa Ala Pro Ala Thr
35 40 45
Ala Ala Trp Arg Arg Leu Arg Val Glu Ala Ile Arg Thr Gln Arg Glu
50 55 60
Lys Gln Arg Ala Glu Val Pro Val Glu Glu Ser Ala Pro Ala
65 70 75

(2) INFORMATION FOR SEQ ID NO:2690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1504272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2690:

```
Leu Ala Ser Xaa Pro Ser Thr Ala Pro Ala Ser Trp Arg Trp Pro Arg
1          5          10          15
Pro Arg Arg Cys Pro Pro Ser Pro Pro Arg Pro Pro Arg Arg Pro Leu
20          25          30
Pro Asp Pro Gly Ser Ser Leu Ser Ala Phe Xaa Arg Pro Pro Leu
35          40          45
Pro Arg Gly Gly Gly Ser Ala Trp Arg Arg Ser Gly Arg Ser Gly Arg
50          55          60
Ser Ser Gly Arg Arg Cys Pro Ser Arg Ser Pro Pro Pro
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:2691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..77
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2691:

```
Ser Arg Xaa Xaa Pro Pro Leu His Gln Arg His Gly Gly Gly Leu Asp
1          5          10          15
Leu Ala Ala Val Arg Gln Ala Arg His Gly Pro Leu Ala Ala Arg Ser
20          25          30
Arg Ile Arg Ala Pro Arg Ser Arg Arg Ser Xaa Gly Pro Arg His Cys
35          40          45
Arg Val Glu Glu Ala Pro Arg Gly Gly Asp Gln Asp Ala Ala Gly Glu
50          55          60
Ala Ala Gly Gly Gly Ala Arg Arg Gly Val Arg Pro Arg
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:2692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..429
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2692:

```
agtcggagca gggcagggtg tgcgtctcag ttcttggttg tgttggtgta agtcacagg      60
tttcttctct tcgctgass tagctagagt gggatcgaga ggaagaagga tgcgtgctg      120
cggaggcaac tgcgggtgcg gcasggantg caagtgcggc assggctgcg gaggggtgcaa      180
gatgtacccg gacatggttg agcaggtgac caccaccacc accaccacaga ctctcatcat      240
gggtgttgcg ccattccacg gccaccgcgt tgctcccttc ggcagccagg atgacagaag      300
taccatttct gccgcgtgag aggctcttca agcagcaaca ttacttccag aacttgacca      360
agcacacctt cctgaaaggc gctacgacgt gatcacctcc gtcgccatcc cccttgcaact      420
cgctgcctc
```

(2) INFORMATION FOR SEQ ID NO:2693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..105
(D) OTHER INFORMATION: / Ceres Seq. ID 1504275
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2693:
Val Gly Ala Gly Gln Gly Leu Arg Leu Ser Ser Trp Leu Cys Cys Cys
1 5 10 15
Lys Leu Thr Gly Phe Phe Ser Ser Arg Xaa Xaa Ala Arg Val Gly Ser
20 25 30
Arg Gly Arg Arg Met Ser Cys Cys Gly Gly Asn Cys Gly Cys Gly Xaa
35 40 45
Xaa Cys Lys Cys Gly Xaa Gly Cys Gly Cys Lys Met Tyr Pro Asp
50 55 60
Met Val Glu Gln Val Thr Thr Thr Thr Thr Thr Gln Thr Leu Ile Met
65 70 75 80
Gly Val Ala Pro Ser Thr Gly His Arg Val Ala Pro Leu Gly Ser Gln
85 90 95
Asp Asp Arg Ser Thr Ile Ser Ala Ala
100 105

(2) INFORMATION FOR SEQ ID NO:2694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1504276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2694:

Met Ser Cys Cys Gly Gly Asn Cys Gly Cys Gly Xaa Xaa Cys Lys Cys
1 5 10 15
Gly Xaa Gly Cys Gly Gly Cys Lys Met Tyr Pro Asp Met Val Glu Gln
20 25 30
Val Thr Thr Thr Thr Thr Thr Gln Thr Leu Ile Met Gly Val Ala Pro
35 40 45
Ser Thr Gly His Arg Val Ala Pro Leu Gly Ser Gln Asp Asp Arg Ser
50 55 60
Thr Ile Ser Ala Ala
65

(2) INFORMATION FOR SEQ ID NO:2695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..244

(D) OTHER INFORMATION: / Ceres Seq. ID 1504277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2695:

agttgatccc atcggttccc ccttcctctt ccccgatccc ctctctcccc cgatcccato	60
caattccact tccacacccc gggcctcgcc gccgacgccg acgccgacgc cgccggccat	120
gtccaagtac ggcaccattc ccacctcttc ctccgcgggc ggaggggcccg tgccccctcg	180
cgcgctccc cgctcgattt catctccgc gcccaaggctc ggggcgcctc ggcstggg	240
acgc	

(2) INFORMATION FOR SEQ ID NO:2696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..81
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504278
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2696:

```
Val Asp Pro Ile Gly Phe Pro Phe Leu Phe Pro Asp Pro Leu Pro Pro
1          5          10          15
Pro Ile Pro Ser Asn Ser Thr Ser Thr Pro Arg Ala Ser Pro Pro Thr
          20          25          30
Pro Thr Pro Thr Pro Pro Ala Met Ser Lys Tyr Gly Thr Ile Pro Thr
          35          40          45
Ser Ser Ser Ala Gly Gly Gly Pro Val Pro Leu Gly Gly Ala Pro Arg
          50          55          60
Ser Ile Ser Ser Pro Ala Pro Arg Leu Gly Ala Pro Arg Xaa Gly Arg
65          70          75          80
Arg
```

(2) INFORMATION FOR SEQ ID NO:2697:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..80
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504279
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2697:

```
Leu Ile Pro Ser Ala Ser Pro Ser Ser Pro Ile Pro Phe Leu Pro
1          5          10          15
Arg Ser His Pro Ile Pro Leu Pro His Pro Gly Pro Arg Arg Arg Arg
          20          25          30
Arg Arg Arg Arg Arg Arg Pro Cys Pro Ser Thr Ala Pro Phe Pro Pro
          35          40          45
Pro Pro Pro Arg Ala Glu Gly Pro Cys Pro Ser Ala Ala Leu Pro Ala
          50          55          60
Arg Phe His Leu Pro Arg Gln Gly Ser Gly Arg Leu Gly Xaa Gly Asp
65          70          75          80
```

(2) INFORMATION FOR SEQ ID NO:2698:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..42
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504280
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2698:

```
Met Ser Lys Tyr Gly Thr Ile Pro Thr Ser Ser Ser Ala Gly Gly Gly
1          5          10          15
Pro Val Pro Leu Gly Gly Ala Pro Arg Ser Ile Ser Ser Pro Ala Pro
          20          25          30
Arg Leu Gly Ala Pro Arg Xaa Gly Arg Arg
```

35 40

(2) INFORMATION FOR SEQ ID NO:2699:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..231

(D) OTHER INFORMATION: / Ceres Seq. ID 1504299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2699:

cctgatttcc tgaacacag atcatcatca ttcattgtca tggctatggc aaactcggca 60
acgatcctga ccgtcgttct ggctctcggg ctacggttcc tccgcgccgc agctccggcc 120
tccgcgcaga actgcggctg cccgccaggc tactgctgca gcaagttcgg ttactgcggc 180
accagcttcg actactgcaa tgccaacacg tgccagtcgg gcccggtgcac g

(2) INFORMATION FOR SEQ ID NO:2700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1504300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2700:

Pro Asp Phe Leu Lys His Arg Ser Ser Phe Met Val Met Ala Met
1 5 10 15
Ala Asn Ser Ala Thr Ile Leu Thr Val Val Leu Ala Leu Gly Leu Ala
20 25 30
Phe Leu Arg Ala Ala Ala Pro Ala Ser Ala Gln Asn Cys Gly Cys Pro
35 40 45
Pro Gly Tyr Cys Cys Ser Lys Phe Gly Tyr Cys Gly Thr Ser Phe Asp
50 55 60
Tyr Cys Asn Ala Asn Thr Cys Gln Ser Gly Pro Cys Thr
65 70 75

(2) INFORMATION FOR SEQ ID NO:2701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1504301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2701:

Met Val Met Ala Met Ala Asn Ser Ala Thr Ile Leu Thr Val Val Leu
1 5 10 15
Ala Leu Gly Leu Ala Phe Leu Arg Ala Ala Ala Pro Ala Ser Ala Gln
20 25 30
Asn Cys Gly Cys Pro Pro Gly Tyr Cys Cys Ser Lys Phe Gly Tyr Cys
35 40 45
Gly Thr Ser Phe Asp Tyr Cys Asn Ala Asn Thr Cys Gln Ser Gly Pro
50 55 60
Cys Thr
65

(2) INFORMATION FOR SEQ ID NO:2702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..64
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2702:

Met	Ala	Met	Ala	Asn	Ser	Ala	Thr	Ile	Leu	Thr	Val	Val	Leu	Ala	Leu
1				5					10					15	
Gly	Leu	Ala	Phe	Leu	Arg	Ala	Ala	Ala	Pro	Ala	Ser	Ala	Gln	Asn	Cys
			20					25					30		
Gly	Cys	Pro	Pro	Gly	Tyr	Cys	Cys	Ser	Lys	Phe	Gly	Tyr	Cys	Gly	Thr
		35				40					45				
Ser	Phe	Asp	Tyr	Cys	Asn	Ala	Asn	Thr	Cys	Gln	Ser	Gly	Pro	Cys	Thr
		50				55					60				

(2) INFORMATION FOR SEQ ID NO:2703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2703:

tacaaggcta	tttatgat	at	tccagcaata	aaagaggatc	caacaaagt	gataccgatt	60
cttaggaaga	tctgttgg	ta	cttggtgcta	gcacctcatg	atcctatgca	atcaagcctt	120
ctcaatgcta	cactagagga	t	taaaaacctt	tcagaaatcc	caaatttcag	gttattactg	180
aagcagctgg	tcacatgga	g	ggtgatacag	tggacaagtc	tgtgggaatt	cttcaaggag	240
gaatatgaga	aggagaagga	t	cttcttggg	ggagctttgg	gtgccaaagc	ttcagaagat	300
ttgaggctga	ggattatcga	a	acataaatatc	ttggttgtat	ccaagtacta	tgcaagggtt	360
accctcaaga	ggcttgccga	t	cttctttgc	ctgactttgc	aggaggcaga	gaagcatctc	420
tcagacatgg	ttaactcgaa	a	atctctagt	g			

(2) INFORMATION FOR SEQ ID NO:2704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..150
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2704:

Tyr	Lys	Ala	Ile	Tyr	Asp	Ile	Pro	Ala	Ile	Lys	Glu	Asp	Pro	Thr	Lys
1				5					10					15	
Trp	Ile	Pro	Ile	Leu	Arg	Lys	Ile	Cys	Trp	Tyr	Leu	Val	Leu	Ala	Pro
			20					25					30		
His	Asp	Pro	Met	Gln	Ser	Ser	Leu	Leu	Asn	Ala	Thr	Leu	Glu	Asp	Lys
		35					40				45				
Asn	Leu	Ser	Glu	Ile	Pro	Asn	Phe	Arg	Leu	Leu	Leu	Lys	Gln	Leu	Val

50	55	60
Thr Met Glu Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu		
65	70	75
Glu Tyr Glu Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys		80
	85	90
Ala Ser Glu Asp Leu Arg Leu Arg Ile Glu His Asn Ile Leu Val		95
	100	105
Val Ser Lys Tyr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu		110
	115	120
Leu Cys Leu Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val		125
	130	135
Asn Ser Lys Ser Leu Val		140
145	150	

(2) INFORMATION FOR SEQ ID NO:2705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..115
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2705:

Met Gln Ser Ser Leu Leu Asn Ala Thr Leu Glu Asp Lys Asn Leu Ser	
1	15
Glu Ile Pro Asn Phe Arg Leu Leu Leu Lys Gln Leu Val Thr Met Glu	
	20
Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu Tyr Glu	
	35
Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys Ala Ser Glu	
	50
Asp Leu Arg Leu Arg Ile Ile Glu His Asn Ile Leu Val Val Ser Lys	
65	80
Tyr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu Leu Cys Leu	
	85
Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val Asn Ser Lys	
	100
Ser Leu Val	110
	115

(2) INFORMATION FOR SEQ ID NO:2706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..85
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2706:

Met Glu Val Ile Gln Trp Thr Ser Leu Trp Glu Phe Phe Lys Glu Glu	
1	15
Tyr Glu Lys Glu Lys Asp Leu Leu Gly Gly Ala Leu Gly Ala Lys Ala	
	20
Ser Glu Asp Leu Arg Leu Arg Ile Ile Glu His Asn Ile Leu Val Val	
	35
Ser Lys Tyr Tyr Ala Arg Val Thr Leu Lys Arg Leu Ala Asp Leu Leu	
	50
	55
	60

Cys Leu Thr Leu Gln Glu Ala Glu Lys His Leu Ser Asp Met Val Asn
65 70 75 80
Ser Lys Ser Leu Val
85

(2) INFORMATION FOR SEQ ID NO:2707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..302
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504307

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2707:

ctcccggctc agacttctgc tgcagcgccct ccgycgccgc cgccgcatct aacgcaktcc	60
ctccgcccga gcccgaggca agatggttct ccagaacgac attgatctgc kcaacccgcc	120
ggcagaactc gagaagctca agcacaagaa aaagagactc gtccagtcgc ccaactcctt	180
cttcatggat gttaagtgcc aggggtgctt cagcataacc actgtkttca gccactccca	240
gactgctgnt gkgtnngtca gaagctatgc agcggatacg ggtacattta tcgacagtkt	300
tc	

(2) INFORMATION FOR SEQ ID NO:2708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..71
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2708:

Pro Gly Ser Asp Phe Cys Cys Ser Ala Ser Xaa Ala Ala Ala Ala Ser	
1 5 10 15	
Asn Ala Xaa Pro Pro Gln Pro Glu Ala Arg Trp Phe Ser Arg Thr	
20 25 30	
Thr Leu Ile Cys Xaa Thr Arg Arg Gln Asn Ser Arg Ser Ser Ser Thr	
35 40 45	
Arg Lys Arg Asp Ser Ser Ser Arg Pro Thr Pro Ser Ser Trp Met Leu	
50 55 60	
Ser Ala Arg Gly Ala Ser Ala	
65 70	

(2) INFORMATION FOR SEQ ID NO:2709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..72
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2709:

Met Val Leu Gln Asn Asp Ile Asp Leu Xaa Asn Pro Pro Ala Glu Leu	
1 5 10 15	
Glu Lys Leu Lys His Lys Lys Lys Arg Leu Val Gln Ser Pro Asn Ser	
20 25 30	
Phe Phe Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr Xaa	

35 40 45
Phe Ser His Ser Gln Thr Ala Xaa Xaa Xaa Val Arg Ser Tyr Ala Ala
50 55 60
Asp Thr Gly Thr Phe Ile Asp Ser
65 70

(2) INFORMATION FOR SEQ ID NO:2710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..38
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2710:

Met Asp Val Lys Cys Gln Gly Cys Phe Ser Ile Thr Thr Xaa Phe Ser
1 5 10 15
His Ser Gln Thr Ala Xaa Xaa Xaa Val Arg Ser Tyr Ala Ala Asp Thr
20 25 30
Gly Thr Phe Ile Asp Ser
35

(2) INFORMATION FOR SEQ ID NO:2711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2711:

accaaggaaa	ttcacaaaga	gatactagtc	cctaccaaag	catacttctt	gaaacactct	60
tgcaatccac	tgagtctctgt	ttgttgagac	ttgagacgca	tagagctagc	gtcgacaatg	120
tcgctcgtga	ggcgcmssaa	cgtgttcgac	cccttctcga	tggacctctg	ggaccccttc	180
gacaccatgt	tccgctccat	cgtcccgtcg	gcggcctcca	ccaactccga	gaccgccgtc	240
ttcgccagc						

(2) INFORMATION FOR SEQ ID NO:2712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..82
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2712:

Gln Gly Asn Ser Gln Arg Asp Thr Ser Pro Tyr Gln Ser Ile Leu Pro
1 5 10 15
Glu Thr Leu Leu Gln Ser Thr Glu Ser Cys Leu Leu Arg Leu Glu Thr
20 25 30
His Arg Ala Ser Val Asp Asn Val Ala Arg Glu Ala Xaa Arg Val
35 40 45
Arg Pro Leu Leu Asp Gly Pro Leu Gly Pro Leu Arg His His Val Pro
50 55 60
Leu His Arg Pro Val Gly Gly Leu His Gln Leu Arg Asp Arg Arg Leu

65
Arg Gln

70

75

80

(2) INFORMATION FOR SEQ ID NO:2713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..44
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2713:

Met	Ser	Leu	Val	Arg	Arg	Xaa	Asn	Val	Phe	Asp	Pro	Phe	Ser	Met	Asp
1			5					10					15		
Leu	Trp	Asp	Pro	Phe	Asp	Thr	Met	Phe	Arg	Ser	Ile	Val	Pro	Ser	Ala
			20				25					30			
Ala	Ser	Thr	Asn	Ser	Glu	Thr	Ala	Val	Phe	Ala	Ser				
			35				40								

(2) INFORMATION FOR SEQ ID NO:2714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..464
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504333

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2714:

cagaataaag	ataaaaaata	tggaactgga	aattaggcgt	agggaatcaa	caggatcagg	60
ctctaacaca	tatgttgaaa	ctgagactct	tgcaaagttt	gagttgatgg	atggtgctcc	120
tgtgagaggt	gaatctattc	cagtgaggct	gttcctgaca	ccctatgagt	tgaccccgac	180
ttaccgcaac	ataaacaaca	aattcagcgt	caagtattac	ctgaatctgg	tccttgtgga	240
cgaggaagat	cggagggtact	tcaagcagca	agagatcaca	atgtaccgtc	tccaagaatc	300
tccccctgcc	tcctagatcc	caacctgttg	catcatgttc	acttctcagg	ttttgtacaa	360
gtggacgctg	aggttagagc	aatgtcctgt	atataaacta	aaatccagaa	gagcgccaca	420
gctggttact	gctatggcca	tgcacgctgc	actgtcgtgt	tcat		

(2) INFORMATION FOR SEQ ID NO:2715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..104
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2715:

Arg	Ile	Lys	Ile	Lys	Asn	Met	Glu	Leu	Glu	Ile	Arg	Arg	Arg	Glu	Ser
1				5					10					15	
Thr	Gly	Ser	Gly	Ser	Asn	Thr	Tyr	Val	Glu	Thr	Glu	Thr	Leu	Ala	Lys
				20				25					30		
Phe	Glu	Leu	Met	Asp	Gly	Ala	Pro	Val	Arg	Gly	Glu	Ser	Ile	Pro	Val
			35				40				45				
Arg	Leu	Phe	Leu	Thr	Pro	Tyr	Glu	Leu	Thr	Pro	Thr	Tyr	Arg	Asn	Ile
			50				55				60				

Asn Asn Lys Phe Ser Val Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp
65 70 75 80
Glu Glu Asp Arg Arg Tyr Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg
85 90 95
Leu Gln Glu Ser Pro Pro Ala Ser
100

(2) INFORMATION FOR SEQ ID NO:2716:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1504335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2716:

Met Glu Leu Glu Ile Arg Arg Arg Glu Ser Thr Gly Ser Gly Ser Asn
1 5 10 15
Thr Tyr Val Glu Thr Glu Thr Leu Ala Lys Phe Glu Leu Met Asp Gly
20 25 30
Ala Pro Val Arg Gly Glu Ser Ile Pro Val Arg Leu Phe Leu Thr Pro
35 40 45
Tyr Glu Leu Thr Pro Thr Tyr Arg Asn Ile Asn Asn Lys Phe Ser Val
50 55 60
Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp Glu Glu Asp Arg Arg Tyr
65 70 75 80
Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg Leu Gln Glu Ser Pro Pro
85 90 95
Ala Ser

(2) INFORMATION FOR SEQ ID NO:2717:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 1504336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2717:

Met Asp Gly Ala Pro Val Arg Gly Glu Ser Ile Pro Val Arg Leu Phe
1 5 10 15
Leu Thr Pro Tyr Glu Leu Thr Pro Thr Tyr Arg Asn Ile Asn Asn Lys
20 25 30
Phe Ser Val Lys Tyr Tyr Leu Asn Leu Val Leu Val Asp Glu Glu Asp
35 40 45
Arg Arg Tyr Phe Lys Gln Gln Glu Ile Thr Met Tyr Arg Leu Gln Glu
50 55 60
Ser Pro Pro Ala Ser
65

(2) INFORMATION FOR SEQ ID NO:2718:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 466 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) NAME/KEY: -
(B) LOCATION: 1..466
(D) OTHER INFORMATION: / Ceres Seq. ID 1504370

ctactacgcc	tgcctctcca	tcatgtcgct	gggtatcctc	ctgcccttcg	ccatcgccat	60
ggagggggccc	aaggtgtggg	cggcgggctg	gcagacagca	gtcgccgaga	tcggtcccaa	120
cttcgtctgg	tgggtggcgg	cgcagagcgt	gttctaccac	ctgtacaacc	aggtgtccta	180
catgtccctg	gacgagatct	cgccgctcac	cttctccatc	ggcaacacca	tgaagcgcct	240
ctccgtcatc	gtcgcgtcca	tcatcatctt	ccagacgccc	gtccagccca	tcaacgcgct	300
cggggccgcc	atgcgccatcc	tccgaacctt	catctacttc	cagcccaagc	agtagccgcc	360
cttggscgcg	ctctctggctc	tcaggcctca	gttcagttca	cggccgaatc	agctcggcgc	420
tcgaagatat	aacagattat	ataacttttt	gaqqatatct	acctaag		

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(A) NAME/KEY: peptide
(B) LOCATION: 1..143
(D) OTHER INFORMATION: / Ceres Seq. ID 1504371

Leu 1	Leu	Arg	Leu	Pro 5	Leu	His	His	Val	Ala 10	Gly	Asp	Pro	Pro	Ala 15	Leu
Arg	His	Arg	His 20	Gly	Gly	Ala	Gln	Gly 25	Val	Gly	Gly	Gly	Leu 30	Ala	Asp
Ser	Ser	Arg 35	Arg	Asp	Arg	Ser	Gln 40	Leu	Arg	Leu	Val	Gly 45	Gly	Gly	Ala
Glu	Arg 50	Val	Leu	Pro	Pro	Val 55	Gln	Pro	Gly	Val	Leu 60	His	Val	Pro	Gly
Arg 65	Asp	Leu	Ala	Ala 70	His	Leu	Leu	His	Arg	Gln 75	His	His	Glu	Ala 80	His
Leu	Arg	His	Arg	Arg 85	Val	His	His	His	Leu 90	Pro	Asp	Ala	Arg	Pro 95	Ala
His	Gln	Arg	Ala 100	Arg	Gly	Arg	His	Arg 105	His	Pro	Arg	Asn	Leu 110	His	Leu
Leu	Pro	Gly 115	Gln	Ala	Val	Ala	Ala 120	Leu	Xaa	Arg	Ala	Ser	Gly 125	Ser	Gln
Ala	Ser	Val	Gln	Phe	Thr	Ala 130	Glu	Ser 135	Ala	Arg	Arg	Ser	Lys 140	Ile	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(A) NAME/KEY: peptide
(B) LOCATION: 1..117
(D) OTHER INFORMATION: / Ceres Seq. ID 1504372

Tyr 1	Tyr	Ala	Cys	Leu 5	Ser	Ile	Met	Ser	Leu 10	Val	Ile	Leu	Leu	Pro 15	Phe
Ala	Ile	Ala	Met 20	Glu	Gly	Pro	Lys	Val 25	Trp	Ala	Ala	Gly	Trp 30	Gln	Thr
Ala	Val	Ala	Glu 35	Ile	Gly	Pro	Asn 40	Phe	Val	Trp	Trp	Val	Ala 45	Ala	Gln

Ser Val Phe Tyr His Leu Tyr Asn Gln Val Ser Tyr Met Ser Leu Asp
50 55 60
Glu Ile Ser Pro Leu Thr Phe Ser Ile Gly Asn Thr Met Lys Arg Ile
65 70 75 80
Ser Val Ile Val Ala Ser Ile Ile Ile Phe Gln Thr Pro Val Gln Pro
85 90 95
Ile Asn Ala Leu Gly Ala Ala Ile Ala Ile Leu Gly Thr Phe Ile Tyr
100 105 110
Ser Gln Ala Lys Gln
115

(2) INFORMATION FOR SEQ ID NO:2721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..110
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2721:

Met Ser Leu Val Ile Leu Leu Pro Phe Ala Ile Ala Met Glu Gly Pro
1 5 10 15
Lys Val Trp Ala Gly Trp Gln Thr Ala Val Ala Glu Ile Gly Pro
20 25 30
Asn Phe Val Trp Trp Val Ala Ala Gln Ser Val Phe Tyr His Leu Tyr
35 40 45
Asn Gln Val Ser Tyr Met Ser Leu Asp Glu Ile Ser Pro Leu Thr Phe
50 55 60
Ser Ile Gly Asn Thr Met Lys Arg Ile Ser Val Ile Val Ala Ser Ile
65 70 75 80
Ile Ile Phe Gln Thr Pro Val Gln Pro Ile Asn Ala Leu Gly Ala Ala
85 90 95
Ile Ala Ile Leu Gly Thr Phe Ile Tyr Ser Gln Ala Lys Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:2722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..452
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2722:

ttagtgatata tatgttatct ggggacaagg aaagtgctgc tatgaatgtg gcttcagttg 60
tcggtatcca ggcagacaag gttcttgctg aagttaaac acatgagaaa aagaagttca 120
tatctgaact ccagaaagag cacaaggtag tcgccatggt tggtagcggc attaatgatg 180
ccgcagcact agcttcagct gatgttgga tgcgaatggg tggaggtgtt ggggcagcta 240
gtgatgtatc ttcagttgta cttatgggca acaggttatc ccagcttata gatgctttag 300
agttgagtaa agagaccatg aagacgggtga agcaaaaatc ttggtgggct ttcctgtata 360
acattgttg actaccatt gctgctggag cattgcttcc agctacggg acgatactga 420
caccatcaat agctggagct ctgatgggt nt

(2) INFORMATION FOR SEQ ID NO:2723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..149
 (D) OTHER INFORMATION: / Ceres Seq. ID 1504375
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2723:
Ser Val Tyr Met Leu Ser Gly Asp Lys Glu Ser Ala Ala Met Asn Val
1 5 10 15
Ala Ser Val Val Gly Ile Gln Ala Asp Lys Val Leu Ala Glu Val Lys
 20 25 30
Pro His Glu Lys Lys Lys Phe Ile Ser Glu Leu Gln Lys Glu His Lys
 35 40 45
Val Val Ala Met Val Gly Asp Gly Ile Asn Asp Ala Ala Ala Leu Ala
50 55 60
Ser Ala Asp Val Gly Ile Ala Met Gly Gly Gly Val Gly Ala Ala Ser
65 70 75 80
Asp Val Ser Ser Val Val Leu Met Gly Asn Arg Leu Ser Gln Leu Ile
 85 90 95
Asp Ala Leu Glu Leu Ser Lys Glu Thr Met Lys Thr Val Lys Gln Asn
 100 105 110
Leu Trp Trp Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro Ile Ala Ala
 115 120 125
Gly Ala Leu Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro Ser Ile Ala
130 135 140
Gly Ala Leu Met Gly
145

(2) INFORMATION FOR SEQ ID NO:2724:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1504376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2724:

Met Leu Ser Gly Asp Lys Glu Ser Ala Ala Met Asn Val Ala Ser Val
1 5 10 15
Val Gly Ile Gln Ala Asp Lys Val Leu Ala Glu Val Lys Pro His Glu
 20 25 30
Lys Lys Lys Phe Ile Ser Glu Leu Gln Lys Glu His Lys Val Val Ala
 35 40 45
Met Val Gly Asp Gly Ile Asn Asp Ala Ala Ala Leu Ala Ser Ala Asp
50 55 60
Val Gly Ile Ala Met Gly Gly Gly Val Gly Ala Ala Ser Asp Val Ser
65 70 75 80
Ser Val Val Leu Met Gly Asn Arg Leu Ser Gln Leu Ile Asp Ala Leu
 85 90 95
Glu Leu Ser Lys Glu Thr Met Lys Thr Val Lys Gln Asn Leu Trp Trp
 100 105 110
Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro Ile Ala Ala Gly Ala Leu
 115 120 125
Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro Ser Ile Ala Gly Ala Leu
130 135 140
Met Gly
145

(2) INFORMATION FOR SEQ ID NO:2725:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..136
(D) OTHER INFORMATION: / Ceres Seq. ID 1504377
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2725:
Met Asn Val Ala Ser Val Val Gly Ile Gln Ala Asp Lys Val Leu Ala
1 5 10 15
Glu Val Lys Pro His Glu Lys Lys Lys Phe Ile Ser Glu Leu Gln Lys
20 25 30
Glu His Lys Val Val Ala Met Val Gly Asp Gly Ile Asn Asp Ala Ala
35 40 45
Ala Leu Ala Ser Ala Asp Val Gly Ile Ala Met Gly Gly Val Gly
50 55 60
Ala Ala Ser Asp Val Ser Ser Val Val Leu Met Gly Asn Arg Leu Ser
65 70 75 80
Gln Leu Ile Asp Ala Leu Glu Leu Ser Lys Glu Thr Met Lys Thr Val
85 90 95
Lys Gln Asn Leu Trp Trp Ala Phe Leu Tyr Asn Ile Val Gly Leu Pro
100 105 110
Ile Ala Ala Gly Ala Leu Leu Pro Ala Thr Gly Thr Ile Leu Thr Pro
115 120 125
Ser Ile Ala Gly Ala Leu Met Gly
130 135

(2) INFORMATION FOR SEQ ID NO:2726:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 440 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..440
(D) OTHER INFORMATION: / Ceres Seq. ID 1504382
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2726:
accacacca cccacgaaa ccgtaagaag cgcagagtgt gagagagaga ggagcatcaa 60
ggacgacgtg ggcaagatga tgcaggtgtt cgtgaagacg ctggcgggga agacgatcac 120
gctggaggtg gagggcagcg acgacgccgt nagaacgtga aggccatgat ccaggggcaag 180
gaaggcatcc cgccggagga gcagcgctc gtcttcgcgg gcaagcagct ggacgacgac 240
ggccgcaccc tggccgacta cggcgtccag aaggagtcga cgctgcacct ggagctgcgc 300
ctccgcggcg gcagcagggg cggctacccc atgggatccc gcccagcctc cgcgagctcg 360
cgcagaagta caacgagaac aagatggtct gccgcaagtg ctatgcgcgg cttccgccta 420
gggcaaccaa ctgccgcaag

(2) INFORMATION FOR SEQ ID NO:2727:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..52
(D) OTHER INFORMATION: / Ceres Seq. ID 1504383
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2727:
Pro His Pro Pro His Glu Thr Val Arg Ser Ala Glu Cys Glu Arg Glu

1 5 10 15
Arg Ser Ile Lys Asp Asp Val Gly Lys Met Met Gln Val Phe Val Lys
20 25 30
Thr Leu Ala Gly Lys Thr Ile Thr Leu Glu Val Glu Gly Ser Asp Asp
35 40 45
Ala Xaa Arg Thr
50

(2) INFORMATION FOR SEQ ID NO:2728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..91
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2728:

Met Ile Gln Gly Lys Glu Gly Ile Pro Pro Glu Glu Gln Arg Leu Val
1 5 10 15
Phe Ala Gly Lys Gln Leu Asp Asp Asp Gly Arg Thr Leu Ala Asp Tyr
20 25 30
Gly Val Gln Lys Glu Ser Thr Leu His Leu Glu Leu Arg Leu Arg Gly
35 40 45
Gly Ser Arg Gly Gly Tyr Pro Met Gly Ser Arg Pro Ala Ser Ala Ser
50 55 60
Ser Arg Arg Ser Thr Thr Arg Thr Arg Trp Ser Ala Ala Ser Ala Met
65 70 75 80
Arg Gly Phe Arg Leu Gly Gln Pro Thr Ala Ala
85 90

(2) INFORMATION FOR SEQ ID NO:2729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..234
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2729:

acatcgaggaa cgccgccgac gccgcagagg agacgcatcg aggttagcac gcgaagaagc 60
gaccatgagg gccaaagtga agaagaagcg catnaggagg ctcaagagga akcgcagaaa 120
gatgaggcag agatccaagt aggcagatcg agatggattg tggacctgac tctcttcggt 180
atatgtacta cctccgttct tgaatatattt taaatatatng tcgttgctcgt cggt

(2) INFORMATION FOR SEQ ID NO:2730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2730:

Thr Ser Gly Thr Pro Pro Thr Pro Gln Arg Arg Arg Ile Glu Val Ser
1 5 10 15

Thr Arg Arg Ser Asp His Glu Gly Gln Val Glu Glu Glu Ala His Xaa
20 25 30
Glu Ala Gln Glu Glu Xaa Gln Lys Asp Glu Ala Glu Ile Gln Val Gly
35 40 45
Arg Ser Arg Trp Ile Val Asp Leu Thr Leu Phe Val Ile Cys Thr Thr
50 55 60
Ser Val Leu Glu Tyr Phe
65 70

(2) INFORMATION FOR SEQ ID NO:2731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..46
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504395

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2731:

His Arg Glu Arg Arg Arg Arg Arg Arg Gly Asp Ala Ser Arg Leu Ala
1 5 10 15
Arg Glu Glu Ala Thr Met Arg Ala Lys Trp Lys Lys Lys Arg Xaa Arg
20 25 30
Arg Leu Lys Arg Xaa Arg Arg Lys Met Arg Gln Arg Ser Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:2732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..474
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2732:

cccagttgat gtggttaagt cgagaatgat ggggtgactca gcctacaaaa gcactctcga 60
ttgtttttgtg aagactctaa agaatgatgg ccctttggca ttttacaaag gcttcctgcc 120
aaacttttgca agactgggat cttggaatgt gattatgttc ttgacatttg agcagggttca 180
aaagctgttt gtgaggaaag cgacaagctg aagatagagt ttttgcagtc aggtggcgta 240
caattgacgc acaggggttt tcttctatag acaaaagggg agaaatgaca cctccccct 300
cgagaattgg ggaacaagga cagatctgac acctcaattg cgagaaataa aaataacagc 360
cgacagttgc atgatccctg aacgaataaa ttcagaacta gaaacagatg tcagtaaaca 420
acatgtggtg aatgttggaa cttgactgct ctagtccagt gggcatctgt tggt

(2) INFORMATION FOR SEQ ID NO:2733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..69
- (D) OTHER INFORMATION: / Ceres Seq. ID 1504401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2733:

Pro Val Asp Val Val Lys Ser Arg Met Met Gly Asp Ser Ala Tyr Lys
1 5 10 15
Ser Thr Leu Asp Cys Phe Val Lys Thr Leu Lys Asn Asp Gly Pro Leu

20 25 30
Ala Phe Tyr Lys Gly Phe Leu Pro Asn Phe Ala Arg Leu Gly Ser Trp
35 40 45
Asn Val Ile Met Phe Leu Thr Leu Glu Gln Val Gln Lys Leu Phe Val
50 55 60
Arg Lys Ala Thr Ser
65

(2) INFORMATION FOR SEQ ID NO:2734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..61

(D) OTHER INFORMATION: / Ceres Seq. ID 1504402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2734:

Met Met Gly Asp Ser Ala Tyr Lys Ser Thr Leu Asp Cys Phe Val Lys
1 5 10 15
Thr Leu Lys Asn Asp Gly Pro Leu Ala Phe Tyr Lys Gly Phe Leu Pro
20 25 30
Asn Phe Ala Arg Leu Gly Ser Trp Asn Val Ile Met Phe Leu Thr Leu
35 40 45
Glu Gln Val Gln Lys Leu Phe Val Arg Lys Ala Thr Ser
50 55 60

(2) INFORMATION FOR SEQ ID NO:2735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..60

(D) OTHER INFORMATION: / Ceres Seq. ID 1504403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2735:

Met Gly Asp Ser Ala Tyr Lys Ser Thr Leu Asp Cys Phe Val Lys Thr
1 5 10 15
Leu Lys Asn Asp Gly Pro Leu Ala Phe Tyr Lys Gly Phe Leu Pro Asn
20 25 30
Phe Ala Arg Leu Gly Ser Trp Asn Val Ile Met Phe Leu Thr Leu Glu
35 40 45
Gln Val Gln Lys Leu Phe Val Arg Lys Ala Thr Ser
50 55 60